

Run on: March 5, 2005, 23:01:24 ; Search time 182.5 Seconds
(without alignments)
4624.171 Million cell updates/sec

Title: US-10-015-385A-193
Perfect score: 2066
Sequence: 1 caagcagtcctcccttgg.....aggggcaaaaaaaaaa 1091
Scoring table: BLOSUM62
Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 4211384
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB ID	Description
RESULT 1				
ID	ABG66676	standard; protein; 254 AA.		
DE	Human novel polypeptide #11.			
PN	WO200244340-A2.			
PD	06-JUN-2002.			
PA	(HYSE-) HYSEQ INC.			
Best Local Similarity:	85.52%	Mismatches: 0		
Query Match:	66.58%	Indels: 43		
RESULT 2				
ID	AAB21304	standard; protein; 248 AA.		
DE	Human KLK-L5 protein #4.			
PN	WO200053776-A2.			
PD	14-SEP-2000.			
PA	(MOUN) MOUNT SINAI HOSPITAL.			
Best Local Similarity:	100.00%	Mismatches: 0		
Query Match:	66.51%	Indels: 0		
RESULT 3				
ID	AAB24428	standard; protein; 248 AA.		
DE	Human PRO1303 protein sequence SEQ ID NO:203.			
PN	WO200032221-A2.			
PD	08-JUN-2000.			
PA	(GETH) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches: 0		
Query Match:	66.51%	Indels: 0		
RESULT 4				
ID	AAB24032	standard; protein; 248 AA.		
DE	Human PRO1303 protein sequence SEQ ID NO:33.			
PN	WO200053750-A1.			
PD	14-SEP-2000.			
PA	(GETH) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches: 0		
Query Match:	66.51%	Indels: 0		
RESULT 5				
ID	AAY99393	standard; protein; 248 AA.		
DE	Human PRO1303 (UNQ669) amino acid sequence SEQ ID NO:194.			
PN	WO200012708-A2.			
PD	09-MAR-2000.			
PA	(GETH) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches: 0		
Query Match:	66.51%	Indels: 0		
RESULT 6				
ID	AAM23994	standard; protein; 248 AA.		
DE	Human EST encoded protein SEQ ID NO: 1519.			
PN	WO200154477-A2.			
PD	02-AUG-2001.			

PA	(HYSE-) HYSEQ INC.			
Best Local Similarity:	100.00%	Mismatches: 0		
Query Match:	66.51%	Indels: 0		
RESULT 7				
ID	AAB66142	standard; protein; 248 AA.		
DE	Protein of the invention #54.			
PN	WO200078961-A1.			
PD	28-DEC-2000.			
PA	(GETH) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches: 0		
Query Match:	66.51%	Indels: 0		
RESULT 8				
ID	ABO33635	standard; protein; 248 AA.		
DE	Novel human secreted and transmembrane protein PRO1303.			
PN	US2003073130-A1.			
PD	17-APR-2003.			
PA	(GETH) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches: 0		
Query Match:	66.51%	Indels: 0		
RESULT 9				
ID	ABO44488	standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.			
PN	US2003044841-A1.			
PD	06-MAR-2003.			
PA	(GETH) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches: 0		
Query Match:	66.51%	Indels: 0		
RESULT 10				
ID	ABO33512	standard; protein; 248 AA.		
DE	Novel human secreted and transmembrane protein PRO1303.			
PN	US2003073129-A1.			
PD	17-APR-2003.			
PA	(GETH) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches: 0		
Query Match:	66.51%	Indels: 0		
RESULT 11				
ID	ADC18063	standard; protein; 248 AA.		
DE	Human PRO polypeptide #54.			
PN	US2003064925-A1.			
PD	03-APR-2003.			
PA	(GETH) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches: 0		
Query Match:	66.51%	Indels: 0		
RESULT 12				
ID	ADD70709	standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.			
PN	US200309625-A1.			
PD	29-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches: 0		
Query Match:	66.51%	Indels: 0		
RESULT 13				
ID	ADD39786	standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.			
PN	US2003083462-A1.			
PD	01-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches: 0		
Query Match:	66.51%	Indels: 0		
RESULT 14				
ID	ADD70232	standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.			
PN	US2003054406-A1.			
PD	20-MAR-2003.			
PA	(GETH) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches: 0		
Query Match:	66.51%	Indels: 0		
RESULT 15				
ID	ADD38353	standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.			
PN	US2003096955-A1.			
PD	22-MAY-2003.			
PA	(GETH) GENENTECH INC.			

Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 16	
ID ADD39309 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003096954-A1.	
PD 22-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 17	
ID ADD38832 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003092061-A1.	
PD 15-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 18	
ID ADD40263 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003082627-A1.	
PD 01-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 19	
ID ADE50484 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003069179-A1.	
PD 10-APR-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 20	
ID ADE20096 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003092883-A1.	
PD 15-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 21	
ID ADE30007 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003082626-A1.	
PD 01-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 22	
ID ADE21565 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003082628-A1.	
PD 01-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 23	
ID ADF29990 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003204053-A1.	
PD 30-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 24	
ID ADF55883 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003204054-A1.	
PD 30-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 25	
ID ADH9387 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003065142-A1.	
PD 03-APR-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 26	
ID ADE36567 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003195347-A1.	
PD 16-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 27	
ID ADF25878 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003199675-A1.	
PD 23-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 28	
ID ADF24777 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003198993-A1.	
PD 23-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 29	
ID ADF29513 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003203401-A1.	
PD 30-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 30	
ID ADE97044 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003195334-A1.	
PD 16-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 31	
ID ADH03082 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003216562-A1.	
PD 20-NOV-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 32	
ID ADH04036 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003220471-A1.	
PD 27-NOV-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 33	
ID ADH03559 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003224478-A1.	
PD 04-DEC-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0

RESULT 34
ID ADH04513 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 66.51% Indels: 0
RESULT 35
ID ADH61514 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 66.51% Indels: 0
RESULT 36
ID ADN10927 standard; protein; 248 AA.
DE Human Kallikrein 12, marker of endocrine cancer.
PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 66.51% Indels: 0
RESULT 37
ID ADL94713 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 66.51% Indels: 0
RESULT 38
ID ADT94373 standard; protein; 248 AA.
DE Human PRO1303 protein.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 66.51% Indels: 0
RESULT 39
ID AAB21303 standard; protein; 254 AA.
DE Human Kik-L5 protein #3.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 85.19% Mismatches: 0
Query Match: 66.43% Indels: 43
RESULT 40
ID ADN10926 standard; protein; 254 AA.
DE Human Kallikrein 12, marker of endocrine cancer.
PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 85.19% Mismatches: 0
Query Match: 66.43% Indels: 43
RESULT 41
ID ADP56174 standard; protein; 254 AA.
DE Human PRO protein sequence SEQ ID NO:2150.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 85.19% Mismatches: 0
Query Match: 66.43% Indels: 43
RESULT 42
ID AAO29516 standard; protein; 248 AA.
DE Human Kallikrein-like protein 5 (18817).
PN WO2003039475-A2.
PD 15-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 99.60% Mismatches: 1
Query Match: 66.17% Indels: 0
RESULT 43

ID AAB21301 standard; protein; 184 AA.
DE Human Kik-L5 protein #1.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 49.32% Indels: 0
RESULT 44
ID AAY28642 standard; protein; 162 AA.
DE Human secreted protein from cDNA clone HKAFV61.
PN WO9940183-A1.
PD 12-AUG-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 64.11% Mismatches: 3
Query Match: 39.25% Indels: 86
RESULT 45
ID AAY32852 standard; protein; 260 AA.
DE Human serine protease protein sequence.
PN JP11225765-A.
PD 24-AUG-1999.
PA (SUNR) SUNTORY LTD.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 46
ID AAY41744 standard; protein; 260 AA.
DE Human PRO322 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 47
ID AAY03220 standard; protein; 260 AA.
DE Amino acid sequence of human tumour antigen derived gene-14 protein.
PN WO9909138-A1.
PD 25-FEB-1999.
PA (UYAR-) UNIV ARKANSAS.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 48
ID AAB21322 standard; protein; 260 AA.
DE Human neuropsin.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 49
ID AAB44300 standard; protein; 260 AA.
DE Human PRO322 (UNQ283) protein sequence SEQ ID NO:395.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 50
ID AAY51131 standard; protein; 260 AA.
DE Human neuropsin protein.
PN JP11318461-A.
PD 24-NOV-1999.
PA (SHIO/) SHIOZAKA S.
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 51
ID AAU12369 standard; protein; 260 AA.
DE Human PRO322 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 52

ID AAB53087 standard; protein; 260 AA.
DE Human angiogenesis-associated protein PRO322, SEQ ID NO:127.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 53
ID ABG23373 standard; protein; 260 AA.
DE Novel human diagnostic protein #23364.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 54
ID ABB48452 standard; protein; 260 AA.
DE Human PRO322 protein sequence SEQ ID NO:72.
PN WO20020690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 55
ID AAU81959 standard; protein; 260 AA.
DE Human PRO322.
PN WO200109327-A2.
PD 08-FEB-2001.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 56
ID ABB95458 standard; protein; 260 AA.
DE Human angiogenesis related protein PRO322 SEQ ID NO: 72.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 57
ID ADI17076 standard; protein; 260 AA.
DE Human NOVX protein homologue SeqID 612.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 58
ID ABO17813 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 59
ID ABO25246 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003004102-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 60
ID ABU81067 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 61
ID ABU72252 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 62
ID ADA05702 standard; protein; 260 AA.
DE Human NOV11h protein SEQ ID NO:62.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 63
ID ABU66767 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 64
ID ABU84932 standard; protein; 260 AA.
DE Human secreted and transmembrane PRO polypeptide #8.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 65
ID ABU59848 standard; protein; 260 AA.
DE Novel secreted and transmembrane protein PRO322.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 66
ID ABU61130 standard; protein; 260 AA.
DE Human PRO322 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 67
ID ABO25038 standard; protein; 260 AA.
DE Human secreted/transmembrane protein (PRO) #198.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 68
ID ABU80399 standard; protein; 260 AA.
DE Human secreted/transmembrane protein PRO322.
PN US2003004102-A1.

PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 69
ID ADBU7043 standard; protein; 260 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 396.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 70
ID ADA45915 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 71
ID ADA76346 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 72
ID ADA18996 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 73
ID ADA61619 standard; protein; 260 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 74
ID ADB19404 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 75
ID ADB27945 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 76
ID ADA86424 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 77
ID ADB15988 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003087350-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 78
ID ADA7774 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 79
ID ADA67569 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 80
ID ADB30576 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 81
ID ADA85872 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 82
ID ADA97084 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 83
ID ADA79388 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 84
ID ADA87527 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 85
ID ADB16729 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 86
ID ADA91821 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

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Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 87
ID ADB14884 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 88
ID ADA24934 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 89
ID ADB18845 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 90
ID ADA94060 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 91
ID ADB19956 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 92
ID ADB13268 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 93
ID ABO43346 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 94
ID ABO19701 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 95
ID ADA12595 standard; protein; 260 AA.
DE Human secreted/transmembrane polypeptide PRO322.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 96
ID ADA74522 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 97
ID ADB24755 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 98
ID ADA82279 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 99
ID ADA75242 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 100
ID ADA85320 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 101
ID ADA84768 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 102
ID ADB30024 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 103
ID ADA80552 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
RESULT 104
ID ADA75794 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%      Mismatches: 96
Query Match: 30.61%      Indels: 13
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RESULT 105
ID ADA47019 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 106
ID ADB25315 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 107
ID ADA93491 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 108
ID ADB26841 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 109
ID ADB31128 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 110
ID ADA61056 standard; protein; 260 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 111
ID ADB24203 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 112
ID ADA96532 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 113
ID ADA81104 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 114
ID ADB28497 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 115
ID ADB26289 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 116
ID ADB21774 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 117
ID ABO19592 standard; protein; 260 AA.
DE Novel human secreted and transmembrane polypeptide #60.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 118
ID ADA77553 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 119
ID ADB18293 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 120
ID ADA86976 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 121
ID ADA88079 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 122
ID ADA46467 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 123
ID ADB28497 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13

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PN US2003082699-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 124
ID ADB29049 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 125
ID ADA77001 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 126
ID ADA8631 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 127
ID ADA97636 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 128
ID ADB27393 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 129
ID ADB22326 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 130
ID ADA67017 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 131
ID ADB22878 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003077111-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 132
ID ADB23651 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 133
ID ADA92373 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 134
ID ADB15436 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 135
ID ADB38688 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 136
ID ADB38136 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 137
ID ADB66608 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 138
ID ADB89688 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 139
ID ADB90420 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 140
ID ADB80561 standard; protein; 260 AA.
DE Ovarian cancer-associated protein #63.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 141
ID ADB39521 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13

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Query Match: 30.61% Indels: 13
RESULT 142
ID ADB73901 standard; protein; 260 AA.
DE Human PRO polypeptide #60.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 143
ID ADB47144 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 144
ID ADB86751 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 145
ID ADB76617 standard; protein; 260 AA.
DE Human PRO polypeptide #60.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 146
ID ADB77356 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 147
ID ADB34513 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 148
ID ADB35617 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 149
ID ADB33961 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 150
ID ADB35065 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 151
ID ADB36169 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 152
ID ADB46564 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 153
ID ADC44043 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 154
ID ADC61803 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 155
ID ADC63767 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 156
ID ADC66867 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 157
ID ADC68991 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 158
ID ADC63051 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 159
ID ADC68116 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 160
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ID ADC41436 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003072745-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 161
ID ADC67491 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003073131-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 162
ID ADC62427 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003073624-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 163
ID ADC42060 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003104998-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 164
ID ADC50437 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003092106-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 165
ID ADC71984 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003092107-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 166
ID ADC59963 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003092105-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 167
ID ADC52970 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein Seq ID396.
PN US2003087365-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 168
ID ADC57324 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein Seq ID396.
PN US2003087366-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 169
ID ADC60515 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087367-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 170
ID ADC50990 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087361-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 171
ID ADC65517 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003087362-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 172
ID ADC54615 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein Seq ID396.
PN US2003087363-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 173
ID ADC53576 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein Seq ID396.
PN US2003087364-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 174
ID ADC59099 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein Seq ID396.
PN US2003087359-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 175
ID ADC55977 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein Seq ID396.
PN US2003087360-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 176
ID ADC58547 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein Seq ID396.
PN US2003087346-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 177
ID ADD03221 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003092104-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Indels: 13
Query Match:
RESULT 178
ID ADC90213 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.

PN US2003087348-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 179
ID ADC69632 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 180
ID ADC48521 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 181
ID ADD10050 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 182
ID ADD4625 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 183
ID ADC80581 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 184
ID ADD09100 standard; protein; 260 AA.
DE Human kallikrein 8 protein SEQ ID NO:2.
PN WO2003085404-A1.
PD 16-OCT-2003.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 185
ID ADD1088 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 186
ID ADD10361 standard; protein; 260 AA.
DE Human secreted/transmembrane PRO polypeptide #36.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 187
ID ADC47969 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194771-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 188
ID ADC80029 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 189
ID ADD11321 standard; protein; 260 AA.
DE Human secreted/transmembrane PRO polypeptide #36.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 190
ID ADD09498 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 191
ID ADD41211 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 192
ID ADD52350 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 193
ID ADD33090 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 194
ID ADD33642 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 195
ID ADD37114 standard; protein; 260 AA.
DE Human secreted/transmembrane PRO polypeptide #36.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 196
ID ABW00074 standard; protein; 260 AA.
DE Human tumour antigen derived gene-14 (TAGD-14) protein.
PN US2002037581-A1.
PD 28-MAR-2002.

PA (UABR-) UAB RES FOUND.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 197
ID ADD51798 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 198
ID ADD02597 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 199
ID ADD02031 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 200
ID ADD54213 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 201
ID ADE49429 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 202
ID ADD92530 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 203
ID ADD91426 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 204
ID ADE04040 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 205
ID ADE32337 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 206
ID ADE22269 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 207
ID ADD79493 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 208
ID ADE35483 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 209
ID ADE16597 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 210
ID ADD73212 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 211
ID ADE42029 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 212
ID ADE17846 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 213
ID ADD91978 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 214
ID ADE33441 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13

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Query Match: 30.61% Indels: 13
RESULT 215
ID ADE33993 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 216
ID ADD80045 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 217
ID ADD93082 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 218
ID ADD72570 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 219
ID ADE19502 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 220
ID ADE18950 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 221
ID ADE43146 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 222
ID ADD95935 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 223
ID ADE22821 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 224
ID ADD78939 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 225
ID ADE32889 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 226
ID ADE42581 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 227
ID ADE17221 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 228
ID ADD80597 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 229
ID ADD89625 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 230
ID ADE40909 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 231
ID ADE04708 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 232
ID ADE92837 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 233
ID ADE17221 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
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ID ADF47235 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 234
ID ADG21546 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 235
ID ADG23187 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 236
ID ADF97522 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 237
ID ADG80586 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 238
ID ADG52992 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003215561-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 239
ID ADG60312 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 240
ID ADG80034 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 241
ID ADH55326 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 242
ID ADH55878 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 243
ID ADI61072 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 244
ID ADI64097 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 245
ID ADH81959 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 246
ID ADH81407 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 247
ID ADM82576 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 248
ID ADN15975 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 249
ID ADN16604 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 250
ID ADN39182 standard; protein; 260 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:500.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 251
ID ADN15423 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.

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PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 252
ID ADN14871 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 253
ID ADI65046 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 254
ID ADI63545 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 255
ID ADC81133 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 256
ID ADD76581 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US200310087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 257
ID ADD87945 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 258
ID ADD86349 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 259
ID ADE75797 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 260
ID ADE48729 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 261
ID ADE41322 standard; protein; 260 AA.
DE Human secreted/transmembrane PRO polypeptide #36.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 262
ID ADE23373 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 263
ID ADE23925 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 264
ID ADE24568 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 265
ID ADD87393 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 266
ID ADE89259 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199082-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 267
ID ADE18398 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 268
ID ADE88707 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 269
ID ADE89830 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003130181-A1.
PD 10-JUL-2003.

PA (ASHK/) ASHKENAZI A J.	PD 23-OCT-2003.	PA (GETH) GENENTECH INC.	Mismatches: 96
PA (BAKE/) BAKER K P.	Best Local Similarity: 48.08%	Indels: 13	
PA (BOTS/) BOTSTEIN D.	Query Match:		
PA (DESN/) DESNOYERS L.	RESULT 276		
PA (EATO/) EATON D L.	ID ADE93389 standard; protein; 260 AA.		
PA (FERR/) FERRARA N.	DE Human PRO polypeptide #198.		
PA (FILV/) FILVAROFF E.	PN US2003199060-A1.		
PA (FONG/) FONG S.	PD 23-OCT-2003.		
PA (GAOW/) GAO W.	PA (GETH) GENENTECH INC.		
PA (GERB/) GERBER H.	Best Local Similarity: 48.08%	Mismatches: 96	
PA (GERR/) GERRITSEN M E.	Indels: 13		
PA (GODD/) GODDARD A.	Query Match:		
PA (GODO/) GODOWSKI P J.	RESULT 277		
PA (GIRM/) GIRMALDI J C.	ID ADF24354 standard; protein; 260 AA.		
PA (GURN/) GURNEY A L.	DE Human secreted/transmembrane protein, PRO322.		
PA (HILL/) HILLAN K J.	PN US2003204055-A1.		
PA (KLJA/) KLJAVIN I J.	PD 30-OCT-2003.		
PA (KUOS/) KUO S S.	PA (GETH) GENENTECH INC.		
PA (NAPI/) NAPIER M A.	Best Local Similarity: 48.08%	Mismatches: 96	
PA (PANJ/) PAN J.	Indels: 13		
PA (PAON/) PAONI N P.	Query Match:		
PA (ROYM/) ROY M A.	RESULT 278		
PA (SHEL/) SHELTON D L.	ID ADF40786 standard; protein; 260 AA.		
PA (STEW/) STEWART T A.	DE Human secreted/transmembrane protein, PRO322.		
PA (TUNA/) TUNAS D.	PN US2003199021-A1.		
PA (WILL/) WILLIAMS P M.	PD 23-OCT-2003.		
PA (WOOD/) WOOD W I.	PA (GETH) GENENTECH INC.		
Best Local Similarity: 48.08%	Best Local Similarity: 48.08%	Mismatches: 96	
Indels: 13	Indels: 13		
Query Match:	Query Match:		
RESULT 270	RESULT 279		
ID ADF61470 standard; protein; 260 AA.	ID ADF23730 standard; protein; 260 AA.		
DE Human secreted/transmembrane protein, PRO322.	DE Human secreted/transmembrane protein, PRO322.		
PN US2003195345-A1.	PN US2003203402-A1.		
PD 16-OCT-2003.	PD 30-OCT-2003.		
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.		
Best Local Similarity: 48.08%	Best Local Similarity: 48.08%	Mismatches: 96	
Indels: 13	Indels: 13		
Query Match:	Query Match:		
RESULT 271	RESULT 280		
ID ADF40162 standard; protein; 260 AA.	ID ADF33713 standard; protein; 260 AA.		
DE Human secreted/transmembrane protein, PRO322.	DE Human secreted/transmembrane protein, PRO322.		
PN US2003198994-A1.	PN US2003194780-A1.		
PD 23-OCT-2003.	PD 16-OCT-2003.		
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.		
Best Local Similarity: 48.08%	Best Local Similarity: 48.08%	Mismatches: 96	
Indels: 13	Indels: 13		
Query Match:	Query Match:		
RESULT 272	RESULT 281		
ID ADF45958 standard; protein; 260 AA.	ID ADF34970 standard; protein; 260 AA.		
DE Human secreted/transmembrane protein, PRO322.	DE Human PRO polypeptide #198.		
PN US2003195148-A1.	PN US2003199029-A1.		
PD 16-OCT-2003.	PD 23-OCT-2003.		
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.		
Best Local Similarity: 48.08%	Best Local Similarity: 48.08%	Mismatches: 96	
Indels: 13	Indels: 13		
Query Match:	Query Match:		
RESULT 273	RESULT 282		
ID ADE94727 standard; protein; 260 AA.	ID ADF27180 standard; protein; 260 AA.		
DE Human PRO polypeptide #198.	DE Human secreted/transmembrane protein, PRO322.		
PN US2003199027-A1.	PN US2003199436-A1.		
PD 23-OCT-2003.	PD 23-OCT-2003.		
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.		
Best Local Similarity: 48.08%	Best Local Similarity: 48.08%	Mismatches: 96	
Indels: 13	Indels: 13		
Query Match:	Query Match:		
RESULT 274	RESULT 283		
ID ADE91138 standard; protein; 260 AA.	ID ADF27816 standard; protein; 260 AA.		
DE Human PRO polypeptide #198.	DE Human secreted/transmembrane protein, PRO322.		
PN US2003199061-A1.	PN US2003199437-A1.		
PD 23-OCT-2003.	PD 23-OCT-2003.		
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.		
Best Local Similarity: 48.08%	Best Local Similarity: 48.08%	Mismatches: 96	
Indels: 13	Indels: 13		
Query Match:	Query Match:		
RESULT 275	RESULT 284		
ID ADE95279 standard; protein; 260 AA.	ID ADE92285 standard; protein; 260 AA.		
DE Human PRO polypeptide #198.	DE Novel human secreted and transmembrane protein PRO322.		
PN US2003199052-A1.	PN US2003199051-A1.		
	PD 23-OCT-2003.		

PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 285
ID ADE90586 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 286
ID ADF41410 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 287
ID ADF33089 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 288
ID ADF25455 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 289
ID ADF26556 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 290
ID ADF34345 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 291
ID ADF46582 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 292
ID ADE91733 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 293
ID ADG02312 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. Mismatches: 96

Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 294
ID ADG22098 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 295
ID ADG20168 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 296
ID ADF98074 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 297
ID ADG24291 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 298
ID ADF98645 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 299
ID ADG03476 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 300
ID ADF99197 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 301
ID ADG16782 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 302
ID ADG05241 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. Mismatches: 96
Best Local Similarity: 48.08% Indels: 13
Query Match: 30.61%
RESULT 303
ID ADG02312 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. Mismatches: 96

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Query Match: 30.61% Indels: 13
RESULT 303
ID ADG19508 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 304
ID ADG13345 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 305
ID ADG08402 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 306
ID ADG15572 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 307
ID ADF96970 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 308
ID ADG06155 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 309
ID ADG23739 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 310
ID ADG04028 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 311
ID ADG24929 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 312
ID ADG07226 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 313
ID ADG07778 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 314
ID ADG55273 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 315
ID ADG60937 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 316
ID ADG62041 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 317
ID ADG82242 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 318
ID ADG57481 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 319
ID ADG56929 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 320
ID ADG55825 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 321
```


ID ADG58585 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207368-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 332
ID ADG70951 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207420-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 333
ID ADG58033 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207363-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 324
ID ADG53617 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207415-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 325
ID ADG71503 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207421-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 326
ID ADG50568 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003207803-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 327
ID ADG81690 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207805-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 328
ID ADH30652 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US200307723-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 329
ID ADH12019 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207419-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 330
ID ADG49944 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.

PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 331
ID ADG51816 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003215908-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 332
ID ADG52441 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207414-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 333
ID ADG54169 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207416-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 334
ID ADG49320 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003216305-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 335
ID ADG81138 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194793-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 336
ID ADG56377 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207366-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 337
ID ADH12643 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207378-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 338
ID ADG48696 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003216560-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 339
ID ADG61489 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207429-A1.

PD 06-NOV-2003.	PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.	Best Local Similarity: 48.08%	Mismatches: 96
Query Match:	Best Local Similarity: 30.61%	Indels: 13	
RESULT 340	DE ADH25617 standard; protein; 260 AA.		
ID ADH25617 standard; protein; 260 AA.	DE Human neurotrophin homologue related protein sequence SEQ ID NO:395.		
PD 04-FEB-2004.	PA (GETH) GENENTECH INC.	Best Local Similarity: 48.08%	Mismatches: 96
Query Match:	Best Local Similarity: 30.61%	Indels: 13	
RESULT 350	DE ADG09928 standard; protein; 260 AA.		
ID ADG09928 standard; protein; 260 AA.	DE Novel human secreted and transmembrane protein PRO322.		
PD 15-JAN-2004.	PA (GETH) GENENTECH INC.	Best Local Similarity: 48.08%	Mismatches: 96
Query Match:	Best Local Similarity: 30.61%	Indels: 13	
RESULT 351	DE ADI15399 standard; protein; 260 AA.		
ID ADI15399 standard; protein; 260 AA.	DE Novel human secreted and transmembrane protein PRO322.		
PD 06-NOV-2003.	PA (GETH) GENENTECH INC.	Best Local Similarity: 48.08%	Mismatches: 96
Query Match:	Best Local Similarity: 30.61%	Indels: 13	
RESULT 352	DE ADG09276 standard; protein; 260 AA.		
ID ADG09276 standard; protein; 260 AA.	DE Novel human secreted and transmembrane protein PRO322.		
PD 15-JAN-2004.	PA (GETH) GENENTECH INC.	Best Local Similarity: 48.08%	Mismatches: 96
Query Match:	Best Local Similarity: 30.61%	Indels: 13	
RESULT 353	DE ADI14731 standard; protein; 260 AA.		
ID ADI14731 standard; protein; 260 AA.	DE Novel human secreted and transmembrane protein PRO322.		
PD 06-NOV-2003.	PA (GETH) GENENTECH INC.	Best Local Similarity: 48.08%	Mismatches: 96
Query Match:	Best Local Similarity: 30.61%	Indels: 13	
RESULT 354	DE ADI18326 standard; protein; 260 AA.		
ID ADI18326 standard; protein; 260 AA.	DE Novel human secreted and transmembrane protein PRO322.		
PD 06-NOV-2003.	PA (GETH) GENENTECH INC.	Best Local Similarity: 48.08%	Mismatches: 96
Query Match:	Best Local Similarity: 30.61%	Indels: 13	
RESULT 355	DE ADI37154 standard; protein; 260 AA.		
ID ADI37154 standard; protein; 260 AA.	DE Human TADG-14 protein.		
PD 23-OCT-2003.	PA (UYAR-) UNIV ARKANSAS.	Best Local Similarity: 48.08%	Mismatches: 96
Query Match:	Best Local Similarity: 30.61%	Indels: 13	
RESULT 356	DE ADJ63607 standard; protein; 260 AA.		
ID ADJ63607 standard; protein; 260 AA.	DE Novel human secreted and transmembrane protein PRO322.		
PD 26-FEB-2004.	PA (GETH) GENENTECH INC.	Best Local Similarity: 48.08%	Mismatches: 96
Query Match:	Best Local Similarity: 30.61%	Indels: 13	
RESULT 357	DE ADJ77502 standard; protein; 260 AA.		
ID ADJ77502 standard; protein; 260 AA.	DE Human PRO polypeptide #198.		
PD 26-FEB-2004.	PA (GETH) GENENTECH INC.	Best Local Similarity: 48.08%	Mismatches: 96
Query Match:	Best Local Similarity: 30.61%	Indels: 13	
RESULT 358	DE ADI39730 standard; protein; 260 AA.		
ID ADI39730 standard; protein; 260 AA.	DE Human TADG-14 protein.		
PD 04-NOV-2003.	PA (GETH) GENENTECH INC.	Best Local Similarity: 48.08%	Mismatches: 96
Query Match:	Best Local Similarity: 30.61%	Indels: 13	
RESULT 359	DE ADH43505 standard; protein; 260 AA.		
ID ADH43505 standard; protein; 260 AA.	DE Human PRO polypeptide #36.		
PD 04-DEC-2003.	PA (GETH) GENENTECH INC.	Best Local Similarity: 48.08%	Mismatches: 96
Query Match:	Best Local Similarity: 30.61%	Indels: 13	
RESULT 360	DE ADG59136 standard; protein; 260 AA.		
ID ADG59136 standard; protein; 260 AA.	DE Human secreted/transmembrane protein, PRO322.		
PD 08-JAN-2004.	PA (GETH) GENENTECH INC.	Best Local Similarity: 48.08%	Mismatches: 96
Query Match:	Best Local Similarity: 30.61%	Indels: 13	
RESULT 361	DE ADG62592 standard; protein; 260 AA.		
ID ADG62592 standard; protein; 260 AA.	DE Human secreted/transmembrane protein, PRO322.		
PD 08-JAN-2004.	PA (GETH) GENENTECH INC.	Best Local Similarity: 48.08%	Mismatches: 96
Query Match:	Best Local Similarity: 30.61%	Indels: 13	
RESULT 362	DE ADG62592 standard; protein; 260 AA.		
ID ADG62592 standard; protein; 260 AA.	DE Human secreted/transmembrane protein, PRO322.		
PD 08-JAN-2004.	PA (GETH) GENENTECH INC.	Best Local Similarity: 48.08%	Mismatches: 96
Query Match:	Best Local Similarity: 30.61%	Indels: 13	
RESULT 363	DE ADI1185 standard; protein; 260 AA.		
ID ADI1185 standard; protein; 260 AA.	DE Human PRO polypeptide #198.		
PD 06-NOV-2003.	PA (GETH) GENENTECH INC.	Best Local Similarity: 48.08%	Mismatches: 96
Query Match:	Best Local Similarity: 30.61%	Indels: 13	
RESULT 364	DE ADI39730 standard; protein; 260 AA.		
ID ADI39730 standard; protein; 260 AA.	DE Human TADG-14 protein.		
PD 04-NOV-2003.	PA (GETH) GENENTECH INC.	Best Local Similarity: 48.08%	Mismatches: 96
Query Match:	Best Local Similarity: 30.61%	Indels: 13	

Best Local Similarity: 48.08%	Mismatches: 96
Query Match: 30.61%	Indels: 13
RESULT 358	
ID ADK82850 standard; protein; 260 AA.	
DE Human PRO polypeptide #36.	
PN US2004043927-A1.	
PD 04-MAR-2004.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.08%	Mismatches: 96
Query Match: 30.61%	Indels: 13
RESULT 359	
ID ADJ65624 standard; protein; 260 AA.	
DE Human PRO polypeptide #198.	
PN US2004038335-A1.	
PD 26-FEB-2004.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.08%	Mismatches: 96
Query Match: 30.61%	Indels: 13
RESULT 360	
ID ADM27760 standard; protein; 260 AA.	
DE Human PRO polypeptide #198.	
PN US2004048333-A1.	
PD 11-MAR-2004.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.08%	Mismatches: 96
Query Match: 30.61%	Indels: 13
RESULT 361	
ID ADM17394 standard; protein; 260 AA.	
DE Human secreted/transmembrane protein, PRO322.	
PN US2004048332-A1.	
PD 11-MAR-2004.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.08%	Mismatches: 96
Query Match: 30.61%	Indels: 13
RESULT 362	
ID ADL07228 standard; protein; 260 AA.	
DE Human secreted/transmembrane protein, PRO322.	
PN US2004063921-A1.	
PD 01-APR-2004.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.08%	Mismatches: 96
Query Match: 30.61%	Indels: 13
RESULT 363	
ID ADM42484 standard; protein; 260 AA.	
DE Human PRO polypeptide #198.	
PN US2004058424-A1.	
PD 25-MAR-2004.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.08%	Mismatches: 96
Query Match: 30.61%	Indels: 13
RESULT 364	
ID ADM62866 standard; protein; 260 AA.	
DE Human NOV11h.	
PN US2004038223-A1.	
PD 26-FEB-2004.	
PA (SMIT) SMITHSON G.	
PA (MILL) MILLET I.	
PA (PEYM) PEYMAN J. A.	
PA (KEKU) KEKUDA R.	
PA (JUJJ) JU J.	
PA (LILL) LI L.	
PA (GUOX) GUO X.	
PA (PATT) PATTURAJAN M.	
PA (SPYT) SPYTEK K. A.	
PA (EDIN) EDINGER S. R.	
PA (ELLE) ELLERMAN K.	
PA (MALY) MALYANKAR U. M.	
PA (ORTT) ORT T.	
PA (GORM) GORMAN L.	
PA (ZERH) ZERHUSEN B. D.	
PA (ANDE) ANDERSON D. W.	
PA (ZHON) ZHONG M.	
PA (CATT) CATTERTON E.	
Best Local Similarity: 48.08%	Mismatches: 96
Query Match: 30.61%	Indels: 13
RESULT 365	
ID ADM04214 standard; protein; 260 AA.	
DE Antipsoriatic protein sequence #302.	
PN WO2004028479-A2.	
PD 08-APR-2004.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.08%	Mismatches: 96
Query Match: 30.61%	Indels: 13
RESULT 366	
ID ADM28346 standard; protein; 260 AA.	
DE Human PRO polypeptide #198.	
PN US2004077064-A1.	
PD 22-APR-2004.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.08%	Mismatches: 96
Query Match: 30.61%	Indels: 13
RESULT 367	
ID ADI95828 standard; protein; 260 AA.	
DE Human PRO polypeptide #198.	
PN US2003077659-A1.	
PD 24-APR-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.08%	Mismatches: 96
Query Match: 30.61%	Indels: 13
RESULT 368	
ID ADI96380 standard; protein; 260 AA.	
DE Novel human secreted and transmembrane protein PRO322.	
PN US2003207354-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.08%	Mismatches: 96
Query Match: 30.61%	Indels: 13
RESULT 369	
ID ADR72883 standard; protein; 260 AA.	
DE Human ovarian cancer-related tumour marker kallikrein 8 (hk8) protein.	
PN WO2004075713-A2.	
PD 10-SEP-2004.	
PA (MOUN) MOUNT SINAI HOSPITAL.	
Best Local Similarity: 48.08%	Mismatches: 96
Query Match: 30.61%	Indels: 13
RESULT 370	
ID AAW87703 standard; protein; 260 AA.	
DE A human serine protease designated HGBAB90.	
PN EP887414-A2.	
PD 30-DEC-1998.	
PA (SMIK) SMITHKLINE BEECHAM PLC.	
Best Local Similarity: 48.25%	Mismatches: 95
Query Match: 30.42%	Indels: 13
RESULT 371	
ID AAB21311 standard; protein; 275 AA.	
DE Human neuropsin.	
PN WO200053776-A2.	
PD 14-SEP-2000.	
PA (MOUN) MOUNT SINAI HOSPITAL.	
Best Local Similarity: 48.25%	Mismatches: 95

Query Match: 30.42% Indels: 13
RESULT 372
ID AAY32853 standard; protein; 305 AA.
DE Human serine protease protein sequence.
PN JP11225765-A.
PD 24-AUG-1999.
PA (SUNR) SONTORY LTD.
Best Local Similarity: 50.85% Mismatches: 90
Query Match: 30.35% Indels: 2
RESULT 373
ID AAB37985 standard; protein; 306 AA.
DE Human secreted protein encoded by gene 2 clone HWJAE49.
PN WO200055371-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 50.85% Mismatches: 90
Query Match: 30.35% Indels: 2
RESULT 374
ID ABP41332 standard; protein; 315 AA.
DE Human ovarian antigen HCOQP78, SEQ ID NO:2464.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 50.85% Mismatches: 90
Query Match: 30.35% Indels: 2
RESULT 375
ID AD117074 standard; protein; 260 AA.
DE Rat NOVX protein homologue Seqid 610.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 47.04% Mismatches: 93
Query Match: 30.28% Indels: 7
RESULT 376
ID AAY06438 standard; protein; 260 AA.
DE Human protease HUPM-7.
PN WO9936550-A2.
PD 22-JUL-1999.
PA (INCY-) INCYTE PHARM INC.
Best Local Similarity: 47.69% Mismatches: 97
Query Match: 30.23% Indels: 13
RESULT 377
ID AAM10694 standard; protein; 260 AA.
DE Human recombinant neuropsin, used for antibody production.
PN JP08245700-A.
PD 24-SEP-1996.
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
Best Local Similarity: 48.99% Mismatches: 93
Query Match: 30.13% Indels: 5
RESULT 378
ID AAM12393 standard; protein; 260 AA.
DE Mouse neuropsin protein.
PN JP08311099-A.
PD 26-NOV-1996.
PA (SHIO/) SHIOZAKA S.
Best Local Similarity: 48.99% Mismatches: 93
Query Match: 30.13% Indels: 5
RESULT 379
ID ABB57219 standard; protein; 260 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:533.
PN WO20018188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Best Local Similarity: 48.99% Mismatches: 93
Query Match: 30.13% Indels: 5
RESULT 380
ID AD117073 standard; protein; 260 AA.
DE Murine NOVX protein homologue Seqid 609.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 48.99% Mismatches: 93
Query Match: 30.13% Indels: 5

RESULT 381
ID ADI39731 standard; protein; 260 AA.
DE Mouse neuropsin protein.
PN US6642013-B1.
PD 04-NOV-2003.
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.
Best Local Similarity: 48.99% Mismatches: 93
Query Match: 30.13% Indels: 5
RESULT 382
ID ADI37155 standard; protein; 260 AA.
DE Mouse neuropsin.
PN US2003199010-A1.
PD 23-OCT-2003.
PA (UYAR-) UNIV ARKANSAS.
Best Local Similarity: 48.99% Mismatches: 93
Query Match: 30.13% Indels: 5
RESULT 383
ID AAB21325 standard; protein; 250 AA.
DE Human TLSP.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 384
ID AAY99390 standard; protein; 250 AA.
DE Human PRO1279 (UNQ649) amino acid sequence SEQ ID NO:170.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 385
ID AAB66139 standard; protein; 250 AA.
DE Protein of the invention #51.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 386
ID AAU12424 standard; protein; 250 AA.
DE Human PRO1279 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 387
ID ABB50479 standard; protein; 250 AA.
DE Human secreted protein encoded by gene 179 SEQ ID NO:427.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 388
ID AAU83684 standard; protein; 250 AA.
DE Human PRO protein, Seq ID No 186.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 389
ID ABG61816 standard; protein; 250 AA.
DE Prostate cancer-associated protein #17.
PN WO200230288-A2.
PD 18-APR-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 390

ID ABB84920 standard; protein; 250 AA.
DE Human PRO1279 protein sequence SEQ ID NO:208.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 391
ID ABB95526 standard; protein; 250 AA.
DE Human angiogenesis related protein PRO1279 SEQ ID NO: 208.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERR/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 392
ID ABO17868 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 393
ID ABU80831 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 394
ID ABO33797 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 395
ID ABU81122 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 396
ID ABU56739 standard; protein; 250 AA.
DE Lung cancer-associated polypeptide #332.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 397
ID ABU66822 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN WO2003049816-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 398
ID ABUS9903 standard; protein; 250 AA.
DE Novel secreted and transmembrane protein PRO1279.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 399
ID ABO25093 standard; protein; 250 AA.
DE Human secreted/transmembrane protein (PRO) #253.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 400
ID ABU82140 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 401
ID ABU67098 standard; protein; 250 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 506.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 402
ID ADA46025 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003023238-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 403
ID ADA76456 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 404
ID ABU72320 standard; protein; 250 AA.
DE Human PRO1279 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 405
ID ADA19106 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 406
ID ADA61729 standard; protein; 250 AA.
DE Homo sapiens.
PN US2003049816-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 407
ID ADB19514 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 408
ID ADB28055 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 409
ID ADA86534 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 410
ID ADB16098 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 411
ID ADA47884 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 412
ID ABO44736 standard; protein; 250 AA.
DE Novel human secreted protein #179.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 413
ID ABO33632 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 414
ID ADA67679 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 415
ID ADB30686 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003068794-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 416
ID ADA85982 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 417
ID ADA97194 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 418
ID ADA79498 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 419
ID ADA87637 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 420
ID ADB16839 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 421
ID ADA91931 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 422
ID ADB14994 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 423
ID ADB18955 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 424
ID ADA94170 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US200307722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

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Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 425
ID ADB20066 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 426
ID ADB13378 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 427
ID ABO43401 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US200304945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 428
ID ADA74632 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 429
ID ADB24865 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US200307713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 430
ID ADA82389 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 431
ID ADA75352 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 432
ID ADA85430 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 433
ID ADA84878 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 434
ID ADB30134 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 435
ID ADA80662 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 436
ID ADA75904 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 437
ID ADA47129 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 438
ID ADB25425 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US200307715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 439
ID ADA93601 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 440
ID ADB26951 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 441
ID ADB31238 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 442
ID ABJ72448 standard; protein; 250 AA.
DE Human PRO1279 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
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RESULT 443
ID ADA61166 standard; protein; 250 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 444
ID ADB24313 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US200307714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 445
ID ADA96642 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 446
ID ADA81214 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 447
ID ADA96090 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 448
ID ADB26399 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 449
ID ADB21884 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 450
ID ABO34343 standard; protein; 250 AA.
DE Human secreted/transmembrane polypeptide PRO 1279.
PN US2003044334-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 451
ID ADA77663 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 452
ID ABO33509 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 453
ID ADA87086 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 454
ID ABO44485 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 455
ID ADA88189 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 456
ID ADA46577 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 457
ID ADB28607 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 458
ID ADB29159 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 459
ID ABO26216 standard; protein; 250 AA.
DE Human protein from novel secreted protein gene 179.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 460
ID ADA77111 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 461
ID ABO33509 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein PRO1279.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 462
ID ADA88741 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 463
ID ADA97746 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 464
ID ADB27503 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 465
ID ADB22436 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 466
ID ADBJ72150 standard; protein; 250 AA.
DE Human membrane bound receptor/protein PRO1279 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 467
ID ADA67127 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 468
ID ADB22988 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 469
ID ADB23761 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 470
ID ADA92483 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082712-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 471
ID ADB15546 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 472
ID ADB83676 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 473
ID ADB80782 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 474
ID ADB73323 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 475
ID ADB38798 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 476
ID ADB78405 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 477
ID ADB38246 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 478
ID ADB66718 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 479
ID ADB85053 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

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Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 480
ID ADB89798 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
RESULT 481
ID ADB90530 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
RESULT 482
ID ADB80596 standard; protein; 250 AA.
DE Ovarian cancer-associated protein #81.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
RESULT 483
ID ADB39631 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
RESULT 484
ID ADB78159 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
RESULT 485
ID ADB87225 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
RESULT 486
ID ADB84807 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
RESULT 487
ID ADB47254 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
RESULT 488
ID ADB83922 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
RESULT 489
ID ADB86861 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
RESULT 490
ID ADB73077 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
RESULT 491
ID ADB77466 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
RESULT 492
ID ADB75388 standard; protein; 250 AA.
DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
RESULT 493
ID ADB34623 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
RESULT 494
ID ADB35727 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
RESULT 495
ID ADB34071 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
RESULT 496
ID ADB35175 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
RESULT 497
ID ADB36279 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 89
Best Local Similarity: 48.19% Indels: 5
Query Match: 29.94%
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RESULT 498
ID ADC46674 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 499
ID ADC18039 standard; protein; 250 AA.
DE Human PRO polypeptide #51.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 500
ID ADC36915 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 501
ID ADC21905 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 502
ID ADC50547 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 503
ID ADC72094 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 504
ID ADC60073 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 505
ID ADC49936 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 506
ID ADC49135 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 507

ID ADC49652 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 508
ID ADC47513 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 509
ID ADC53080 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein Seq ID506.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 510
ID ADC57434 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein Seq ID506.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 511
ID ADC60625 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 512
ID ADC51100 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 513
ID ADC65627 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 514
ID ADC54725 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein Seq ID506.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 515
ID ADC53686 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein Seq ID506.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 516
ID ADC59209 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein Seq ID506.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 517
ID ADC56087 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein Seq ID506.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 518
ID ADC58657 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein Seq ID506.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 519
ID ADC47288 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 520
ID ADD03331 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 521
ID ADC90323 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 522
ID ADC69742 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 523
ID ADC48631 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 524
ID ADD10160 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 525
ID ADC78133 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003105013-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 526
ID ADD04735 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 527
ID ADD06368 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 528
ID ADC80691 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 529
ID ADD11198 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 530
ID ADD10497 standard; protein; 250 AA.
DE Human secreted/transmembrane PRO polypeptide #104.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 531
ID ADC48079 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 532
ID ADC77887 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 533
ID ADC80139 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 534
ID ADD11457 standard; protein; 250 AA.
DE Human secreted/transmembrane PRO polypeptide #104.
PN US2003105013-A1.

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PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 535
ID ADD09608 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 536
ID ADD50850 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 537
ID ADD41321 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 538
ID ADD2460 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 539
ID ADD51096 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 540
ID ADD70685 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US200309625-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 541
ID ADD39762 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 542
ID ADD53200 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 543
ID ADD53752 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 544
ID ADD70208 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 545
ID ADD37250 standard; protein; 250 AA.
DE Human secreted/transmembrane PRO polypeptide #104.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 546
ID ADD38329 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 547
ID ADD39285 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 548
ID ADD51908 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 549
ID ADD02707 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 550
ID ADD50577 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 551
ID ADD02141 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 552
ID ADD54323 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.

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Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 553	
ID AD50331 standard; protein; 250 AA.	
DE Human PRO polypeptide #93.	
PN US2003096970-A1.	
PD 22-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 554	
ID ADD3808 standard; protein; 250 AA.	
DE Human secreted/transmembrane protein PRO1279.	
PN US2003092061-A1.	
PD 15-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 555	
ID ADD40239 standard; protein; 250 AA.	
DE Human secreted/transmembrane protein PRO1279.	
PN US2003082627-A1.	
PD 01-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 556	
ID ADD51342 standard; protein; 250 AA.	
DE Novel human secreted and transmembrane protein PRO1279.	
PN US2003105289-A1.	
PD 05-JUN-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 557	
ID ADE50460 standard; protein; 250 AA.	
DE Human secreted/transmembrane protein PRO1279.	
PN US2003069179-A1.	
PD 10-APR-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 558	
ID ADD92640 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003199030-A1.	
PD 23-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 559	
ID ADD91516 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003199055-A1.	
PD 23-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 560	
ID ADE04150 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003199057-A1.	
PD 23-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 561	
ID ADE20072 standard; protein; 250 AA.	
DE Human secreted/transmembrane protein PRO1279.	
PN US2003092883-A1.	
PD 15-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5

Query Match: 29.94%	Indels: 5
RESULT 562	
ID ADE32447 standard; protein; 250 AA.	
DE Novel human secreted and transmembrane protein PRO1279.	
PN US2003194765-A1.	
PD 16-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 563	
ID ADE22379 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003199056-A1.	
PD 23-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 564	
ID ADD79603 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003203428-A1.	
PD 30-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 565	
ID ADE42139 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003194772-A1.	
PD 16-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 566	
ID ADE17956 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003199023-A1.	
PD 23-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 567	
ID ADD92088 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003199053-A1.	
PD 23-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 568	
ID ADE33551 standard; protein; 250 AA.	
DE Novel human secreted and transmembrane protein PRO1279.	
PN US2003194767-A1.	
PD 16-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 569	
ID ADE34103 standard; protein; 250 AA.	
DE Novel human secreted and transmembrane protein PRO1279.	
PN US2003194791-A1.	
PD 16-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 570	
ID ADD80155 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003207417-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5

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RESULT 571
ID ADE49983 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 572
ID ADD93192 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 573
ID ADE19612 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 574
ID ADE21541 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 575
ID ADE19060 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 576
ID ADE43256 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 577
ID ADD96045 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 578
ID ADE22931 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 579
ID ADD79049 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 580
ID ADE32999 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 581
ID ADE42691 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 582
ID ADD80707 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 583
ID ADD89735 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 584
ID ADE41019 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 585
ID ADE04818 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 586
ID ADE92947 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 587
ID ADF29966 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 588
ID ADF55859 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 589
ID ADG21656 standard; protein; 250 AA.
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DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 590
ID ADG323297 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 591
ID ADF97632 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 592
ID ADG80696 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 593
ID ADG80144 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 594
ID ADH55436 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 595
ID ADH55988 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 596
ID ADH99363 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 597
ID ADI64207 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 598
ID ADI65156 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 599
ID ADH82069 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 600
ID ADH81517 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 601
ID ADM82686 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 602
ID ADN16085 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 603
ID ADN16714 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 604
ID ADN39242 standard; protein; 250 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:560.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 605
ID ADN15533 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 606
ID ADN14981 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 607
ID ADI63655 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207387-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 608
ID ADC4889 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 609
ID ADC81243 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 610
ID ADE21060 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 611
ID ADR05904 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 612
ID ADP7691 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 613
ID ADD75133 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 614
ID ADP75879 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 615
ID ADR85111 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 616
ID ADR86937 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 617
ID ADR20814 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 618
ID ADR39111 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US200309362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 619
ID ADR8055 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 620
ID ADR86459 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 621
ID ADR05658 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 622
ID ADD73643 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 623
ID ADE75907 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 624
ID ADD78483 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 625
ID ADE41458 standard; protein; 250 AA.
DE Human secreted/transmembrane PRO polypeptide #104.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 626			
ID ADE23483 standard; protein; 250 AA.			
DE Human PRO polypeptide #253.			
PN US2003092108-A1.			
PD 15-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 627			
ID ADE21306 standard; protein; 250 AA.			
DE Novel human secreted and transmembrane protein PRO1279.			
PN US2003100736-A1.			
PD 29-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 628			
ID AD077421 standard; protein; 250 AA.			
DE Novel human secreted and transmembrane protein PRO1279.			
PN US2003100732-A1.			
PD 29-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 629			
ID ADE20568 standard; protein; 250 AA.			
DE Novel human secreted and transmembrane protein PRO1279.			
PN US2003100733-A1.			
PD 29-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 630			
ID AD075633 standard; protein; 250 AA.			
DE Human PRO polypeptide #93.			
PN US2003100064-A1.			
PD 29-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 631			
ID AD074149 standard; protein; 250 AA.			
DE Human PRO polypeptide #93.			
PN US2003100708-A1.			
PD 29-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 632			
ID AD074395 standard; protein; 250 AA.			
DE Human PRO polypeptide #93.			
PN US2003100709-A1.			
PD 29-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 633			
ID AD076125 standard; protein; 250 AA.			
DE Novel human secreted and transmembrane protein PRO1279.			
PN US2003100718-A1.			
PD 29-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 634			
ID AD085617 standard; protein; 250 AA.			
DE Novel human secreted and transmembrane protein PRO1279.			
PN US2003100721-A1.			
PD 29-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 635			
ID ADE24035 standard; protein; 250 AA.			
DE Human PRO polypeptide #253.			
PN US2003092110-A1.			
PD 15-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 636			
ID ADE24678 standard; protein; 250 AA.			
DE Human PRO polypeptide #253.			
PN US2003092111-A1.			
PD 15-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 637			
ID AD087503 standard; protein; 250 AA.			
DE Human PRO polypeptide #253.			
PN US2003203439-A1.			
PD 30-OCT-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 638			
ID ADE05166 standard; protein; 250 AA.			
DE Human PRO polypeptide #93.			
PN US2003100726-A1.			
PD 29-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 639			
ID ADD75379 standard; protein; 250 AA.			
DE Human PRO polypeptide #93.			
PN US2003100714-A1.			
PD 29-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 640			
ID ADD76923 standard; protein; 250 AA.			
DE Novel human secreted and transmembrane protein PRO1279.			
PN US2003100715-A1.			
PD 29-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 641			
ID AD086691 standard; protein; 250 AA.			
DE Novel human secreted and transmembrane protein PRO1279.			
PN US2003100719-A1.			
PD 29-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 642			
ID AD089369 standard; protein; 250 AA.			
DE Human PRO polypeptide #253.			
PN US2003199062-A1.			
PD 23-OCT-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		
RESULT 643			
ID AD078159 standard; protein; 250 AA.			
DE Novel human secreted and transmembrane protein PRO1279.			
PN US2003100731-A1.			
PD 29-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 48.19%	Mismatches: 89		
Query Match: 29.94%	Indels: 5		

RESULT 644
ID ADE18508 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 645
ID ADE88817 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 646
ID ADD77667 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 647
ID ADD77913 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 648
ID ADD85371 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 649
ID ADD73903 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 650
ID ADD74641 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 651
ID ADD77169 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 652
ID ADD85863 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 653
ID ADE05412 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 654
ID ADD74887 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 655
ID ADE96543 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 656
ID ADE94837 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 657
ID ADE91248 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 658
ID ADE25854 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 659
ID ADE95389 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 660
ID ADE93499 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 661
ID ADF24753 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 662
ID ADE29489 standard; protein; 250 AA.

DE Human secreted/transmembrane protein PRO1279.	PN US2003207360-A1.		
PN US2003203401-A1.	PD 06-NOV-2003.		
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 663			
ID ADF35080 standard; protein; 250 AA.			
DE Human PRO polypeptide #253.			
PN US2003199029-A1.			
PD 23-OCT-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 664			
ID ADE97020 standard; protein; 250 AA.			
DE Human secreted/transmembrane protein PRO1279.			
PN US2003195334-A1.			
PD 16-OCT-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 665			
ID ADE92395 standard; protein; 250 AA.			
DE Novel human secreted and transmembrane protein PRO1279.			
PN US2003199051-A1.			
PD 23-OCT-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 666			
ID ADE90696 standard; protein; 250 AA.			
DE Human PRO polypeptide #253.			
PN US2003199063-A1.			
PD 23-OCT-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 667			
ID ADE91843 standard; protein; 250 AA.			
DE Novel human secreted and transmembrane protein PRO1279.			
PN US2003199058-A1.			
PD 23-OCT-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 668			
ID ADG05699 standard; protein; 250 AA.			
DE Novel human secreted and transmembrane protein PRO1279.			
PN US2003096959-A1.			
PD 22-MAY-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 669			
ID ADG27253 standard; protein; 250 AA.			
DE Human PRO polypeptide #93.			
PN US2003096962-A1.			
PD 22-MAY-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 670			
ID ADG02422 standard; protein; 250 AA.			
DE Human PRO polypeptide #253.			
PN US2003207352-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 671			
ID ADG22208 standard; protein; 250 AA.			
DE Novel human secreted and transmembrane protein PRO1279.			
PN US2003207351-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 672			
ID ADG20278 standard; protein; 250 AA.			
DE Human PRO polypeptide #253.			
PN US2003207376-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 673			
ID ADF98184 standard; protein; 250 AA.			
DE Human PRO polypeptide #253.			
PN US2003207422-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 674			
ID ADG24401 standard; protein; 250 AA.			
DE Novel human secreted and transmembrane protein PRO1279.			
PN US2003207426-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 675			
ID ADF98755 standard; protein; 250 AA.			
DE Human PRO polypeptide #253.			
PN US2003208055-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 676			
ID ADG03586 standard; protein; 250 AA.			
DE Human PRO polypeptide #253.			
PN US2003207351-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 677			
ID ADF99307 standard; protein; 250 AA.			
DE Human PRO polypeptide #253.			
PN US2003207353-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 678			
ID ADG16892 standard; protein; 250 AA.			
DE Human PRO polypeptide #253.			
PN US2003207359-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 679			
ID ADG05351 standard; protein; 250 AA.			
DE Human PRO polypeptide #253.			
PN US2003207375-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 48.19%	Mismatches: 89	
Query Match: 29.94%	Indels: 5		
RESULT 680			
ID ADG19618 standard; protein; 250 AA.			
DE Human PRO polypeptide #253.			
PN US2003207425-A1.			

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 681
ID ADG11316 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 682
ID ADG13455 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 683
ID ADG08512 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 684
ID ADG15682 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 685
ID ADG12095 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 686
ID ADF97080 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 687
ID ADG06265 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 688
ID ADG23849 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 689
ID ADG04138 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207423-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 690
ID ADG25039 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 691
ID ADF94652 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 692
ID ADG07336 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 693
ID ADG07888 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 694
ID ADG06748 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 695
ID ADG55383 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 696
ID ADG61047 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 697
ID ADG62151 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 698
ID ADH03058 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 699
ID ADG82352 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 700
ID ADG57591 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 701
ID ADG57039 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 702
ID ADG55935 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 703
ID ADG58695 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 704
ID ADG71061 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 705
ID ADH04012 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 706
ID ADH03535 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 707
ID ADH39092 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 708
ID ADG58143 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 709
ID ADG53727 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 710
ID ADG71613 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 711
ID ADG81800 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 712
ID ADH30762 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 713
ID ADH12129 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 714
ID ADG52551 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 715
ID ADG54279 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 716
ID ADG81248 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 717

ID ADG56487 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
FN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 718
ID ADH12753 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
FN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 719
ID ADG61599 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
FN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 720
ID ADH28686 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
FN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 721
ID ADG54831 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
FN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 722
ID ADG59871 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
FN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 723
ID ADH43641 standard; protein; 250 AA.
DE Human PRO polypeptide #104.
FN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 724
ID ADG34182 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
FN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 725
ID ADH04489 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
FN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 726
ID ADI181295 standard; protein; 250 AA.

DE Human PRO polypeptide #253.
FN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 727
ID ADI33652 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
FN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 728
ID ADH69746 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
FN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 729
ID ADH61490 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
FN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 730
ID ADG10038 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
FN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 731
ID ADI15509 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
FN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 732
ID ADG09386 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
FN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 733
ID ADI14841 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
FN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 734
ID ADI29907 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
FN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 735
ID ADI18436 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.

PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 736
ID ADM27304 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US200404179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 737
ID ADJ63717 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 738
ID ADJ77612 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 739
ID ADK62986 standard; protein; 250 AA.
DE Human PRO polypeptide #104.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 740
ID ADK66662 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 741
ID ADJ65734 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 742
ID ADM27870 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 743
ID ADM42594 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 744
ID ADL94689 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2004073015-A1.

PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 745
ID ADM28456 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 746
ID ADI95938 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 747
ID ADI96490 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 748
ID ADR72632 standard; protein; 250 AA.
DE Human renal cell carcinoma-related kallikrein 11 (hK11) protein 2.
PN WO2004077060-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 749
ID ADR72890 standard; protein; 250 AA.
DE Human ovarian cancer-related tumour marker kallikrein 11 (hK11) protein2.
PN WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 750
ID ADS34892 standard; protein; 250 AA.
DE Human autoimmune disease-related protein - SEQ ID 106.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 751
ID AAY42439 standard; protein; 282 AA.
DE CASB12 amino acid sequence.
PN WO9949055-A1.
PD 30-SEP-1999.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 752
ID AAB11712 standard; protein; 282 AA.
DE Human serine protease BSSP6 (hBSSP6) SEQ ID NO:2.
PN WO200031257-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 753
ID AAY43636 standard; protein; 282 AA.
DE A human prostate-associated serum protease (PRASP).
PN WO9941387-A2.
PD 19-AUG-1999.

PA (INCY-) INCYTE PHARM INC.
Best Local Similarity: 48.13% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 754
ID ADN11325 standard; protein; 282 AA.
DE Human kallikrein-11, marker for prostate cancer.
PN WO2004029616-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 48.13% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 755
ID ADQ17587 standard; protein; 282 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 404.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 48.13% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 756
ID ADR72631 standard; protein; 282 AA.
DE Human renal cell carcinoma-related kallikrein 11 (hk11) protein 1.
PN WO2004077060-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 48.13% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 757
ID ADR72889 standard; protein; 282 AA.
DE Human ovarian cancer-related tumour marker kallikrein 11 (hk11) protein1.
PN WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 48.13% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 758
ID ADS34893 standard; protein; 282 AA.
DE Human autoimmune disease-related protein - SEQ ID 107.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 48.13% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 759
ID AAY42440 standard; protein; 281 AA.
DE CASB12 polypeptide derived from Expressed Sequence Tag products.
PN WO9949055-A1.
PD 30-SEP-1999.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Best Local Similarity: 47.98% Mismatches: 89
Query Match: 29.65% Indels: 5
RESULT 760
ID AAU82732 standard; protein; 320 AA.
DE Amino acid sequence of novel human protease #31.
PN WO200200860-A2.
PD 03-JAN-2002.
PA (SUCG-) SUCEN INC.
Best Local Similarity: 41.90% Mismatches: 100
Query Match: 29.55% Indels: 51
RESULT 761
ID AAEL19166 standard; protein; 320 AA.
DE Human protease, PRTS-3 protein.
PN WO200208396-A2.
PD 31-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 41.90% Mismatches: 100
Query Match: 29.55% Indels: 51
RESULT 762
ID AAB36482 standard; protein; 288 AA.
DE Fusion gene with human serine protease catalytic domain protein #13.
PN WO200066709-A2.
PD 09-NOV-2000.
PA (ORTH) ORTHO-MCNEIL PHARM RES INC.

Best Local Similarity: 51.10% Mismatches: 87
Query Match: 29.16% Indels: 3
RESULT 763
ID AAB67542 standard; protein; 288 AA.
DE Amino acid sequence of catalytic domain in PFEK1-6XHIS-TAG.
PN WO200116289-A2.
PD 08-MAR-2001.
PA (ORTH) ORTHO-MCNEIL PHARM INC.
Best Local Similarity: 51.10% Mismatches: 87
Query Match: 29.16% Indels: 3
RESULT 764
ID AAY36093 standard; protein; 250 AA.
DE Extended human secreted protein sequence, SEQ ID NO. 478.
PN WO9931236-A2.
PD 24-JUN-1999.
PA (GEST) GENSET.
Best Local Similarity: 47.39% Mismatches: 91
Query Match: 29.11% Indels: 5
RESULT 765
ID ADP19401 standard; protein; 250 AA.
DE Human secreted polypeptide #252.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Best Local Similarity: 47.39% Mismatches: 91
Query Match: 29.11% Indels: 5
RESULT 766
ID AAB11714 standard; protein; 275 AA.
DE Human serine protease BSSP6 (hBSSP6) SEQ ID NO.6.
PN WO200031257-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Best Local Similarity: 44.16% Mismatches: 88
Query Match: 29.09% Indels: 30
RESULT 767
ID ADI17075 standard; protein; 225 AA.
DE Murine NOVX protein homologue Segid 611.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 49.78% Mismatches: 86
Query Match: 28.99% Indels: 2
RESULT 768
ID AAU79390 standard; protein; 256 AA.
DE Novel human kallikrein KLK15.
PN WO200214485-A2.
PD 21-FEB-2002.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 47.08% Mismatches: 88
Query Match: 28.99% Indels: 16
RESULT 769
ID ADN10932 standard; protein; 256 AA.
DE Human kallikrein 15, marker of endocrine cancer.
PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 47.08% Mismatches: 88
Query Match: 28.99% Indels: 16
RESULT 770
ID AAB36483 standard; protein; 289 AA.
DE Fusion gene with human serine protease catalytic domain protein #14.
PN WO200066709-A2.
PD 09-NOV-2000.
PA (ORTH) ORTHO-MCNEIL PHARM RES INC.
Best Local Similarity: 49.14% Mismatches: 79
Query Match: 28.97% Indels: 5
RESULT 771
ID AAB67543 standard; protein; 289 AA.
DE Amino acid sequence of catalytic domain in PFEK1-6XHIS-TAG.
PN WO200116289-A2.
PD 08-MAR-2001.
PA (ORTH) ORTHO-MCNEIL PHARM INC.
Best Local Similarity: 49.14% Mismatches: 79

Query Match:	28.97%	Indels:	5
RESULT 772			
ID AAE08017 standard; protein; 248 AA.			
DE Human PS133 consensus protein sequence.			
PN US6232456-B1.			
PD 15-MAY-2001.			
PA (ABB0) ABBOTT LAB.			
Best Local Similarity: 47.79%	Mismatches:	87	
Query Match: 28.92%	Indels:	7	
RESULT 773			
ID AAB11713 standard; protein; 276 AA.			
DE Mouse serine protease BSSP6 (mBSSP6) SEQ ID NO:4.			
PN WO200031257-A1.			
PD 02-JUN-2000.			
PA (FUSO) FUSO PHARM IND LTD.			
Best Local Similarity: 47.01%	Mismatches:	95	
Query Match: 28.92%	Indels:	5	
RESULT 774			
ID ADI117077 standard; protein; 260 AA.			
DE Human NOVX protein homologue SeqID 613.			
PN WO200268649-A2.			
PD 06-SEP-2002.			
PA (CURA-) CURAGEN CORP.			
Best Local Similarity: 46.54%	Mismatches:	100	
Query Match: 28.82%	Indels:	13	
RESULT 775			
ID ADC31389 standard; protein; 298 AA.			
DE Human novel polypeptide sequence, SEQ ID NO:1471.			
PN WO2003029271-A2.			
PD 10-APR-2003.			
PA (HYSE-) HYSEQ INC.			
Best Local Similarity: 48.12%	Mismatches:	79	
Query Match: 28.80%	Indels:	14	
RESULT 776			
ID AAB21312 standard; protein; 228 AA.			
DE Human KLK-L3.			
PN WO200053776-A2.			
PD 14-SEP-2000.			
PA (MOUN) MOUNT SINAI HOSPITAL.			
Best Local Similarity: 49.33%	Mismatches:	77	
Query Match: 28.65%	Indels:	4	
RESULT 777			
ID AAW08475 standard; protein; 247 AA.			
DE Porcine trypsinogen.			
PN WO9700316-A1.			
PD 03-JAN-1997.			
PA (NOVO) NOVO-NORDISK AS.			
Best Local Similarity: 45.56%	Mismatches:	83	
Query Match: 27.73%	Indels:	10	
RESULT 778			
ID ABB98258 standard; protein; 247 AA.			
DE Pig trypsinogen SEQ ID NO 1.			
PN WO200261064-A2.			
PD 08-AUG-2002.			
PA (HOFF) ROCHE DIAGNOSTICS GMBH.			
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.			
Best Local Similarity: 45.56%	Mismatches:	83	
Query Match: 27.73%	Indels:	10	
RESULT 779			
ID ADJ92132 standard; protein; 247 AA.			
DE Pig pro-trypsin.			
PN US2004043455-A1.			
PD 04-MAR-2004.			
PA (NOVO) NOVOZYMES BIOTECH INC.			
Best Local Similarity: 45.56%	Mismatches:	83	
Query Match: 27.73%	Indels:	10	
RESULT 780			
ID ABU26666 standard; protein; 267 AA.			
DE Human protein modification + maintenance molecule protein SEQ ID NO 20.			
PN WO2003000844-A2.			
PD 03-JAN-2003.			
PA (INCY-) INCYTE GENOMICS INC.			
Best Local Similarity: 44.81%	Mismatches:	88	
Query Match:			
Query Match:	27.66%	Indels:	25
RESULT 781			
ID AAB21306 standard; protein; 251 AA.			
DE Human KLK-L6 protein #2.			
PN WO200053776-A2.			
PD 14-SEP-2000.			
PA (MOUN) MOUNT SINAI HOSPITAL.			
Best Local Similarity: 46.85%	Mismatches:	87	
Query Match: 27.57%	Indels:	15	
RESULT 782			
ID ADNI0930 standard; protein; 251 AA.			
DE Human Kallikrein 14, marker of endocrine cancer.			
PN WO2004029285-A2.			
PD 08-APR-2004.			
PA (MOUN) MOUNT SINAI HOSPITAL.			
Best Local Similarity: 46.85%	Mismatches:	87	
Query Match: 27.57%	Indels:	15	
RESULT 783			
ID AAB21298 standard; protein; 250 AA.			
DE Human KLK-L3 protein #2.			
PN WO200053776-A2.			
PD 14-SEP-2000.			
PA (MOUN) MOUNT SINAI HOSPITAL.			
Best Local Similarity: 46.67%	Mismatches:	89	
Query Match: 27.52%	Indels:	15	
RESULT 784			
ID ABP64969 standard; protein; 250 AA.			
DE Human protein SEQ ID 629.			
PN WO200259280-A2.			
PD 01-AUG-2002.			
PA (HYSE-) HYSEQ INC.			
Best Local Similarity: 46.67%	Mismatches:	89	
Query Match: 27.52%	Indels:	15	
RESULT 785			
ID ABR55400 standard; protein; 250 AA.			
DE Amino acid sequence of human Kallikrein 9 (hK9).			
PN WO2003033731-A2.			
PD 24-APR-2003.			
PA (MOUN) MOUNT SINAI HOSPITAL.			
Best Local Similarity: 46.67%	Mismatches:	89	
Query Match: 27.52%	Indels:	15	
RESULT 786			
ID ADR05516 standard; protein; 250 AA.			
DE Antipsoriatic protein sequence #924.			
PN WO2004028479-A2.			
PD 08-APR-2004.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 46.67%	Mismatches:	89	
Query Match: 27.52%	Indels:	15	
RESULT 787			
ID AAB21300 standard; protein; 277 AA.			
DE Human KLK-L4 protein #2.			
PN WO200053776-A2.			
PD 14-SEP-2000.			
PA (MOUN) MOUNT SINAI HOSPITAL.			
Best Local Similarity: 46.77%	Mismatches:	80	
Query Match: 27.44%	Indels:	16	
RESULT 788			
ID ABO00554 standard; protein; 277 AA.			
DE Novel human polypeptide #141.			
PN WO2003023013-A2.			
PD 20-MAR-2003.			
PA (HYSE-) HYSEQ INC.			
Best Local Similarity: 46.77%	Mismatches:	80	
Query Match: 27.44%	Indels:	16	
RESULT 789			
ID ADL71094 standard; protein; 277 AA.			
DE Human Kallikrein 13 protein SEQ ID NO:1.			
PN WO2004021009-A2.			
PD 11-MAR-2004.			
PA (MOUN) MOUNT SINAI HOSPITAL.			
Best Local Similarity: 46.77%	Mismatches:	80	
Query Match: 27.44%	Indels:	16	

RESULT 790
 ID ADN04184 standard; protein; 277 AA.
 DE Antipsoriatic protein sequence #287.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 46.77% Mismatches: 80
 Query Match: 27.44% Indels: 16
 RESULT 791
 ID ADRI4575 standard; protein; 277 AA.
 DE Human NF-kappaB pathway-associated protein SeqID576.
 PN WO2004065577-A2.
 PD 05-AUG-2004.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Best Local Similarity: 46.77% Mismatches: 80
 Query Match: 27.44% Indels: 16
 RESULT 792
 ID AAU16971 standard; protein; 251 AA.
 DE Human novel secreted protein, SEQ ID 212.
 PN WO200155441-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 46.85% Mismatches: 89
 Query Match: 27.42% Indels: 15
 RESULT 793
 ID AAU23217 standard; protein; 247 AA.
 DE Novel human enzyme polypeptide #303.
 PN WO200155301-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 46.85% Mismatches: 90
 Query Match: 27.32% Indels: 15
 RESULT 794
 ID AAV16777 standard; protein; 293 AA.
 DE Human keratinocyte derived protease (KDP).
 PN WO9918219-A1.
 PD 15-APR-1999.
 PA (PROC) PROCTER & GAMBLE CO.
 Best Local Similarity: 45.34% Mismatches: 83
 Query Match: 27.32% Indels: 5
 RESULT 795
 ID AAY30524 standard; protein; 293 AA.
 DE Human PDSP-1 protein.
 PN WO9946391-A2.
 PD 16-SEP-1999.
 PA (MILL-) MILLENNIUM BIOTHEAPEUTICS INC.
 Best Local Similarity: 45.34% Mismatches: 83
 Query Match: 27.32% Indels: 5
 RESULT 796
 ID AAY38412 standard; protein; 293 AA.
 DE Human secreted protein encoded by gene No. 27.
 PN WO9935158-A1.
 PD 15-JUL-1999.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 45.34% Mismatches: 83
 Query Match: 27.32% Indels: 5
 RESULT 797
 ID AAY38426 standard; protein; 293 AA.
 DE Human secreted protein encoded by gene No. 27.
 PN WO9935158-A1.
 PD 15-JUL-1999.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 45.34% Mismatches: 83
 Query Match: 27.32% Indels: 5
 RESULT 798
 ID AAY66726 standard; protein; 293 AA.
 DE Membrane-bound protein PRO1132.
 PN WO9963088-A2.
 PD 09-DEC-1999.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 45.34% Mismatches: 83
 Query Match: 27.32% Indels: 5
 RESULT 799
 ID ADA56974 standard; protein; 293 AA.
 DE Human secreted protein #257.
 PN WO2002102994-A2.

ID AAB21296 standard; protein; 293 AA.
 DE Human KIK-L2 protein.
 PN WO200053776-A2.
 PD 14-SEP-2000.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Best Local Similarity: 45.34% Mismatches: 83
 Query Match: 27.32% Indels: 5
 RESULT 800
 ID AAU12399 standard; protein; 293 AA.
 DE Human PRO1132 polypeptide sequence.
 PN WO200140466-A2.
 PD 07-JUN-2001.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 45.34% Mismatches: 83
 Query Match: 27.32% Indels: 5
 RESULT 801
 ID AAB65249 standard; protein; 293 AA.
 DE Human PRO1132 (UNQ570) protein sequence SEQ ID NO:309.
 PN WO200073454-A1.
 PD 07-DEC-2000.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 45.34% Mismatches: 83
 Query Match: 27.32% Indels: 5
 RESULT 802
 ID AAU81966 standard; protein; 293 AA.
 DE Human PRO1132.
 PN WO200109327-A2.
 PD 08-FEB-2001.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 45.34% Mismatches: 83
 Query Match: 27.32% Indels: 5
 RESULT 803
 ID ABU58064 standard; protein; 293 AA.
 DE Human PRO polypeptide #96.
 PN US2003027163-A1.
 PD 06-FEB-2003.
 Best Local Similarity: 45.34% Mismatches: 83
 Query Match: 27.32% Indels: 5
 RESULT 804
 ID ABU59142 standard; protein; 293 AA.
 DE Novel human secreted or transmembrane protein PRO1132.
 PN US2002132252-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 45.34% Mismatches: 83
 Query Match: 27.32% Indels: 5
 RESULT 805
 ID ABU82654 standard; protein; 293 AA.
 DE Human secreted/transmembrane protein PRO1132.
 PN US2003032023-A1.
 PD 13-FEB-2003.
 Best Local Similarity: 45.34% Mismatches: 83
 Query Match: 27.32% Indels: 5
 RESULT 806
 ID AB017843 standard; protein; 293 AA.
 DE Novel human secreted and transmembrane protein PRO1132.
 PN US2003032156-A1.
 PD 13-FEB-2003.
 Best Local Similarity: 45.34% Mismatches: 83
 Query Match: 27.32% Indels: 5
 RESULT 807
 ID ADA57425 standard; protein; 293 AA.
 DE Human secreted protein #257.
 PN WO2002102994-A2.
 PD 27-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 45.34% Mismatches: 83
 Query Match: 27.32% Indels: 5
 RESULT 808
 ID ADA56974 standard; protein; 293 AA.
 DE Human secreted protein #257.
 PN WO2002102994-A2.

PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 809
ID ADA57427 standard; protein; 293 AA.
DE Human secreted protein #257.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 810
ID ADA57428 standard; protein; 293 AA.
DE Human secreted protein #257.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 811
ID ABU60573 standard; protein; 293 AA.
DE Human secreted/transmembrane protein, #130.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 812
ID ABU13955 standard; protein; 293 AA.
DE Human PRO1132 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 813
ID ABU81097 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 814
ID ABU72540 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 815
ID ABU66797 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 816
ID ADA41303 standard; protein; 293 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 817
ID ADA41305 standard; protein; 293 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 818
ID ADA40825 standard; protein; 293 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 819
ID ADA41306 standard; protein; 293 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 820
ID ABU59878 standard; protein; 293 AA.
DE Novel secreted and transmembrane protein PRO1132.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 821
ID ABU59289 standard; protein; 293 AA.
DE Human secreted/transmembrane protein, #130.
PN US2003027162-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 822
ID AB025986 standard; protein; 293 AA.
DE Human PRO1132 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 823
ID AB025068 standard; protein; 293 AA.
DE Human secreted/transmembrane protein (PRO) #228.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 824
ID ABU58995 standard; protein; 293 AA.
DE Human secreted/transmembrane protein, #130.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 825
ID ABU92373 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 826
ID ABU59438 standard; protein; 293 AA.
DE Novel human secreted or transmembrane protein PRO1346.
PN US2003027985-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 827

ID ABU67073 standard; protein; 293 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 456.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 828
ID ABU92204 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 829
ID ABU10910 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 830
ID ABU81662 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2002171164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 831
ID ABU88601 standard; protein; 293 AA.
DE Human secreted and transmembrane polypeptide PRO1132.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 832
ID ABO34115 standard; protein; 293 AA.
DE Human PRO1132 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 833
ID ADA45975 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 834
ID ADA76406 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 835
ID ADA19056 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 836
ID ADA61679 standard; protein; 293 AA.
DE Homo sapiens.
PN US2003049816-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 837
ID ADB19464 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 838
ID ADB28005 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 839
ID ADA86484 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 840
ID ADB16048 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 841
ID ADA37820 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 842
ID ADA47834 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 843
ID ADA1506 standard; protein; 293 AA.
DE Human secreted/transmembrane polypeptide PRO1132.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 844
ID ADA10293 standard; protein; 293 AA.
DE Human secreted/transmembrane protein, PRO1132.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 845
ID ADA67629 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83

Query Match: 27.32% Indels: 5
RESULT 846
ID ADB30636 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003068734-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 847
ID ADA85932 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082693-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 848
ID ADA17837 standard; protein; 293 AA.
DE Human PRO1132 polypeptide.
PN US2003054987-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 849
ID ADA97144 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082705-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 850
ID ADA79448 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082763-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 851
ID ADA87587 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087345-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 852
ID ADB16789 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003087349-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 853
ID ADA27945 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003054359-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 854
ID ADA91881 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082694-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 855
ID ADB14944 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082701-A1.

DE Human PRO polypeptide #228.
PN US2003087351-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 856
ID ADB18905 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003073211-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 857
ID ADA94120 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077722-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 858
ID ADB20016 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082691-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 859
ID ADB13328 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082710-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 860
ID ABO43376 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003044945-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 861
ID ADA94525 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003059832-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 862
ID ADA74582 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003068798-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 863
ID ADB24815 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US200307713-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 864
ID ADA82339 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082701-A1.

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PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 865
ID ADA75302 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 866
ID ADA85380 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 867
ID ADA84828 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 868
ID ADB30084 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 869
ID ADA80612 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 870
ID ADA75854 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 871
ID ADA38750 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 872
ID ADA47079 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 873
ID ADB25375 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US200307715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 874
ID ADA93551 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 875
ID ADB26901 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 876
ID ADB31188 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 877
ID ADA92871 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 878
ID ADA61116 standard; protein; 293 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 879
ID ADB4263 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US200307714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 880
ID ADA96592 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 881
ID ADA81164 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 882
ID ADA96040 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
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RESULT 883
ID ADB26349 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 884
ID ADB21834 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 885
ID ADA77613 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 886
ID ADB18353 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 887
ID ADA87036 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 888
ID ADA88139 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 889
ID ADA46527 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 890
ID ADB28557 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 891
ID ADB29109 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 892
ID ABO53201 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 893
ID ADA77061 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 894
ID ADA22432 standard; protein; 293 AA.
DE Human secreted/transmembrane polypeptide PRO1132.
PN US2003040473-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 895
ID ADA88691 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 896
ID ADA97696 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 897
ID ADB27453 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003022339-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 898
ID ADB22386 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 899
ID ABO22571 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 900
ID ADA06598 standard; protein; 293 AA.
DE Human secreted/transmembrane PRO polypeptide #96.
PN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 901
ID ADA39291 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003059782-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 902


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ID ADA67077 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 903
ID ADB22938 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US200307711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 904
ID ADB23711 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 905
ID ADA92433 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 906
ID ADB15496 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 907
ID ADB38748 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 908
ID ADB96317 standard; protein; 293 AA.
DE Human PRO polypeptide #98.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 909
ID ADB38196 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 910
ID ADB66668 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 911
ID ADB99748 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 912
ID ADB90480 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 913
ID ADB80490 standard; protein; 293 AA.
DE Ovarian cancer-associated protein #27.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 914
ID ADB39581 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 915
ID ADB47204 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 916
ID ADB86811 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 917
ID ADB77416 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 918
ID ADB34573 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 919
ID ADB35677 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 920
ID ADB34021 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US200307716-A1.
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PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 921
ID ADB35125 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 922
ID ADB36229 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 923
ID ADB46624 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 924
ID ADC57789 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 925
ID ADC55153 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 926
ID ADC12020 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 927
ID ADC56442 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 928
ID ADC07497 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 929
ID ADC11487 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 930
ID ADC50497 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 931
ID ADC72044 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 932
ID ADC60023 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 933
ID ADC53030 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 934
ID ADC57384 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 935
ID ADC60575 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 936
ID ADC51050 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 937
ID ADC65577 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 938
ID ADC54675 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 939
ID ADC53636 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087364-A1.

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PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 940
ID ADC59159 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 941
ID ADC56037 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 942
ID ADC58607 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 943
ID ADC14609 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 944
ID ADD08141 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 945
ID ADD03281 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 946
ID ADC90273 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 947
ID ADC81966 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 948
ID ADC69692 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5

RESULT 949
ID ADC48581 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 950
ID ADD10110 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 951
ID ADD07608 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 952
ID ADD04685 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 953
ID ADC82499 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 954
ID ADC80641 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 955
ID ADD11148 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 956
ID ADC48029 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 957
ID ADD08679 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 958
ID ADC80089 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.

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PN US2003087358-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 959
ID ADD06928 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 960
ID ADD09558 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 961
ID ADC83175 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 962
ID ADD41271 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 963
ID ADD52410 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 964
ID ADD53150 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194782-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 965
ID ADD53702 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 966
ID ADD55282 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 967
ID ADD56240 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 968
ID ADD51858 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 969
ID ADD02657 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 970
ID ADD02091 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 971
ID ADD54273 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 972
ID ADD54678 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 973
ID ADD92590 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 974
ID ADD91486 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 975
ID ADE804100 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 976
ID ADE26832 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 977
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ID ADE32397 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 978
ID ADE22329 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 979
ID ADD79553 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 980
ID ADE42089 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 981
ID ADE17906 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 982
ID ADD92038 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 983
ID ADE33501 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 984
ID ADE34053 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 985
ID ADD80105 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 986
ID ADD93142 standard; protein; 293 AA.

Human PRO polypeptide #228.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 987
ID ADE19562 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 988
ID ADE19010 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 989
ID ADE43206 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 990
ID ADD95995 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 991
ID ADE22881 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 992
ID ADD78999 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 993
ID ADE26299 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 994
ID ADE32949 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 995
ID ADE42641 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199032-A1.

PA (GETH) GENENTECH INC. Best Local Similarity: 45.34% Query Match: 27.32% RESULT 1005	Mismatches: 83 Indels: 5
ID AG80646 standard; protein; 293 AA. DE Human PRO polypeptide #228. FN US2003207373-A1. PD 06-NOV-2003.	
PA (GETH) GENENTECH INC. Best Local Similarity: 45.34% Query Match: 27.32% RESULT 1006	Mismatches: 83 Indels: 5
ID AG80094 standard; protein; 293 AA. DE Human PRO polypeptide #228. FN US2003207372-A1. PD 06-NOV-2003.	
PA (GETH) GENENTECH INC. Best Local Similarity: 45.34% Query Match: 27.32% RESULT 1007	Mismatches: 83 Indels: 5
ID ADH5386 standard; protein; 293 AA. DE Novel human secreted and transmembrane protein PRO1132. FN US2003207381-A1. PD 06-NOV-2003.	
PA (GETH) GENENTECH INC. Best Local Similarity: 45.34% Query Match: 27.32% RESULT 1008	Mismatches: 83 Indels: 5
ID ADH5938 standard; protein; 293 AA. DE Novel human secreted and transmembrane protein PRO1132. FN US2003207379-A1. PD 06-NOV-2003.	
PA (GETH) GENENTECH INC. Best Local Similarity: 45.34% Query Match: 27.32% RESULT 1009	Mismatches: 83 Indels: 5
ID ADI35490 standard; protein; 293 AA. DE Human PRO polypeptide #96. FN US2003050457-A1. PD 13-MAR-2003.	
PA (GETH) GENENTECH INC. Best Local Similarity: 45.34% Query Match: 27.32% RESULT 1010	Mismatches: 83 Indels: 5
ID ADI64157 standard; protein; 293 AA. DE Novel human secreted and transmembrane protein PRO1132. FN US2003207385-A1. PD 06-NOV-2003.	
PA (GETH) GENENTECH INC. Best Local Similarity: 45.34% Query Match: 27.32% RESULT 1011	Mismatches: 83 Indels: 5
ID ADI65106 standard; protein; 293 AA. DE Novel human secreted and transmembrane protein PRO1132. FN US2003207386-A1. PD 06-NOV-2003.	
PA (GETH) GENENTECH INC. Best Local Similarity: 45.34% Query Match: 27.32% RESULT 1012	Mismatches: 83 Indels: 5
ID ADI63605 standard; protein; 293 AA. DE Novel human secreted and transmembrane protein PRO1132. FN US2003207387-A1. PD 06-NOV-2003.	
PA (GETH) GENENTECH INC. Best Local Similarity: 45.34% Query Match: 27.32% RESULT 1013	Mismatches: 83 Indels: 5
ID ADH82019 standard; protein; 293 AA. DE Novel human secreted and transmembrane protein PRO1132. FN US2003207388-A1. PD 06-NOV-2003.	
PA (GETH) GENENTECH INC. Best Local Similarity: 45.34% Query Match: 27.32% RESULT 1014	Mismatches: 83 Indels: 5
ID ADH82019 standard; protein; 293 AA. DE Novel human secreted and transmembrane protein PRO1132. FN US2003207388-A1. PD 06-NOV-2003.	
PA (GETH) GENENTECH INC. Best Local Similarity: 45.34% Query Match: 27.32% RESULT 1015	Mismatches: 83 Indels: 5

Query Match: 27.32% Indels: 5
RESULT 1014
ID ADH99982 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003049682-A1.
PD 13-MAR-2003.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1015
ID ADH81467 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1016
ID ADM82636 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1017
ID ADN16035 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1018
ID ADN16664 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1019
ID ADN39198 standard; protein; 293 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:516.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1020
ID ADN15483 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1021
ID ADN14931 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1022
ID ADC81193 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1023
ID ADE18458 standard; protein; 293 AA.

ID ADD76641 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1024
ID ADH88005 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1025
ID ADH86409 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1026
ID ADE75857 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1027
ID ADE23433 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1028
ID ADE23985 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1029
ID ADE24628 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1030
ID ADH87453 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1031
ID ADE89319 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1032
ID ADE18458 standard; protein; 293 AA.

DE Human PRO polypeptide #228.
PD US2003194794-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1033
ID ADE88767 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1034
ID ADE94787 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1035
ID ADE91198 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1036
ID ADF35435 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1037
ID ADE95339 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1038
ID ADE93449 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1039
ID ADF35030 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1040
ID ADE92345 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1041
ID ADE90646 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199063-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1042
ID ADE91793 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1043
ID ADG11685 standard; protein; 293 AA.
DE Human PRO1132 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1044
ID ADG02372 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1045
ID ADG22158 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1046
ID ADG20228 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1047
ID ADF98134 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1048
ID ADG24351 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1049
ID ADF98705 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1050
ID ADG03536 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207351-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match: 45.34% Mismatches: 83
Indels: 5
RESULT 1051
ID ADF9257 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1052
ID ADG16842 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1053
ID ADG05301 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1054
ID ADG19568 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1055
ID ADG13405 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1056
ID ADG08462 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1057
ID ADG15632 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1058
ID ADF97030 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1059
ID ADG06215 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1060
ID ADG23799 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1061
ID ADG04088 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1062
ID ADG24989 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1063
ID ADG07286 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1064
ID ADG07838 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1065
ID ADG55333 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1066
ID ADG60997 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1067
ID ADG62101 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1068
ID ADG82302 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5

Query Match: 27.32% Indels: 5
RESULT 1069
ID ADG57541 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207362-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1070
ID ADG56989 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207364-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1071
ID ADG55885 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207365-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1072
ID ADG58645 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207368-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1073
ID ADG71011 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207420-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1074
ID ADG58093 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207363-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1075
ID ADG53677 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207415-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1076
ID ADG71563 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207421-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1077
ID ADG81750 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207805-A1.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1078
ID ADG61549 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.

ID ADH19555 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1079
ID ADH30712 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1080
ID ADG52501 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1081
ID ADG52501 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1082
ID ADG54229 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1083
ID ADG81198 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1084
ID ADG56437 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1085
ID ADH12703 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1086
ID ADH21048 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1087
ID ADG61549 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.

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PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1088
ID ADH20088 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1089
ID ADH28636 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1090
ID ADG54781 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1091
ID ADG59821 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1092
ID ADI81245 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1093
ID ADG09988 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1094
ID ADI15459 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1095
ID ADG09336 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1096
ID ADI14791 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207383-A1.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1097
ID ADI18386 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1098
ID ADJ63667 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1099
ID ADJ77562 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1100
ID ADJ5684 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1101
ID ADM27820 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1102
ID ADK52481 standard; protein; 293 AA.
DE Human kallikrein 5 protein.
PN WO2004021008-A2.
PD 11-MAR-2004.
PA (MOUN ) MOUNT SINAI HOSPITAL.
PA (YOUS ) YOUSEF G.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1103
ID ADM42544 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1104
ID ADM28406 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1105
ID ADI95888 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077659-A1.
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PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1106
ID AD196440 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PD US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1107
ID ADR72621 standard; protein; 293 AA.
DE Human renal cell carcinoma-related kallikrein 5 (hK5) protein.
PD WO2004077060-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1108
ID ADR72873 standard; protein; 293 AA.
DE Human ovarian cancer-related tumour marker kallikrein 5 (hK5) protein.
PD WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1109
ID AAY14072 standard; protein; 322 AA.
DE Human BS247 specific epitope.
PD WO9220227-A1.
PD 06-MAY-1999.
PA (ABBO) ABBOTT LAB.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 1110
ID AAW07620 standard; protein; 276 AA.
DE Human NES1 polypeptide.
PD WO9639175-A1.
PD 12-DEC-1996.
PA (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
Best Local Similarity: 45.91% Mismatches: 92
Query Match: 27.30% Indels: 18
RESULT 1111
ID AAB21327 standard; protein; 276 AA.
DE Human NES1.
PD WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 45.91% Mismatches: 92
Query Match: 27.30% Indels: 18
RESULT 1112
ID ABG96356 standard; protein; 276 AA.
DE Human ovarian cancer marker OV32.
PD WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 45.91% Mismatches: 92
Query Match: 27.30% Indels: 18
RESULT 1113
ID AAU82729 standard; protein; 276 AA.
DE Amino acid sequence of novel human protease #28.
PD WO200200860-A2.
PD 03-JAN-2002.
PA (SUGE-) SUGEN INC.
Best Local Similarity: 45.91% Mismatches: 92
Query Match: 27.30% Indels: 18
RESULT 1114
ID ADB80527 standard; protein; 276 AA.
DE Ovarian cancer-associated protein #46.
PD WO2002102235-A2.
PD 27-DEC-2002.

PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 45.91% Mismatches: 92
Query Match: 27.30% Indels: 18
RESULT 1115
ID ADE40473 standard; protein; 276 AA.
DE Human kallikrein 10 (gene ID 2045) protein.
PD WO2003070883-A2.
PD 28-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 45.91% Mismatches: 92
Query Match: 27.30% Indels: 18
RESULT 1116
ID ADN39880 standard; protein; 276 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C250.
PD WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 45.91% Mismatches: 92
Query Match: 27.30% Indels: 18
RESULT 1117
ID ADN04446 standard; protein; 276 AA.
DE Antipsoriatic protein sequence #416.
PD WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.91% Mismatches: 92
Query Match: 27.30% Indels: 18
RESULT 1118
ID ADQ89070 standard; protein; 276 AA.
DE Human urological disorder related protein 2045 SEQ:22.
PD WO2004065576-A2.
PD 05-AUG-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 45.91% Mismatches: 92
Query Match: 27.30% Indels: 18
RESULT 1119
ID ADR72628 standard; protein; 276 AA.
DE Human renal cell carcinoma-related kallikrein 10 (hK10) protein.
PD WO2004077060-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 45.91% Mismatches: 92
Query Match: 27.30% Indels: 18
RESULT 1120
ID ADR72886 standard; protein; 276 AA.
DE Human ovarian cancer-related tumour marker kallikrein 10 (hK10) protein.
PD WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 45.91% Mismatches: 92
Query Match: 27.30% Indels: 18
RESULT 1121
ID AAB21305 standard; protein; 237 AA.
DE Human K1K-L6 protein #1.
PD WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 48.10% Mismatches: 84
Query Match: 27.20% Indels: 8
RESULT 1122
ID AAB21299 standard; protein; 256 AA.
DE Human K1K-L4 protein #1.
PD WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 49.12% Mismatches: 78
Query Match: 27.18% Indels: 5
RESULT 1123
ID AAB21309 standard; protein; 287 AA.
DE Human K1K-L2.
PD WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.

Best Local Similarity: 46.0% Mismatches: 80
 Query Match: 27.1% Indels: 5
 RESULT 1124
 ID ABB98259 standard; protein; 228 AA.
 DE Synthetic shortened trypsinogen SEQ ID NO 23.
 PN WO200261064-A2.
 PD 08-AUG-2002.
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 Best Local Similarity: 46.7% Mismatches: 77
 Query Match: 27.1% Indels: 6
 RESULT 1125
 ID AAB21310 standard; protein; 239 AA.
 DE Human zyme.
 PN WO200053776-A2.
 PD 14-SEP-2000.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Best Local Similarity: 46.6% Mismatches: 83
 Query Match: 27.1% Indels: 10
 RESULT 1126
 ID AAR44532 standard; protein; 244 AA.
 DE Zyme APP-cleaving protease.
 PN EP576152-A1.
 PD 29-DEC-1993.
 PA (ELIL) LILLY & CO ELI.
 Best Local Similarity: 46.6% Mismatches: 83
 Query Match: 27.1% Indels: 10
 RESULT 1127
 ID AAW22985 standard; protein; 244 AA.
 DE Human serine protease 59 (SP59).
 PN JP09149790-A.
 PD 10-JUN-1997.
 PA (SUNR) SUNTORY LTD.
 Best Local Similarity: 46.6% Mismatches: 83
 Query Match: 27.1% Indels: 10
 RESULT 1128
 ID AAW51006 standard; protein; 244 AA.
 DE Protease M, a novel serine protease.
 PN WO9811238-A2.
 PD 19-MAR-1998.
 PA (DAND) DANA FARBEN CANCER INST INC.
 Best Local Similarity: 46.6% Mismatches: 83
 Query Match: 27.1% Indels: 10
 RESULT 1129
 ID AAB21323 standard; protein; 244 AA.
 DE Human zyme.
 PN WO200053776-A2.
 PD 14-SEP-2000.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Best Local Similarity: 46.6% Mismatches: 83
 Query Match: 27.1% Indels: 10
 RESULT 1130
 ID AAE37572 standard; protein; 244 AA.
 DE Human 2047 protein.
 PN WO2003037258-A2.
 PD 08-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Best Local Similarity: 46.6% Mismatches: 83
 Query Match: 27.1% Indels: 10
 RESULT 1131
 ID ADB80567 standard; protein; 244 AA.
 DE Ovarian cancer-associated protein #66.
 PN WO2002102235-A2.
 PD 27-DEC-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Best Local Similarity: 46.6% Mismatches: 83
 Query Match: 27.1% Indels: 10
 RESULT 1132
 ID ADN39212 standard; protein; 244 AA.
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:530.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.

Best Local Similarity: 46.6% Mismatches: 83
 Query Match: 27.1% Indels: 10
 RESULT 1133
 ID ADN04074 standard; protein; 244 AA.
 DE Antipsoriatic protein sequence #232.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 46.6% Mismatches: 83
 Query Match: 27.1% Indels: 10
 RESULT 1134
 ID ADN29289 standard; protein; 244 AA.
 DE Human kallikrein 6 associated protein.
 PN US2004097452-A1.
 PD 20-MAY-2004.
 PA (ISIS-) ISIS PHARM INC.
 Best Local Similarity: 46.6% Mismatches: 83
 Query Match: 27.1% Indels: 10
 RESULT 1135
 ID ADQ89076 standard; protein; 244 AA.
 DE Human urological disorder related protein 2047 SEQ:28.
 PN WO2004065576-A2.
 PD 05-AUG-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Best Local Similarity: 46.6% Mismatches: 83
 Query Match: 27.1% Indels: 10
 RESULT 1136
 ID ADR72624 standard; protein; 244 AA.
 DE Human renal cell carcinoma-related kallikrein 6 (hk6) protein.
 PN WO2004077060-A2.
 PD 10-SEP-2004.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Best Local Similarity: 46.6% Mismatches: 83
 Query Match: 27.1% Indels: 10
 RESULT 1137
 ID ADR72876 standard; protein; 244 AA.
 DE Human ovarian cancer-related tumour marker kallikrein 6 (hk6) protein.
 PN WO2004075713-A2.
 PD 10-SEP-2004.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Best Local Similarity: 46.6% Mismatches: 83
 Query Match: 27.1% Indels: 10
 RESULT 1138
 ID ABG96357 standard; protein; 244 AA.
 DE Human ovarian cancer marker OV33.
 PN WO200271928-A2.
 PD 19-SEP-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Best Local Similarity: 46.8% Mismatches: 83
 Query Match: 27.1% Indels: 10
 RESULT 1139
 ID AAB21297 standard; protein; 296 AA.
 DE Human CLK-L3 protein #1.
 PN WO200053776-A2.
 PD 14-SEP-2000.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Best Local Similarity: 46.12% Mismatches: 79
 Query Match: 26.9% Indels: 30
 RESULT 1140
 ID ADA05734 standard; protein; 252 AA.
 DE Human NOV18b protein SEQ ID NO:94.
 PN WO2003029424-A2.
 PD 10-APR-2003.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 44.6% Mismatches: 88
 Query Match: 26.8% Indels: 19
 RESULT 1141
 ID ADN62898 standard; protein; 252 AA.
 DE Human NOV18b.
 PN US2004038223-A1.
 PD 26-FEB-2004.
 PA (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.

PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUGJ/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATT/) PATURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERR/) ZERHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIWW/) JI W.
 PA (MILL/) MILLER C E.
 PA (RST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENA/) PENA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.
 PA (BERG/) BERGHS C.
 PA (DIPI/) DIPIPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 Best Local Similarity: 44.66% Mismatches: 88
 Query Match: 26.86% Indels: 19
 RESULT 1142
 ID AAB21302 standard; protein; 111 AA.
 DE Human Kik-L5 protein #2.
 PN WO200053776-A2.
 PD 14-SEP-2000.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Best Local Similarity: 55.78% Mismatches: 0
 Query Match: 26.86% Indels: 88
 RESULT 1143
 ID ADN10928 standard; protein; 111 AA.
 DE Human kallikrein 12, marker of endocrine cancer.
 PN WO2004029285-A2.
 PD 08-APR-2004.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Best Local Similarity: 55.78% Mismatches: 0
 Query Match: 26.86% Indels: 88
 RESULT 1144
 ID AAR67888 standard; protein; 253 AA.
 DE Human stratum corneum chymotrophic recombinant enzyme (SCCE).
 PN WO9500851-A1.
 PD 05-JAN-1995.
 PA (SYMB-) SYMBICOM AB.
 Best Local Similarity: 44.57% Mismatches: 90
 Query Match: 26.86% Indels: 16
 RESULT 1145
 ID AAW05383 standard; protein; 253 AA.
 DE Human amyloid precursor protein protease.
 PN WO9631122-A1.
 PD 10-OCT-1996.
 PA (ELIL) LILLY & CO ELI.
 Best Local Similarity: 44.57% Mismatches: 90
 Query Match: 26.86% Indels: 16
 RESULT 1146
 ID AAY08025 standard; protein; 253 AA.
 DE Mouse protease-related protein (PVP).
 PN DE19736198-C1.
 PD 24-DEC-1998.
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 Best Local Similarity: 42.52% Mismatches: 89

Query Match: 26.86% Indels: 10
 RESULT 1147
 ID ABB84421 standard; peptide; 253 AA.
 DE Human SCCE protein N-terminal fragment SEQ ID 48.
 PN WO200262135-A2.
 PD 15-AUG-2002.
 PA (EGEL/) EGELRUD T.
 PA (HANS/) HANSSON L.
 Best Local Similarity: 44.57% Mismatches: 90
 Query Match: 26.86% Indels: 16
 RESULT 1148
 ID ABB84406 standard; protein; 253 AA.
 DE Human SCCE protein.
 PN WO200262135-A2.
 PD 15-AUG-2002.
 PA (EGEL/) EGELRUD T.
 PA (HANS/) HANSSON L.
 Best Local Similarity: 44.57% Mismatches: 90
 Query Match: 26.86% Indels: 16
 RESULT 1149
 ID AAU82740 standard; protein; 253 AA.
 DE Amino acid sequence of novel human protease #39.
 PN WO200200860-A2.
 PD 03-JAN-2002.
 PA (SUGE-) SUGEN INC.
 Best Local Similarity: 44.57% Mismatches: 90
 Query Match: 26.86% Indels: 16
 RESULT 1150
 ID ABU07440 standard; protein; 253 AA.
 DE Protein differentially regulated in prostate cancer #43.
 PN WO200281638-A2.
 PD 17-OCT-2002.
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 Best Local Similarity: 44.57% Mismatches: 90
 Query Match: 26.86% Indels: 16
 RESULT 1151
 ID ABU07471 standard; protein; 253 AA.
 DE Protein differentially regulated in prostate cancer #74.
 PN WO200281638-A2.
 PD 17-OCT-2002.
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 Best Local Similarity: 44.57% Mismatches: 90
 Query Match: 26.86% Indels: 16
 RESULT 1152
 ID ABR58471 standard; protein; 253 AA.
 DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
 PN WO2003029468-A1.
 PD 10-APR-2003.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 44.57% Mismatches: 90
 Query Match: 26.86% Indels: 16
 RESULT 1153
 ID ADS80484 standard; protein; 253 AA.
 DE Ovarian cancer-associated protein #24.
 PN WO2002102235-A2.
 PD 27-DEC-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Best Local Similarity: 44.57% Mismatches: 90
 Query Match: 26.86% Indels: 16
 RESULT 1154
 ID ADJ68833 standard; protein; 253 AA.
 DE Human heat mitochondrial protein as a therapeutic target SegID639.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Best Local Similarity: 44.57% Mismatches: 90
 Query Match: 26.86% Indels: 16
 RESULT 1155
 ID ADN31960 standard; protein; 253 AA.
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:498.
 PN WO2003042861-A2.
 PD 22-MAY-2003.

PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Best Local Similarity: 44.57% Mismatches: 90
 Query Match: 26.86% Indels: 16
 RESULT 1156
 ID ADL06515 standard; protein; 253 AA.
 DE Human tumour-associated antigenic target (TAT) polypeptide #14.
 PN WO2004016225-A2.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 44.57% Mismatches: 90
 Query Match: 26.86% Indels: 16
 RESULT 1157
 ID ADN04182 standard; protein; 253 AA.
 DE Antipsoriatic protein sequence #286.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 44.57% Mismatches: 90
 Query Match: 26.86% Indels: 16
 RESULT 1158
 ID ADR7280 standard; protein; 253 AA.
 DE Human ovarian cancer-related tumour marker kallikrein 7 (hk7) protein.
 PN WO2004075713-A2.
 PD 10-SEP-2004.
 PA (MOON) MOUNT SINAI HOSPITAL.
 Best Local Similarity: 44.57% Mismatches: 90
 Query Match: 26.86% Indels: 16
 RESULT 1159
 ID ADN2896 standard; protein; 250 AA.
 DE Human NOV18a.
 PN US2004038223-A1.
 PD 26-FEB-2004.
 PA (SMIT) SMITHSON G.
 PA (MILL) MILLET I.
 PA (PEYM) PEYMAN J A.
 PA (KEKU) KEKUDA R.
 PA (JUOJ) JU J.
 PA (LILL) LI L.
 PA (GUOX) GUO X.
 PA (PATT) PATTURAJAN M.
 PA (SPVT) SPYTEK K A.
 PA (EDIN) EDINGER S R.
 PA (ELLE) ELLERMAN K.
 PA (MALY) MALYANKAR U M.
 PA (ORTT) ORT T.
 PA (GORM) GORMAN L.
 PA (ZERH) ZERHUSEN B D.
 PA (ANDE) ANDERSON D W.
 PA (ZHON) ZHONG W.
 PA (CATT) CATTERTON E.
 PA (JTWI) JI W.
 PA (MILL) MILLER C E.
 PA (RSTI) RASTELLI L.
 PA (STON) STONE D J.
 PA (PENA) PENA C E A.
 PA (SHEN) SHENOY S G.
 PA (SHIM) SHIMKETS R A.
 PA (ROTH) ROTHENBERG M E.
 PA (LEAC) LEACH M D.
 PA (AGEE) AGEH M L.
 PA (BERG) BERGHS C.
 PA (DIPI) DIPIPO V A.
 PA (EISE) EISEN A.
 PA (GANG) GANGOLLI E A.
 PA (RIEG) RIEGER D K.
 PA (SPAD) SPADERNA S K.
 Best Local Similarity: 44.84% Mismatches: 90
 Query Match: 26.77% Indels: 12
 RESULT 1160
 ID AAV7494 standard; protein; 229 AA.
 DE Bovine trypsinogen.
 PN WO200005384-A1.
 PD 03-FEB-2000.
 PA (PROD-) PRODIGENE INC.
 Best Local Similarity: 46.29% Mismatches: 77
 Query Match: 26.72% Indels: 6
 RESULT 1161
 ID AAR51638 standard; protein; 230 AA.
 DE Bovine trypsinogen.
 PN EP597681-A1.
 PD 18-MAY-1994.
 PA (ELIL) LILLY & CO ELI.
 Best Local Similarity: 47.53% Mismatches: 73
 Query Match: 26.72% Indels: 6
 RESULT 1162
 ID AAY91926 standard; protein; 231 AA.
 DE Recombinant trypsin.
 PN WO200017332-A1.
 PD 30-MAR-2000.
 PA (ELIL) LILLY & CO ELI.
 Best Local Similarity: 46.29% Mismatches: 77
 Query Match: 26.72% Indels: 6
 RESULT 1163
 ID AAB80953 standard; protein; 231 AA.
 DE Bovine met-phe-trypsinogen.
 PN WO200119970-A2.
 PD 22-MAR-2001.
 PA (ELIL) LILLY & CO ELI.
 Best Local Similarity: 46.29% Mismatches: 77
 Query Match: 26.72% Indels: 6
 RESULT 1164
 ID ADA05732 standard; protein; 250 AA.
 DE Human NOV18a protein SEQ ID NO:92.
 PN WO2003029424-A2.
 PD 10-APR-2003.
 PA (CURA) CURAGEN CORP.
 Best Local Similarity: 44.84% Mismatches: 90
 Query Match: 26.72% Indels: 12
 RESULT 1165
 ID ABB84420 standard; peptide; 249 AA.
 DE Porcine SCCE protein N-terminal fragment SEQ ID 47.
 PN WO200262135-A2.
 PD 15-AUG-2002.
 PA (EGEL) EGELRUD T.
 PA (HANS) HANSSON L.
 Best Local Similarity: 45.35% Mismatches: 82
 Query Match: 26.67% Indels: 26
 RESULT 1166
 ID AAB35701 standard; protein; 247 AA.
 DE Human trypsin hL amino acid sequence.
 PN JP2000253887-A.
 PD 19-SEP-2000.
 PA (TTPH) TT PHARMA KK.
 Best Local Similarity: 44.05% Mismatches: 89
 Query Match: 26.60% Indels: 11
 RESULT 1167
 ID AAU86677 standard; protein; 247 AA.
 DE Novel human connective tissue related polypeptide #243.
 PN WO200155343-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 46.06% Mismatches: 92
 Query Match: 26.50% Indels: 15
 RESULT 1168
 ID AAU23752 standard; protein; 247 AA.
 DE Novel human enzyme polypeptide #838.
 PN WO200155301-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 46.06% Mismatches: 92
 Query Match: 26.50% Indels: 15
 RESULT 1169
 ID AAU17043 standard; protein; 247 AA.
 DE Human novel secreted protein, SEQ ID 284.
 PN WO200155441-A2.
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.			
Best Local Similarity:	46.06%	Mismatches:	92
Query Match:	26.50%	Indels:	15
RESULT 1170			
ID ADB60011 standard; protein; 247 AA.			
DE Connective tissue antigen (CTA) #243.			
FN US2003054375-A1.			
PD 20-MAR-2003.			
PA (HUMA-) HUMAN GENOME SCI INC.			
Best Local Similarity:	46.06%	Mismatches:	92
Query Match:	26.50%	Indels:	15
RESULT 1171			
ID AAW81767 standard; peptide; 223 AA.			
DE Bovine TRYP peptide fragment.			
FN JP10287696-A.			
PD 27-OCT-1998.			
PA (IYAK-) IYAKU BUNSHI SEKKEI KENKYUSHO KK.			
Best Local Similarity:	46.05%	Mismatches:	77
Query Match:	26.48%	Indels:	6
RESULT 1172			
ID AAI69973 standard; protein; 223 AA.			
DE TRYP protein.			
FN WO962004-A1.			
PD 02-DEC-1999.			
PA (MEDI-) INST MEDICINAL MOLECULAR DESIGN INC.			
Best Local Similarity:	46.05%	Mismatches:	77
Query Match:	26.48%	Indels:	6
RESULT 1173			
ID ABG31841 standard; protein; 223 AA.			
DE Example protein #3 used in three-dimensional structure analysis method.			
FN WO200257954-A1.			
PD 25-JUL-2002.			
PA (MITU) MITSUBISHI CHEM CORP.			
PA (UMEY/) UMEYAMA H.			
Best Local Similarity:	46.05%	Mismatches:	77
Query Match:	26.48%	Indels:	6
RESULT 1174			
ID ADC73287 standard; protein; 223 AA.			
DE Bovine pTPC E protein - SEQ ID 13.			
FN WO2003050755-A1.			
PD 24-JUL-2003.			
PA (AJIN) AJINOMOTO CO INC.			
PA (UMEY/) UMEYAMA H.			
Best Local Similarity:	46.05%	Mismatches:	77
Query Match:	26.48%	Indels:	6
RESULT 1175			
ID ADD35545 standard; protein; 223 AA.			
DE Cationic bovine trypsinogen TRY1.			
FN WO2003040093-A2.			
PD 15-MAY-2003.			
PA (FARB) BAYER AG.			
Best Local Similarity:	46.05%	Mismatches:	77
Query Match:	26.48%	Indels:	6
RESULT 1176			
ID AAR53637 standard; protein; 224 AA.			
DE Bovine trypsin.			
FN EP597681-A1.			
PD 18-MAY-1994.			
PA (ELIL) LILLY & CO ELI.			
Best Local Similarity:	46.05%	Mismatches:	77
Query Match:	26.48%	Indels:	6
RESULT 1177			
ID AAY91925 standard; protein; 233 AA.			
DE Trypsinogen analogue.			
FN WO200017332-A1.			
PD 30-MAR-2000.			
PA (ELIL) LILLY & CO ELI.			
Best Local Similarity:	46.05%	Mismatches:	77
Query Match:	26.48%	Indels:	6
RESULT 1178			
ID ADI39734 standard; protein; 244 AA.			
DE Human protease M (prom) protein.			
FN US6642013-B1.			

PD	04-NOV-2003.
PA	(UYAR-) UNIV ARKANSAS MEDICAL SCI.
Best Local Similarity:	45.83%
Query Match:	26.43%
RESULT 1179	
ID	ADI317158 standard; protein; 244 AA.
DE	Human protease m (Protm).
PN	US2003199010-A1.
PD	23-OCT-2003.
PA	(UYAR-) UNIV ARKANSAS.
Best Local Similarity:	45.83%
Query Match:	26.43%
RESULT 1180	
ID	RAY78974 standard; protein; 247 AA.
DE	Canine cationic trypsinogen amino acid sequence.
PN	WO200009739-A1.
PD	24-FEB-2000.
PA	(FUJY) FUJI YAKUHIN KOGYO KK.
Best Local Similarity:	45.56%
Query Match:	26.43%
RESULT 1181	
ID	ADA05742 standard; protein; 247 AA.
DE	Human NOVI8f protein SEQ ID NO:102.
PN	WO2003029424-A2.
PD	10-APR-2003.
PA	(CURA-) CURAGEN CORP.
Best Local Similarity:	45.45%
Query Match:	26.43%
RESULT 1182	
ID	ADN62906 standard; protein; 247 AA.
DE	Human NOVI8f.
PN	US2004038223-A1.
PD	26-FEB-2004.
PA	(SMIT/) SMITHSON G.
PA	(MILL/) MILLET I.
PA	(PEYN/) PEYMAN J A.
PA	(KEKU/) KEKUDA R.
PA	(JUJG/) JU J.
PA	(LILF/) LI L.
PA	(GUOX/) GUO X.
PA	(PATT/) PATTURAJAN M.
PA	(SPVT/) SPYTEK K.A.
PA	(EDIN/) EDINGER S.R.
PA	(ELLE/) ELLERMAN K.
PA	(NALY/) MALYANKAR U M.
PA	(ORTT/) ORT T.
PA	(GORM/) GORMAN L.
PA	(ZERH/) ZERHUSEN B D.
PA	(ANDE/) ANDERSON D W.
PA	(ZHON/) ZHONG M.
PA	(CAIT/) CATTERTON E.
PA	(JIWW/) JI W.
PA	(MILL/) MILLER C.E.
PA	(RAST/) RASTELLI L.
PA	(STON/) STONE D J.
PA	(PENB/) PENNA C E A.
PA	(SHEN/) SHENOY S.G.
PA	(SHIM/) SHIMKETS R A.
PA	(ROTH/) ROTHENBERG M E.
PA	(LEAC/) LEACH M D.
PA	(AGEE/) AGEER M L.
PA	(BERG/) BERGHS C.
PA	(DIPI/) DIPIPO V A.
PA	(EISE/) EISEN A.
PA	(GANG/) GANGOLLI E A.
PA	(RIEG/) RIEGER D K.
PA	(SPAD/) SPADERNA S K.
Best Local Similarity:	45.45%
Query Match:	26.43%
RESULT 1183	
ID	AAB98502 standard; protein; 225 AA.
DE	Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.
PN	WO200129056-A1.

PD 26-APR-2001.	PA (COLM/) COLMAN S D.		
PA (UYAR-) UNIV ARKANSAS.	PA (WOLE/) WOLENC A R.		
Best Local Similarity: 46.52%	PA (PENA/) PENA C E A.	Mismatches: 81	
Query Match: 26.38%	PA (FURT/) FURTAK K.	Indels: 8	
RESULT 1184	PA (GROS/) GROSSE W M.		
ID AAY78975 standard; protein; 246 AA.	PA (ALSO/) ALSOBROOK J P.		
DE Canine anionic trypsinogen amino acid sequence.	PA (LEFL/) LEFLEY D M.		
PD WO200009739-A1.	PA (RIEG/) RIEGER D K.		
PD 24-FEB-2000.	PA (BURG/) BURGESS C E.		
Best Local Similarity: 44.22%	Best Local Similarity: 44.35%	Mismatches: 103	
Query Match: 26.38%	Query Match: 26.11%	Indels: 5	
RESULT 1185	RESULT 1191		
ID AAB21326 standard; protein; 257 AA.	ID ABB78122 standard; peptide; 223 AA.		
DE Human HSCCE.	DE Amino acid sequence of trypsin.		
PD WO200053776-A2.	PN US2002072863-A1.		
PD 14-SEP-2000.	PD 13-JUN-2002.		
PA (MOUN) MOUNT SINAI HOSPITAL.	PA (FUJI) FUJITSU LTD.		
Best Local Similarity: 44.11%	Best Local Similarity: 45.61%	Mismatches: 78	
Query Match: 26.33%	Query Match: 26.04%	Indels: 6	
RESULT 1186	RESULT 1192		
ID AAW64260 standard; protein; 246 AA.	ID ABB83322 standard; protein; 223 AA.		
DE Human amyloid beta-protein precursor inhibitor.	DE Partial trypsin sequence.		
PD WO9824886-A1.	PN US2002035434-A1.		
PD 11-JUN-1998.	PD 21-MAR-2002.		
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.	PA (FUJI) FUJITSU LTD.		
Best Local Similarity: 44.53%	Best Local Similarity: 45.61%	Mismatches: 78	
Query Match: 26.28%	Query Match: 26.04%	Indels: 6	
RESULT 1187	RESULT 1193		
ID ADC73299 standard; protein; 220 AA.	ID ABB94419 standard; peptide; 243 AA.		
DE Stereostereorelated 2PTC_E protein.	DE Bovine SCCE protein N-terminal fragment SEQ ID 46.		
PD WO2003060765-A1.	PN WO200262135-A2.		
PD 24-JUL-2003.	PD 15-AUG-2002.		
PA (AJIN) AJINOMOTO CO INC.	PA (EGEL/) EGELRUD T.		
PA (UMEY/) UMEYAMA H.	PA (HANS/) HANSSON L.		
Best Local Similarity: 46.85%	Best Local Similarity: 43.70%	Mismatches: 83	
Query Match: 26.19%	Query Match: 25.82%	Indels: 23	
RESULT 1188	RESULT 1194		
ID ADC73301 standard; protein; 279 AA.	ID ABB04644 standard; protein; 240 AA.		
DE Stereostereorelated 2PTC protein.	DE Engraulis japonicus trypsinogen (atry I) SEQ ID NO:1.		
PD WO2003060765-A1.	PN JP2001269173-A.		
PD 24-JUL-2003.	PD 02-OCT-2001.		
PA (AJIN) AJINOMOTO CO INC.	PA (NISE) JAPAN TOBACCO INC.		
PA (UMEY/) UMEYAMA H.	Best Local Similarity: 45.71%	Mismatches: 87	
Best Local Similarity: 46.85%	Query Match: 25.41%	Indels: 10	
Query Match: 26.19%	RESULT 1195		
RESULT 1189	ID AAW64261 standard; protein; 232 AA.		
ID ADI16686 standard; protein; 259 AA.	DE Kallikrein substrate binding site.		
DE Human NOVX protein to treat human pathological conditions SeqID222.	PN WO9824886-A1.		
PD 06-SEP-2002.	PD 11-JUN-1998.		
PA (CURA) CURAGEN CORP.	PA (BGHM) BRIGHAM & WOMENS HOSPITAL.		
Best Local Similarity: 44.35%	Best Local Similarity: 43.64%	Mismatches: 79	
Query Match: 26.11%	Query Match: 25.36%	Indels: 14	
RESULT 1190	RESULT 1196		
ID ADN42340 standard; protein; 259 AA.	ID ABB94423 standard; peptide; 249 AA.		
DE Human novel proteinNOV 62.	DE Murine SCCE protein N-terminal fragment SEQ ID 50.		
PD US2004033493-A1.	PN WO200262135-A2.		
PD 19-FEB-2004.	PD 15-AUG-2002.		
PA (TCHE/) TCHERNEV V T.	PA (EGEL/) EGELRUD T.		
PA (SPYT/) SPYTEK K A.	PA (HANS/) HANSSON L.		
PA (ZERR/) ZERRHUSEN B D.	Best Local Similarity: 42.97%	Mismatches: 97	
PA (PATT/) PATTURAJAN M.	Query Match: 25.24%	Indels: 9	
PA (SHIM/) SHIMKETS R A.	RESULT 1197		
PA (LILL/) LI L.	ID ABR96164 standard; protein; 261 AA.		
PA (GANG/) GANGOLLI E A.	DE Human NOV13a protein SEQ ID NO:70.		
PA (PADI/) PADIGARU M.	PN WO200290568-A2.		
PA (ANDE/) ANDERSON D W.	PD 14-NOV-2002.		
PA (RAST/) RASTELLI L.	PA (CURA) CURAGEN CORP.		
PA (MILL/) MILLER C E.	Best Local Similarity: 40.00%	Mismatches: 91	
PA (GERL/) GERLACH V.	Query Match: 25.15%	Indels: 17	
PA (TAUP/) TAUFIER R J.	RESULT 1198		
PA (GUSE/) GUSEV V Y.	ID ADL15205 standard; protein; 232 AA.		
	DE Pancreatic kallikrein #1.		
	PN CN1384199-A.		

PD 11-DEC-2002.
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY. 73
Best Local Similarity: 44.54% Mismatches: 14
Query Match: 25.12% Indels: 14
RESULT 1199
ID AAW94493 standard; protein; 268 AA.
DE Human kallikrein.
PN WO9842849-A1.
PD 01-OCT-1998.
PA (INCY-) INCYTE PHARM INC. 95
Best Local Similarity: 42.42% Mismatches: 20
Query Match: 25.10% Indels: 20
RESULT 1200
ID ABG70276 standard; protein; 247 AA.
DE Human Serine Protease TLSP-like protein.
PN WO200255702-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP. 77
Best Local Similarity: 42.51% Mismatches: 36
Query Match: 24.98% Indels: 36
RESULT 1201
ID ADL27347 standard; peptide; 464 AA.
DE Amino acid sequence of trypsinogen-3aa-sp55.
PN WO2004019878-A2.
PD 11-MAR-2004.
PA (COMP-) COMPOUND THERAPEUTICS INC. 114
Best Local Similarity: 38.56% Mismatches: 34
Query Match: 24.54% Indels: 34
RESULT 1202
ID ABB04645 standard; protein; 241 AA.
DE Engraulis japonicus trypsinogen (stry II) SEQ ID NO:2.
PN JP2001269173-A.
PD 02-OCT-2001.
PA (NIBS) JAPAN TOBACCO INC. 92
Best Local Similarity: 45.87% Mismatches: 10
Query Match: 24.39% Indels: 10
RESULT 1203
ID AAU87693 standard; protein; 247 AA.
DE Human pancreatic tumour protein #5.
PN WO200212331-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP. 91
Best Local Similarity: 43.27% Mismatches: 10
Query Match: 24.25% Indels: 10
RESULT 1204
ID ADN04140 standard; protein; 247 AA.
DE Antipsoriatic protein sequence #265.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC. 91
Best Local Similarity: 43.27% Mismatches: 10
Query Match: 24.25% Indels: 10
RESULT 1205
ID ADN99594 standard; protein; 247 AA.
DE Novel human protein sequence #410.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC. 91
Best Local Similarity: 43.27% Mismatches: 10
Query Match: 24.25% Indels: 10
RESULT 1206
ID ADQ30589 standard; protein; 247 AA.
DE Pancreas cancer marker - trypsin II precursor.
PN WO2004055519-A2.
PD 01-JUL-2004.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F. 91
Best Local Similarity: 43.27% Mismatches: 10
Query Match: 24.25% Indels: 10
RESULT 1207
ID ABR41530 standard; protein; 261 AA.
DE Human DITP protein modification/maintenance protein.

PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC. 91
Best Local Similarity: 43.27% Mismatches: 10
Query Match: 24.25% Indels: 10
RESULT 1208
ID ADL27346 standard; peptide; 461 AA.
DE Amino acid sequence of trypsinogen-0aa-sp55.
PN WO2004019878-A2.
PD 11-MAR-2004.
PA (COMP-) COMPOUND THERAPEUTICS INC. 112
Best Local Similarity: 38.24% Mismatches: 37
Query Match: 24.23% Indels: 37
RESULT 1209
ID AAB03862 standard; protein; 223 AA.
DE Human neurosin amino acid sequence.
PN WO200031284-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD. 69
Best Local Similarity: 43.46% Mismatches: 36
Query Match: 24.20% Indels: 36
RESULT 1210
ID ADL27345 standard; peptide; 280 AA.
DE Amino acid sequence of trypsinogen.
PN WO2004019878-A2.
PD 11-MAR-2004.
PA (COMP-) COMPOUND THERAPEUTICS INC. 101
Best Local Similarity: 41.03% Mismatches: 24
Query Match: 24.15% Indels: 24
RESULT 1211
ID AAB21294 standard; protein; 254 AA.
DE Human KLK-L1 protein #2.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL. 87
Best Local Similarity: 43.10% Mismatches: 8
Query Match: 24.10% Indels: 8
RESULT 1212
ID AAM01174 standard; protein; 254 AA.
DE Human prostate-specific amino acid sequence P703P.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP. 87
Best Local Similarity: 43.10% Mismatches: 8
Query Match: 24.10% Indels: 8
RESULT 1213
ID AAU69819 standard; protein; 254 AA.
DE Human prostate cDNA encoded protein #27.
PN WO200173032-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP. 87
Best Local Similarity: 43.10% Mismatches: 8
Query Match: 24.10% Indels: 8
RESULT 1214
ID AAG99059 standard; protein; 254 AA.
DE Human prostate-specific amino acid of P703P.
PN WO200134802-A2.
PD 17-MAY-2001.
PA (CORI-) CORIXA CORP. 87
Best Local Similarity: 43.10% Mismatches: 8
Query Match: 24.10% Indels: 8
RESULT 1215
ID ABU71710 standard; protein; 254 AA.
DE Prostate cancer specific antigen P703P #7.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ) XU J. 87
Best Local Similarity: 43.10% Mismatches: 8
Query Match: 24.10% Indels: 8
RESULT 1216
ID ABR41530 standard; protein; 261 AA.
DE Human DITP protein modification/maintenance protein.

PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P D.
 PA (HOUG/) HOUGHTON R L.
 PA (DBAS/) Y DE BASSOLS C V.
 PA (FOYT/) FOY T M.
 Best Local Similarity: 43.10% Mismatches: 87
 Query Match: 24.10% Indels: 8

RESULT 1216
 ID ABB95279 standard; protein; 254 AA.
 DE Human P703P putative full length protein SEQ ID NO 525.
 PN US200202248-A1.
 PD 21-FEB-2002.
 PA (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 Best Local Similarity: 43.10% Mismatches: 87
 Query Match: 24.10% Indels: 8

RESULT 1217
 ID ABP54360 standard; protein; 254 AA.
 DE Human KLK4 protein SEQ ID NO:13.
 PN WO200277243-A1.
 PD 03-OCT-2002.
 PA (UYQU-) UNIV. QUEENSLAND TECHNOLOGY.
 Best Local Similarity: 43.10% Mismatches: 87
 Query Match: 24.10% Indels: 8

RESULT 1218
 ID ABP54357 standard; protein; 254 AA.
 DE Human KLK4 protein SEQ ID NO:6.
 PN WO200277243-A1.
 PD 03-OCT-2002.
 PA (UYQU-) UNIV. QUEENSLAND TECHNOLOGY.
 Best Local Similarity: 43.10% Mismatches: 87
 Query Match: 24.10% Indels: 8

RESULT 1219
 ID ABR54391 standard; protein; 254 AA.
 DE Prostate tumour specific protein sequence SEQ ID 525.
 PN WO200289747-A2.
 PD 14-NOV-2002.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 43.10% Mismatches: 87
 Query Match: 24.10% Indels: 8

RESULT 1220
 ID ADB13975 standard; protein; 254 AA.
 DE Human prostate specific protein P703P.
 PN US2003185830-A1.
 PD 02-OCT-2003.
 PA (CORI-) CORIXA CORP.

Best Local Similarity: 43.10% Mismatches: 87
 Query Match: 24.10% Indels: 8

RESULT 1221
 ID ADG26391 standard; protein; 254 AA.
 DE Human prostate-specific polypeptide #60.
 PN US2003157089-A1.
 PD 21-AUG-2003.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 43.10% Mismatches: 87
 Query Match: 24.10% Indels: 8

RESULT 1222
 ID AAB74830 standard; protein; 1079 AA.
 DE Prostate tumour antigen amino acid sequence for a fusion protein.
 PN WO200125272-A2.
 PD 12-APR-2001.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 43.10% Mismatches: 87
 Query Match: 24.10% Indels: 8

RESULT 1223
 ID ABU71860 standard; protein; 1079 AA.
 DE Prostate specific antigen fusion protein #2.
 PN US2002192763-A1.
 PD 19-DEC-2002.
 PA (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P D.
 PA (HOUG/) HOUGHTON R L.
 PA (DBAS/) Y DE BASSOLS C V.
 PA (FOYT/) FOY T M.
 Best Local Similarity: 43.10% Mismatches: 87
 Query Match: 24.10% Indels: 8

RESULT 1224
 ID ADI17268 standard; protein; 230 AA.
 DE Polypeptide homologous to a human NOVX domain SeqID 804.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 47.44% Mismatches: 73
 Query Match: 24.08% Indels: 17

RESULT 1225
 ID ADI17276 standard; protein; 230 AA.
 DE Polypeptide homologous to a human NOVX domain SeqID 812.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 47.44% Mismatches: 73
 Query Match: 24.08% Indels: 17

RESULT 1226
 ID ADJ83075 standard; protein; 230 AA.
 DE Trypsin-like serine protease protein - SEQ ID 66.
 PN US2003170630-A1.
 PD 11-SEP-2003.
 PA (ALSO/) ALSOBROOK J P.
 PA (TCHE/) TCHERNEV V T.
 PA (LIUX/) LIU X.
 PA (SPYT/) SPYTEK K A.
 PA (ZERH/) ZERHUSEN B D.

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PA (PATT//) PATTURAJAN M.
PA (LEPL//) LEFLEY D M.
PA (BURG//) BURGESS C E.
PA (SHIM//) SHIMKETS R A.
PA (GROS//) GROSSE W M.
PA (SZEK//) SZEKERES E S.
PA (VERN//) VERNET C A M.
PA (LILL//) LI L.
PA (CASW//) CASMAN S J.
PA (BOLD//) BOLDOG F L.
PA (GORM//) GORMAN L.
PA (GANG//) GANGOLLI E A.
PA (FERN//) FERNANDES E R.
PA (RIEG//) RIEGER D K.
PA (EDIN//) EDINGER S R.
PA (GUNT//) GUNTHER E.
PA (MILL//) MILLET I.
PA (SCIO//) SCIORE P.
PA (ELLE//) ELLERMAN K.
PA (MACD//) MACDOUGALL J R.
PA (SMIT//) SMITHSON G.
PA (SMIT//) SMITHSON G.
Best Local Similarity: 47.44% Mismatches: 73
Query Match: 24.08% Indels: 17
RESULT 1227
ID ADL27348 standard; peptide; 485 AA.
DE Amino acid sequence of trypsinogen-20aa-sp55.
PN WO2004019878-A2.
PD 11-WAR-2004.
PA (COMP-) COMPOUND THERAPEUTICS INC.
PA (AFEY//) AFEYAN N B.
Best Local Similarity: 42.74% Mismatches: 96
Query Match: 24.08% Indels: 11
RESULT 1228
ID AAB21307 standard; protein; 249 AA.
DE Human prostate.
PN WO2000053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 43.10% Mismatches: 87
Query Match: 24.08% Indels: 8
RESULT 1229
ID AAB21320 standard; protein; 254 AA.
DE Human prostate.
PN WO2000053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 43.10% Mismatches: 87
Query Match: 24.06% Indels: 8
RESULT 1230
ID AAV72525 standard; protein; 254 AA.
DE Human prostate antigen #3.
PN WO200104143-A2.
PD 18-JAN-2001.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.10% Mismatches: 87
Query Match: 24.06% Indels: 8
RESULT 1231
ID AAU74901 standard; protein; 254 AA.
DE Protein sequence of prostate homologue #3.
PN WO200200708-A2.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Best Local Similarity: 43.10% Mismatches: 87
Query Match: 24.06% Indels: 8
RESULT 1232
ID AAU74932 standard; protein; 254 AA.
DE Amino acid sequence of prostate protein fragment #3.
PN WO200200867-A1.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Best Local Similarity: 43.10% Mismatches: 87
Query Match: 24.06% Indels: 8
RESULT 1233
ID AAW60592 standard; protein; 248 AA.
DE Human prostate-specific kallikrein (HPSK) protein.
PN WO9820117-A1.
PD 14-MAY-1998.
PA (INCY-) INCYTE PHARM INC.
PA (INCY-) INCYTE PHARM INC.
Best Local Similarity: 43.44% Mismatches: 84
Query Match: 24.03% Indels: 13
RESULT 1234
ID AAY72524 standard; protein; 248 AA.
DE Human prostate antigen #2.
PN WO200104143-A2.
PD 18-JAN-2001.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.44% Mismatches: 84
Query Match: 24.03% Indels: 13
RESULT 1235
ID AAU74770 standard; protein; 248 AA.
DE Protein sequence of prostate homologue #2.
PN WO200200708-A2.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Best Local Similarity: 43.44% Mismatches: 84
Query Match: 24.03% Indels: 13
RESULT 1236
ID AAU74931 standard; protein; 248 AA.
DE Amino acid sequence of prostate protein fragment #2.
PN WO200200867-A1.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Best Local Similarity: 43.44% Mismatches: 84
Query Match: 24.03% Indels: 13
RESULT 1237
ID ABU71889 standard; protein; 585 AA.
DE Prostate cancer specific antigen fusion protein #3.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJJ//) XU J.
PA (DILL//) DILLON D C.
PA (MITC//) MITCHAM J L.
PA (HARL//) HARLOCKER S L.
PA (JIAN//) JIANG Y.
PA (KALO//) KALOS M D.
PA (FANG//) FANGER G R.
PA (RETT//) RETTER M W.
PA (STOL//) STOLK J A.
PA (DAYC//) DAY C H.
PA (VEDV//) VEDVICK T S.
PA (CART//) CARTER D.
PA (LISX//) LI S X.
PA (WANG//) WANG A.
PA (SKEI//) SKEIKY Y A W.
PA (HEPL//) HEPLER W T.
PA (HEND//) HENDERSON R A.
PA (HURA//) HURAL J.
PA (MCNE//) MCNEILL P D.
PA (HOUG//) HOUGHTON R L.
PA (DBAS//) Y DE BASSOLS C V.
PA (FOYT//) FOY T M.
Best Local Similarity: 40.14% Mismatches: 110
Query Match: 24.03% Indels: 17
RESULT 1238
ID ABR54580 standard; protein; 585 AA.
DE Prostate tumour-related protein SEQ ID 1020.
PN WO200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 40.14% Mismatches: 110
Query Match: 24.03% Indels: 17
RESULT 1239
ID ADB14470 standard; protein; 585 AA.
DE FOPF/hFAP fusion protein, FOPF3.

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PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 40.14% Mismatches: 110
Query Match: 24.03% Indels: 17
RESULT 1240
ID ADG26993 standard; protein; 585 AA.
DE Human prostate-specific polypeptide #249.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 40.14% Mismatches: 110
Query Match: 24.03% Indels: 17
RESULT 1241
ID ABG76997 standard; protein; 262 AA.
DE Human kallikrein protein variant #1.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUIL/) HUI L.
Best Local Similarity: 40.38% Mismatches: 99
Query Match: 23.96% Indels: 18
RESULT 1242
ID ADR90673 standard; protein; 246 AA.
DE Human trypsinogen partial protein.
PN WO2004078777-A2.
PD 16-SEP-2004.
PA (BIOR-) BIOREXIS PHARM CORP.
Best Local Similarity: 41.94% Mismatches: 97
Query Match: 23.94% Indels: 11
RESULT 1243
ID AAB21321 standard; protein; 247 AA.
DE Human trypsinogen.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN ) MOUNT SINAI HOSPITAL.
Best Local Similarity: 41.94% Mismatches: 97
Query Match: 23.94% Indels: 11
RESULT 1244
ID ABR54239 standard; protein; 247 AA.
DE Human NOV35a protein SEQ ID NO:146.
PN WO2003023001-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 41.94% Mismatches: 97
Query Match: 23.94% Indels: 11
RESULT 1245
ID ABR54241 standard; protein; 247 AA.
DE Human NOV35c protein SEQ ID NO:150.
PN WO2003023001-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 41.94% Mismatches: 97
Query Match: 23.94% Indels: 11
RESULT 1246
ID ADQ30588 standard; protein; 247 AA.
DE Pancreas cancer marker - trypsin I precursor.
PN WO2004055519-A2.
PD 01-JUL-2004.
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.
Best Local Similarity: 41.94% Mismatches: 97
Query Match: 23.94% Indels: 11
RESULT 1247
ID AAM01173 standard; protein; 254 AA.
DE Human prostate-specific amino acid mature form of P703P.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 42.68% Mismatches: 88
Query Match: 23.91% Indels: 8
RESULT 1248
ID ABR54390 standard; protein; 254 AA.
DE Prostate tumour specific protein sequence SEQ ID 523.
PN WO200289747-A2.
PD 14-NOV-2002.
ID AAG99058 standard; protein; 254 AA.
DE Human prostate-specific mature protein of P703P.
PN WO200134802-A2.
PD 17-MAY-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 42.68% Mismatches: 88
Query Match: 23.91% Indels: 8
RESULT 1249
ID ABU71709 standard; protein; 254 AA.
DE Prostate cancer associated protein #12.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISK/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DEAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Best Local Similarity: 42.68% Mismatches: 88
Query Match: 23.91% Indels: 8
RESULT 1251
ID ABB95278 standard; protein; 254 AA.
DE Human P703P mature protein SEQ ID NO 523.
PN US2002022248-A1.
PD 21-FEB-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISK/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
Best Local Similarity: 42.68% Mismatches: 88
Query Match: 23.91% Indels: 8
RESULT 1252
ID ABR54390 standard; protein; 254 AA.
DE Prostate tumour specific protein sequence SEQ ID 523.
PN WO200289747-A2.
PD 14-NOV-2002.
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PA (CORI-) CORIXA CORP.
 Best Local Similarity: 42.68% Mismatches: 88
 Query Match: 23.91% Indels: 8
 RESULT 1253
 ID ADB13973 standard; protein; 254 AA.
 DE Human mature prostate specific protein P703P.
 PN US2003185830-A1.
 PD 02-OCT-2003.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 42.68% Mismatches: 88
 Query Match: 23.91% Indels: 8
 RESULT 1254
 ID ADG26389 standard; protein; 254 AA.
 DE Human prostate-specific polypeptide #59.
 PN US2003157089-A1.
 PD 21-AUG-2003.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 42.68% Mismatches: 88
 Query Match: 23.91% Indels: 8
 RESULT 1255
 ID AAB21319 standard; protein; 262 AA.
 DE Human KLK2.
 PN WO200053776-A2.
 PD 14-SEP-2000.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Best Local Similarity: 40.38% Mismatches: 99
 Query Match: 23.91% Indels: 18
 RESULT 1256
 ID ABG76996 standard; protein; 262 AA.
 DE Human kallikrein protein.
 PN WO200261131-A2.
 PD 08-AUG-2002.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA (TSUC) TSUCHIHASHI Z.
 PA (HUIL) HUI L.
 Best Local Similarity: 40.38% Mismatches: 99
 Query Match: 23.91% Indels: 18
 RESULT 1257
 ID ADL15197 standard; protein; 262 AA.
 DE Human pancreatic kallikrein.
 PN CN1384199-A.
 PD 11-DEC-2002.
 PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.
 Best Local Similarity: 40.38% Mismatches: 99
 Query Match: 23.91% Indels: 18
 RESULT 1258
 ID ADL64969 standard; protein; 262 AA.
 DE Human kallikrein protein (KLK1).
 PN US2004033582-A1.
 PD 19-FEB-2004.
 PA (EDMO) EDMONDS M.
 PA (HUIL) HUI L.
 PA (PERR) PERRONE M.
 PA (POWE) POWELL J R.
 PA (RAWA) RAVANATHAN C S.
 PA (SWAN) SWANSON B.
 PA (TSUC) TSUCHIHASHI Z.
 PA (ZERR) ZERBA K.
 Best Local Similarity: 40.38% Mismatches: 99
 Query Match: 23.91% Indels: 18
 RESULT 1259
 ID ADQ39654 standard; protein; 262 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1317.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Best Local Similarity: 40.38% Mismatches: 99
 Query Match: 23.91% Indels: 18
 RESULT 1260
 ID ADS34891 standard; protein; 262 AA.
 DE Human autoimmune disease-related protein - SEQ ID 105.
 PN WO2004083403-A2.
 PD 30-SEP-2004.

PA (APPL-) APPLERA CORP.
 Best Local Similarity: 40.38% Mismatches: 99
 Query Match: 23.91% Indels: 18
 RESULT 1261
 ID ABR54277 standard; protein; 240 AA.
 DE Human trypsinogen protein SEQ ID NO:341.
 PN WO2003023001-A2.
 PD 20-MAR-2003.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 42.56% Mismatches: 93
 Query Match: 23.89% Indels: 11
 RESULT 1262
 ID AAB21316 standard; protein; 241 AA.
 DE Human trypsinogen.
 PN WO200053776-A2.
 PD 14-SEP-2000.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Best Local Similarity: 42.56% Mismatches: 93
 Query Match: 23.89% Indels: 11
 RESULT 1263
 ID ADN04297 standard; protein; 247 AA.
 DE Antipsoriatic protein sequence #343.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 42.15% Mismatches: 89
 Query Match: 23.86% Indels: 10
 RESULT 1264
 ID AAB21308 standard; protein; 253 AA.
 DE Human EMSP.
 PN WO200053776-A2.
 PD 14-SEP-2000.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Best Local Similarity: 42.80% Mismatches: 85
 Query Match: 23.86% Indels: 12
 RESULT 1265
 ID AAB21324 standard; protein; 258 AA.
 DE Human EMSP.
 PN WO200053776-A2.
 PD 14-SEP-2000.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Best Local Similarity: 42.80% Mismatches: 85
 Query Match: 23.86% Indels: 12
 RESULT 1266
 ID AAW71005 standard; protein; 262 AA.
 DE Human prostate-associated kallikrein designated HPAK.
 PN WO9832865-A1.
 PD 30-JUL-1998.
 PA (INCY) INCYTE PHARM INC.
 Best Local Similarity: 40.38% Mismatches: 100
 Query Match: 23.86% Indels: 18
 RESULT 1267
 ID ABP74711 standard; protein; 262 AA.
 DE Human glandular kallikrein 1 precursor protein SEQ ID NO:600.
 PN WO200281646-A2.
 PD 17-OCT-2002.
 PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
 Best Local Similarity: 40.38% Mismatches: 100
 Query Match: 23.86% Indels: 18
 RESULT 1268
 ID ADL15204 standard; protein; 262 AA.
 DE Pancreatic kallikrein #1.
 PN CN1384199-A.
 PD 11-DEC-2002.
 PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.
 Best Local Similarity: 40.38% Mismatches: 100
 Query Match: 23.86% Indels: 18
 RESULT 1269
 ID ADM72846 standard; protein; 263 AA.
 DE Human glandular kallikrein 1 protein SEQ ID NO:105.
 PN WO2004022709-A2.
 PD 18-NAR-2004.
 PA (MANN-) MANNKIND CORP.

Best Local Similarity: 40.38% Mismatches: 100
 Query Match: 23.86% Indels: 18
 RESULT 1270
 ID AAB98503 standard; protein; 225 AA.
 DE Human trypsin serine protease catalytic domain.
 PN WO200129056-A1.
 PD 26-APR-2001.
 PA (UYAR-) UNIV ARKANSAS.
 Best Local Similarity: 43.67% Mismatches: 89
 Query Match: 23.81% Indels: 6
 RESULT 1271
 ID AAW93488 standard; protein; 230 AA.
 DE Human TRYI trypsinogen variant protein.
 PN WO9910503-A1.
 PD 04-MAR-1999.
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 Best Local Similarity: 43.67% Mismatches: 89
 Query Match: 23.81% Indels: 6
 RESULT 1272
 ID AAB21315 standard; protein; 256 AA.
 DE Human KUK1.
 PN WO200053776-A2.
 PD 14-SEP-2000.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Best Local Similarity: 41.11% Mismatches: 94
 Query Match: 23.81% Indels: 18
 RESULT 1273
 ID AAP95121 standard; protein; 262 AA.
 DE Kallikrein encoded by clone lambda HK65a.
 PN EP297913-A.
 PD 04-JAN-1989.
 PA (AMGE-) AMGEN.
 Best Local Similarity: 40.38% Mismatches: 100
 Query Match: 23.81% Indels: 18
 RESULT 1274
 ID ABG76998 standard; protein; 262 AA.
 DE Human kallikrein protein variant #2.
 PN WO200261131-A2.
 PD 08-AUG-2002.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (HUIL/) HUI L.
 Best Local Similarity: 40.38% Mismatches: 100
 Query Match: 23.81% Indels: 18
 RESULT 1275
 ID AAB54293 standard; protein; 267 AA.
 DE Human pancreatic cancer antigen protein sequence SEQ ID NO:745.
 PN WO200055320-A1.
 PD 21-SEP-2000.
 PA (HUNA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 40.38% Mismatches: 100
 Query Match: 23.81% Indels: 18
 RESULT 1276
 ID ABG77002 standard; protein; 262 AA.
 DE Human kallikrein 1 polymorphic sequence.
 PN WO200261131-A2.
 PD 08-AUG-2002.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (HUIL/) HUI L.
 Best Local Similarity: 40.38% Mismatches: 100
 Query Match: 23.77% Indels: 18
 RESULT 1277
 ID ADA05744 standard; protein; 224 AA.
 DE Human NOV18g; protein SEQ ID NO:104.
 PN WO2003029424-A2.
 PD 10-APR-2003.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 45.29% Mismatches: 75
 Query Match: 23.72% Indels: 16
 RESULT 1278
 ID ADN62908 standard; protein; 224 AA.
 DE Human NOV18g.

PN US2004038223-A1.
 PD 26-FEB-2004.
 PA (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUJ/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATT/) PATTURAJAN M.
 PA (SPVT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERR/) ZERHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIWW/) JI W.
 PA (MILL/) MILLER C E.
 PA (STON/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENA/) PENNA C E A.
 PA (SHEN/) SHENOY S G.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.
 PA (AGEE/) AGEE M L.
 PA (BERG/) BERGHS C.
 PA (DIFI/) DIPPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 Best Local Similarity: 45.29% Mismatches: 75
 Query Match: 23.72% Indels: 16
 RESULT 1279
 ID AAE00397 standard; protein; 234 AA.
 DE Human serine protease, PROST 07.
 PN WO200125446-A1.
 PD 12-APR-2001.
 PA (SCHD) SCHERING AG.
 Best Local Similarity: 43.04% Mismatches: 85
 Query Match: 23.69% Indels: 7
 RESULT 1280
 ID ABM3250 standard; protein; 333 AA.
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:3499.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Best Local Similarity: 40.00% Mismatches: 106
 Query Match: 23.67% Indels: 19
 RESULT 1281
 ID ABU71888 standard; protein; 585 AA.
 DE Prostate cancer associated protein #72.
 PN US2002192763-A1.
 PD 19-DEC-2002.
 PA (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.

PA (SKEI/) SKEIKY Y A W. 96
 PA (HEPL/) HEPLER W T. 44
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J. P D.
 PA (MCNE/) MCNEILL P D.
 PA (HOUG/) HOUGHTON R L.
 PA (DBAS/) Y DE BASSOLS C V.
 PA (FOVT/) FOY T M.
 Best Local Similarity: 37.24% Mismatches: 96
 Indels: 44
 Query Match:
 RESULT 1282
 ID AAY25510 standard; protein; 231 AA.
 DE Human prostate serine protease protein.
 PN EP936270-A2.
 PD 18-AUG-1999.
 PA (BADI) BASF AG.
 Best Local Similarity: 43.99% Mismatches: 80
 Indels: 7
 Query Match:
 RESULT 1283
 ID ABR96163 standard; protein; 274 AA.
 DE Human NOV12a protein SEQ ID NO:68.
 PN WO200290568-A2.
 PD 14-NOV-2002.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 40.82% Mismatches: 101
 Indels: 18
 Query Match:
 RESULT 1284
 ID ADN04726 standard; protein; 247 AA.
 DE Antipsoriatic protein sequence #544.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 42.32% Mismatches: 92
 Indels: 10
 Query Match:
 RESULT 1285
 ID ADN99593 standard; protein; 247 AA.
 DE Novel human protein sequence #409.
 PN WO2004038003-A2.
 PD 06-MAY-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Best Local Similarity: 42.32% Mismatches: 92
 Indels: 10
 Query Match:
 RESULT 1286
 ID AAM01227 standard; protein; 449 AA.
 DE P703P and PSA fusion amino acid sequence.
 PN WO200151633-A2.
 PD 19-JUL-2001.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 44.14% Mismatches: 80
 Indels: 7
 Query Match:
 RESULT 1287
 ID AAU69872 standard; protein; 449 AA.
 DE Human prostate serum antigen/P703P fusion protein.
 PN WO200173032-A2.
 PD 04-OCT-2001.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 44.14% Mismatches: 80
 Indels: 7
 Query Match:
 RESULT 1288
 ID ABU71763 standard; protein; 449 AA.
 DE Prostate cancer specific antigen fusion protein #1.
 PN US2002192763-A1.
 PD 19-DEC-2002.
 PA (XUJJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.

PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P D.
 PA (HOUG/) HOUGHTON R L.
 PA (DBAS/) Y DE BASSOLS C V.
 PA (FOVT/) FOY T M.
 Best Local Similarity: 44.14% Mismatches: 80
 Indels: 7
 Query Match:
 RESULT 1289
 ID ABR95332 standard; protein; 449 AA.
 DE Human P703P/PSA fusion protein SEQ ID NO 617.
 PN US2002022448-A1.
 PD 21-FEB-2002.
 PA (XUJJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 Best Local Similarity: 44.14% Mismatches: 80
 Indels: 7
 Query Match:
 RESULT 1290
 ID ABR54444 standard; protein; 449 AA.
 DE Prostate tumour specific protein sequence SEQ ID 617.
 PN WO200289747-A2.
 PD 14-NOV-2002.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 44.14% Mismatches: 80
 Indels: 7
 Query Match:
 RESULT 1291
 ID ADB14067 standard; protein; 449 AA.
 DE Human prostate specific protein P703P/PSA fusion protein.
 PN US2003185830-A1.
 PD 02-OCT-2003.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 44.14% Mismatches: 80
 Indels: 7
 Query Match:
 RESULT 1292
 ID ADG26483 standard; protein; 449 AA.
 DE Human prostate-specific polypeptide #113.
 PN US2003157089-A1.
 PD 21-AUG-2003.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 44.14% Mismatches: 80
 Indels: 7
 Query Match:
 RESULT 1293
 ID ABU71890 standard; protein; 801 AA.
 DE Prostate cancer specific antigen fusion protein #4.
 PN US2002192763-A1.
 PD 19-DEC-2002.
 PA (XUJJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.

PA (FANG/) FANGER G R.	Query Match:	23.28%	Indels:	18
PA (RETT/) RETTER M W.	RESULT 1301			
PA (STOL/) STOLK J A.	ID AAY72522 standard; protein; 312 AA.			
PA (DAYC/) DAY C H.	DE NS1-P703P-His fusion protein.			
PA (VEDV/) VEDVICK T S.	PN WO200104143-A2.			
PA (CART/) CARTER D.	PD 18-JAN-2001.			
PA (LISX/) LI S X.	PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.			
PA (WANG/) WANG A.	PA (CORI-) CORIXA CORP.			
PA (SKEI/) SKEIKY Y A W.	Best Local Similarity: 42.49%	Mismatches:	82	
PA (HEPL/) HEPLER W T.	Query Match:	23.18%	Indels:	12
PA (HEND/) HENDERSON R A.	RESULT 1302			
PA (HURA/) HURAL J. P D.	ID AAU74768 standard; protein; 312 AA.			
PA (MCNE/) MCNEILL P D.	DE Amino acid sequence of wild-type NS1-P703-His fusion protein.			
PA (HOUG/) HOUGHTON R L.	PN WO200200708-A2.			
PA (DBAS/) Y DE BASSOLS C V.	PD 03-JAN-2002.			
PA (FOYT/) FOY T M.	PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.			
Best Local Similarity: 44.14%	Query Match:	23.18%	Mismatches:	82
Query Match:			Indels:	12
RESULT 1294				
ID AAY31160 standard; protein; 224 AA.				
DE Human trypsin serine protease protein domain.				
PN US5948892-A.				
PD 07-SEP-1999.				
PA (AMGE-) AMGEN INC.				
Best Local Similarity: 43.42%	Mismatches:	89		
Query Match:	Indels:	6		
RESULT 1295				
ID ADL15207 standard; protein; 261 AA.				
DE Pancreatic kallikrein #3.				
PN CN1384199-A.				
PD 11-DEC-2002.				
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.				
Best Local Similarity: 40.23%	Mismatches:	96		
Query Match:	Indels:	19		
RESULT 1296				
ID ABM83249 standard; protein; 261 AA.				
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3498.				
PN WO2004023973-A2.				
PD 25-MAR-2004.				
PA (INCY-) INCYTE CORP.				
Best Local Similarity: 43.50%	Mismatches:	82		
Query Match:	Indels:	6		
RESULT 1297				
ID AAW57740 standard; protein; 240 AA.				
DE Trypsinogen-like protein.				
PN JP10099080-A.				
PD 21-APR-1998.				
PA (SHIS) SHISSIDO CO LTD.				
Best Local Similarity: 42.49%	Mismatches:	84		
Query Match:	Indels:	11		
RESULT 1298				
ID ADL15206 standard; protein; 260 AA.				
DE Pancreatic kallikrein #2.				
PN CN1384199-A.				
PD 11-DEC-2002.				
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.				
Best Local Similarity: 39.77%	Mismatches:	98		
Query Match:	Indels:	16		
RESULT 1299				
ID AAB21293 standard; protein; 237 AA.				
DE Human KUK-L1 protein #1.				
PN WO200053776-A2.				
PD 14-SEP-2000.				
PA (MOUN) MOUNT SINAI HOSPITAL.				
Best Local Similarity: 42.24%	Mismatches:	89		
Query Match:	Indels:	7		
RESULT 1300				
ID AAP70568 standard; protein; 262 AA.				
DE Human kallikrein-like substance has hypotensive activity.				
PN JP62126980-A.				
PD 09-JUN-1987.				
PA (NAKA/) NAKANISHI S.				
Best Local Similarity: 40.00%	Mismatches:	101		
Query Match:				
RESULT 1301				
ID AAY72522 standard; protein; 312 AA.				
DE NS1-P703P-His fusion protein.				
PN WO200104143-A2.				
PD 18-JAN-2001.				
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.				
PA (CORI-) CORIXA CORP.				
Best Local Similarity: 42.49%	Mismatches:	82		
Query Match:	Indels:	12		
RESULT 1302				
ID AAU74768 standard; protein; 312 AA.				
DE Amino acid sequence of wild-type NS1-P703-His fusion protein.				
PN WO200200708-A2.				
PD 03-JAN-2002.				
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.				
Best Local Similarity: 42.49%	Mismatches:	82		
Query Match:	Indels:	12		
RESULT 1303				
ID AAB08449 standard; protein; 375 AA.				
DE A human prostate specific antigen variant polypeptide.				
PN WO200049158-A2.				
PD 24-AUG-2000.				
PA (COMP-) COMPUGEN LTD.				
Best Local Similarity: 37.42%	Mismatches:	111		
Query Match:	Indels:	46		
RESULT 1304				
ID AAU01290 standard; protein; 216 AA.				
DE Human serine protease HETAA37p.				
PN WO200123587-A2.				
PD 05-APR-2001.				
PA (SMIK) SMITHKLINE BEECHAM PLC.				
Best Local Similarity: 44.34%	Mismatches:	82		
Query Match:	Indels:	7		
RESULT 1305				
ID AAY72526 standard; protein; 226 AA.				
DE Human prostate antigen P703PDE5 sequence.				
PN WO200104143-A2.				
PD 18-JAN-2001.				
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.				
PA (CORI-) CORIXA CORP.				
Best Local Similarity: 43.84%	Mismatches:	79		
Query Match:	Indels:	7		
RESULT 1306				
ID AAU74902 standard; protein; 226 AA.				
DE Protein sequence of prostate homologue #4.				
PN WO200200708-A2.				
PD 03-JAN-2002.				
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.				
Best Local Similarity: 43.84%	Mismatches:	79		
Query Match:	Indels:	7		
RESULT 1307				
ID AAU74933 standard; protein; 226 AA.				
DE Amino acid sequence of prostate protein fragment #4.				
PN WO200200867-A1.				
PD 03-JAN-2002.				
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.				
Best Local Similarity: 43.84%	Mismatches:	79		
Query Match:	Indels:	7		
RESULT 1308				
ID ABU71886 standard; protein; 344 AA.				
DE Human prostate specific antigen (PSA) epitope #26.				
PN US2002192763-A1.				
PD 19-DEC-2002.				
PA (XUJ/) XU J.				

PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISK/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P D.
 PA (HOUG/) HOUGHTON R L.
 PA (DBAS/) Y DE BASSOLS C V.
 PA (FOYT/) FOY T M.
 Best Local Similarity: 43.84% Mismatches: 79
 Query Match: 23.11% Indels: 7
 RESULT 1310
 ID ABM82601 standard; protein; 239 AA.
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:2850.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Best Local Similarity: 40.08% Mismatches: 72
 Query Match: 23.02% Indels: 55
 RESULT 1311
 ID ABM82602 standard; protein; 239 AA.
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:2851.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Best Local Similarity: 40.08% Mismatches: 72
 Query Match: 23.02% Indels: 55
 RESULT 1312
 ID ABM82603 standard; protein; 239 AA.
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:2852.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Best Local Similarity: 40.08% Mismatches: 72
 Query Match: 23.02% Indels: 55
 RESULT 1313
 ID ADN99649 standard; protein; 280 AA.
 DE Novel human protein sequence #465.
 PN WO2004038003-A2.
 PD 06-MAY-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Best Local Similarity: 37.72% Mismatches: 96
 Query Match: 22.89% Indels: 44
 RESULT 1314
 ID RAY82008 standard; protein; 220 AA.
 DE Human immunogenic prostate tumour protein sequence SEQ ID NO:327.
 PN WO200004149-A2.
 PD 27-JAN-2000.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 43.78% Mismatches: 78
 Query Match: 22.87% Indels: 7
 RESULT 1315
 ID AAW01123 standard; protein; 220 AA.
 DE Human prostate-specific amino acid sequence P703PDE6.
 PN WO200151633-A2.
 PD 19-JUL-2001.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 43.78% Mismatches: 78
 Query Match: 22.87% Indels: 7
 RESULT 1316
 ID AAU69768 standard; protein; 220 AA.

DE Human prostate cDNA encoded protein #8.
 PN WO200173032-A2.
 PD 04-OCT-2001.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 43.78% Mismatches: 78
 Query Match: 22.87% Indels: 7
 RESULT 1317
 ID AAB74806 standard; protein; 220 AA.
 DE Prostate tumour antigen predicted amino acid sequence for P703PDES.
 PN WO200125272-A2.
 PD 12-APR-2001.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 43.78% Mismatches: 78
 Query Match: 22.87% Indels: 7
 RESULT 1318
 ID AAG99008 standard; protein; 220 AA.
 DE Human prostate-specific amino acid sequence P703PDES.
 PN WO200134802-A2.
 PD 17-MAY-2001.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 43.78% Mismatches: 78
 Query Match: 22.87% Indels: 7
 RESULT 1319
 ID AAG62147 standard; protein; 220 AA.
 DE Human P703P inventive antigen SEQ ID NO: 330.
 PN WO200125273-A2.
 PD 12-APR-2001.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 43.78% Mismatches: 78
 Query Match: 22.87% Indels: 7
 RESULT 1320
 ID ABU71659 standard; protein; 220 AA.
 DE Prostate cancer specific antigen P703P #4.
 PN US2002192763-A1.
 PD 19-DEC-2002.
 PA (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISK/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P D.
 PA (HOUG/) HOUGHTON R L.
 PA (DBAS/) Y DE BASSOLS C V.
 PA (FOYT/) FOY T M.
 Best Local Similarity: 43.78% Mismatches: 78
 Query Match: 22.87% Indels: 7
 RESULT 1321
 ID ABB95228 standard; protein; 220 AA.
 DE Human P703PDES protein SEQ ID NO 327.
 PN US2002022248-A1.
 PD 21-FEB-2002.
 PA (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.

PA (DAYC/) DAY C H.	22.77%	Indels: 13
PA (VEDV/) VEDVICK T S.		
PA (CART/) CARTER D.		
PA (LISX/) LI S X.		
PA (WANG/) WANG A.		
PA (SKEI/) SKEIKY Y A W.		
PA (HEPL/) HEPLER W T.		
PA (HEND/) HENDERSON R A.		
Best Local Similarity: 43.78%		
Query Match: 22.87%		
Mismatches: 78		
Indels: 7		
RESULT 1322		
ID ABR54340 standard; protein; 220 AA.		
DE Prostate tumour specific protein sequence SEQ ID 327.		
PN WO200289747-A2.		
PD 14-NOV-2002.		
PA (CORI-) CORIXA CORP.		
Best Local Similarity: 43.78%		
Query Match: 22.87%		
Mismatches: 78		
Indels: 7		
RESULT 1323		
ID ADB13777 standard; protein; 220 AA.		
DE Human prostate specific protein P703PDB5.		
PN US2003185830-A1.		
PD 02-OCT-2003.		
PA (CORI-) CORIXA CORP.		
Best Local Similarity: 43.78%		
Query Match: 22.87%		
Mismatches: 78		
Indels: 7		
RESULT 1324		
ID ADG26193 standard; protein; 220 AA.		
DE Human prostate-specific polypeptide #9.		
PN US2003157089-A1.		
PD 21-AUG-2003.		
PA (CORI-) CORIXA CORP.		
Best Local Similarity: 43.78%		
Query Match: 22.87%		
Mismatches: 78		
Indels: 7		
RESULT 1325		
ID ADI3732 standard; protein; 262 AA.		
DE Human glandular kallikrein (HK2) protein.		
PN US6642013-B1.		
PD 04-NOV-2003.		
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.		
Best Local Similarity: 38.93%		
Query Match: 22.87%		
Mismatches: 102		
Indels: 19		
RESULT 1326		
ID ADI37156 standard; protein; 262 AA.		
DE Human glandular kallikrein (hHK2) protein.		
PN US2003199010-A1.		
PD 23-OCT-2003.		
PA (UYAR-) UNIV ARKANSAS.		
Best Local Similarity: 38.93%		
Query Match: 22.87%		
Mismatches: 102		
Indels: 19		
RESULT 1327		
ID AAP92314 standard; protein; 245 AA.		
DE Human recombinant kallikrein gene.		
PN EP297913-A.		
PD 04-JAN-1989.		
PA (AMGE-) AMGEN.		
Best Local Similarity: 40.17%		
Query Match: 22.80%		
Mismatches: 97		
Indels: 12		
RESULT 1328		
ID AAB21313 standard; protein; 255 AA.		
DE Human PSA.		
PN WO200053776-A2.		
PD 14-SEP-2000.		
PA (MOUN) MOUNT SINAI HOSPITAL.		
Best Local Similarity: 40.40%		
Query Match: 22.77%		
Mismatches: 103		
Indels: 13		
RESULT 1329		
ID AAU06276 standard; protein; 257 AA.		
DE Prostate specific Antigen (PSA) polypeptide.		
PN WO200145728-A2.		
PD 28-JUN-2001.		
PA (EPIN-) EPIMUNE INC.		
Best Local Similarity: 40.40%		
Mismatches: 103		
Query Match: 22.77%		
Indels: 13		
RESULT 1330		
ID AAW13649 standard; protein; 261 AA.		
DE Human prostatic specific antigen.		
PN WO9711172-A1.		
PD 27-MAR-1997.		
PA (WORC-) WORCESTER FOUND BIOMEDICAL RES.		
Best Local Similarity: 40.40%		
Query Match: 22.77%		
Mismatches: 103		
Indels: 13		
RESULT 1331		
ID AAY56048 standard; protein; 261 AA.		
DE Human prostate-specific antigen.		
PN WO9961068-A1.		
PD 02-DEC-1999.		
PA (UYPE-) UNIV PENNSYLVANIA.		
Best Local Similarity: 40.40%		
Query Match: 22.77%		
Mismatches: 103		
Indels: 13		
RESULT 1332		
ID AAY77842 standard; protein; 261 AA.		
DE Human prostate-specific antigen (PSA) sequence.		
PN WO9960984-A2.		
PD 02-DEC-1999.		
PA (ENTR-) ENTREMED INC.		
Best Local Similarity: 40.40%		
Query Match: 22.77%		
Mismatches: 103		
Indels: 13		
RESULT 1333		
ID AAB21317 standard; protein; 261 AA.		
DE Human PSA.		
PN WO200053776-A2.		
PD 14-SEP-2000.		
PA (MOUN) MOUNT SINAI HOSPITAL.		
Best Local Similarity: 40.40%		
Query Match: 22.77%		
Mismatches: 103		
Indels: 13		
RESULT 1334		
ID AAB74821 standard; protein; 261 AA.		
DE Prostate tumour antigen amino acid sequence for PSA.		
PN WO200125272-A2.		
PD 12-APR-2001.		
PA (CORI-) CORIXA CORP.		
Best Local Similarity: 40.40%		
Query Match: 22.77%		
Mismatches: 103		
Indels: 13		
RESULT 1335		
ID AAG62144 standard; protein; 261 AA.		
DE Human prostate specific membrane antigen SEQ ID NO: 327.		
PN WO200125273-A2.		
PD 12-APR-2001.		
PA (CORI-) CORIXA CORP.		
Best Local Similarity: 40.40%		
Query Match: 22.77%		
Mismatches: 103		
Indels: 13		
RESULT 1336		
ID AAG62146 standard; protein; 261 AA.		
DE Human prostate specific antigen SEQ ID NO: 329.		
PN WO200125273-A2.		
PD 12-APR-2001.		
PA (CORI-) CORIXA CORP.		
Best Local Similarity: 40.40%		
Query Match: 22.77%		
Mismatches: 103		
Indels: 13		
RESULT 1337		
ID ABU71859 standard; protein; 261 AA.		
DE Human prostatic specific membrane antigen (PSMA).		
PN US2002192763-A1.		
PD 19-DEC-2002.		
PA (XUJG/) XU J.		
PA (DILL/) DILLON D C.		
PA (MITC/) MITCHAM J L.		
PA (HARL/) HARLOCKER S L.		
PA (JIAN/) JIANG Y.		
PA (KALO/) KALOS M D.		
PA (FANG/) FANGER G R.		
PA (RETT/) RETTER M W.		
PA (STOL/) STOLK J A.		
PA (DAYC/) DAY C H.		
PA (VEDV/) VEDVICK T S.		

PA (CART/) CARTER D.
PA (LISK/) LJ S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Best Local Similarity: 40.40% Mismatches: 103
Query Match: 22.77% Indels: 13
RESULT 1338
ID ABP74202 standard; protein; 261 AA.
DE Human PSA protein SEQ ID NO:78.
PN WO200281646-A2.
PD 17-OCT-2002.
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
Best Local Similarity: 40.40% Mismatches: 103
Query Match: 22.77% Indels: 13
RESULT 1339
ID ADB82777 standard; protein; 261 AA.
DE Human protein sequence useful for the treatment of cancer (SeqID 1558).
PN WO2003050236-A2.
PD 19-JUN-2003.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 40.40% Mismatches: 103
Query Match: 22.77% Indels: 13
RESULT 1340
ID ADC09580 standard; protein; 261 AA.
DE PSA protein #SEQ ID 78.
PN WO2003008537-A2.
PD 30-JAN-2003.
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
Best Local Similarity: 40.40% Mismatches: 103
Query Match: 22.77% Indels: 13
RESULT 1341
ID ADJ59022 standard; protein; 261 AA.
DE Human PSA precursor protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Best Local Similarity: 40.40% Mismatches: 103
Query Match: 22.77% Indels: 13
RESULT 1342
ID ADI39733 standard; protein; 261 AA.
DE Human prostate specific antigen (PSA) protein.
PN US6642013-B1.
PD 04-NOV-2003.
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.
Best Local Similarity: 40.40% Mismatches: 103
Query Match: 22.77% Indels: 13
RESULT 1343
ID ADI37157 standard; protein; 261 AA.
DE Human prostate specific antigen (hPSA).
PN US2003199010-A1.
PD 23-OCT-2003.
PA (UYAR-) UNIV ARKANSAS.
Best Local Similarity: 40.40% Mismatches: 103
Query Match: 22.77% Indels: 13
RESULT 1344
ID ADM72819 standard; protein; 261 AA.
DE Human PSA protein SEQ ID NO:78.
PN WO2004022709-A2.
PD 18-MAR-2004.
PA (MANN-) MANNKIND CORP.
Best Local Similarity: 40.40% Mismatches: 103
Query Match: 22.77% Indels: 13
RESULT 1345
ID ABM82166 standard; protein; 261 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO2109, SEQ:5591.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 40.40% Mismatches: 103
Query Match: 22.77% Indels: 13
RESULT 1346
ID AAG62154 standard; protein; 692 AA.
DE Human WT1/PSA fusion protein SEQ ID NO: 357.
PN WO200125273-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 40.40% Mismatches: 103
Query Match: 22.77% Indels: 13
RESULT 1347
ID AAB67545 standard; protein; 284 AA.
DE Amino acid sequence of protease MH2 catalytic domain in PFEK2-6XHIS-TAG.
PN WO200116289-A2.
PD 08-MAR-2001.
PA (ORTH) ORTHO-MCNEIL PHARM INC.
Best Local Similarity: 43.75% Mismatches: 82
Query Match: 22.70% Indels: 8
RESULT 1348
ID AAY72521 standard; protein; 312 AA.
DE NSI-p703P mutated-His fusion protein.
PN WO200104143-A2.
PD 18-JAN-2001.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 42.06% Mismatches: 83
Query Match: 22.70% Indels: 12
RESULT 1349
ID AAU74767 standard; protein; 312 AA.
DE Amino acid sequence of NSI-p703 mutated-His fusion protein.
PN WO200200708-A2.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Best Local Similarity: 42.06% Mismatches: 83
Query Match: 22.70% Indels: 12
RESULT 1350
ID AAU74928 standard; protein; 312 AA.
DE Amino acid sequence of NSI-p703P mutated-His fusion protein.
PN WO200200867-A1.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Best Local Similarity: 42.06% Mismatches: 83
Query Match: 22.70% Indels: 12
RESULT 1351
ID ADJ59024 standard; protein; 261 AA.
DE Human PSA precursor protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Best Local Similarity: 40.40% Mismatches: 103
Query Match: 22.68% Indels: 13
RESULT 1352
ID AAU74903 standard; protein; 231 AA.
DE Amino acid sequence of p703 mutated-His fusion protein.
PN WO200200708-A2.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Best Local Similarity: 43.38% Mismatches: 80
Query Match: 22.63% Indels: 7
RESULT 1353
ID AAU74934 standard; protein; 231 AA.
DE Amino acid sequence of p703P mutated-His fusion protein.
PN WO200200867-A1.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Best Local Similarity: 43.38% Mismatches: 80
Query Match: 22.63% Indels: 7
RESULT 1354
ID AAP81243 standard; protein; 247 AA.
DE Human spleen trypsin III (trypsinogen III).

PN JP63160582-A.
PD 04-JUL-1988.
PA (SANY) SANKYO CO LTD.
Best Local Similarity: 40.91% Mismatches: 92
Query Match: 22.60% Indels: 10
RESULT 1355
ID AAR82703 standard; protein; 247 AA.
DE Human pancreatic trypsin III.
PN JP07184655-A.
PD 25-JUL-1995.
PA (SANY) SANKYO CO LTD.
Best Local Similarity: 40.91% Mismatches: 92
Query Match: 22.60% Indels: 10
RESULT 1356
ID ADJ59026 standard; protein; 261 AA.
DE Human PSA analogue (Y154) precursor protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USHS) US DEPT HEALTH & HUMAN SERVICES.
Best Local Similarity: 40.40% Mismatches: 104
Query Match: 22.58% Indels: 13
RESULT 1357
ID ABB84422 standard; peptide; 226 AA.
DE Rat SCE protein N-terminal fragment SEQ ID 48.
PN WO2002621135-A2.
PD 15-AUG-2002.
PA (EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
Best Local Similarity: 42.67% Mismatches: 87
Query Match: 22.48% Indels: 9
RESULT 1358
ID ADJ59028 standard; protein; 261 AA.
DE Human PSA analogue (L155/Y154) precursor protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USHS) US DEPT HEALTH & HUMAN SERVICES.
Best Local Similarity: 40.40% Mismatches: 104
Query Match: 22.48% Indels: 13
RESULT 1359
ID ADP27546 standard; protein; 281 AA.
DE Human kallikrein-3 (KLK-3) EHT103 protien b variant SeqID 20.
PN FR2848569-A1.
PD 18-JUN-2004.
PA (EXON-) EXONHIT THERAPEUTICS SA.
Best Local Similarity: 39.70% Mismatches: 105
Query Match: 22.48% Indels: 23
RESULT 1360
ID ADP27545 standard; protein; 297 AA.
DE Human kallikrein-3 (KLK-3) EHT103 protien a variant SeqID 19.
PN FR2848569-A1.
PD 18-JUN-2004.
PA (EXON-) EXONHIT THERAPEUTICS SA.
Best Local Similarity: 39.70% Mismatches: 105
Query Match: 22.48% Indels: 23
RESULT 1361
ID ADA50549 standard; protein; 237 AA.
DE Rhesus macaque prostate specific antigen (PSA/KLK3), SEQ ID NO:4.
PN WO2003031569-A2.
PD 17-APR-2003.
PA (CENZ) CENTOCOR INC.
Best Local Similarity: 42.62% Mismatches: 96
Query Match: 22.46% Indels: 12
RESULT 1362
ID ADM12395 standard; protein; 261 AA.
DE Human prostate-specific antigen protein.
PN US2003235594-A1.
PD 25-DEC-2003.
PA (ANTI-) ANTIGEN EXPRESS INC.
Best Local Similarity: 40.00% Mismatches: 104
Query Match: 22.43% Indels: 13
RESULT 1363
ID ADR66838 standard; protein; 248 AA.
DE Human prostatic carcinoma derived DNA SEQ ID 131 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Best Local Similarity: 40.25% Mismatches: 101
Query Match: 22.39% Indels: 11
RESULT 1364
ID ADR66277 standard; protein; 248 AA.
DE Human prostatic carcinoma derived protein SEQ ID 131 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Best Local Similarity: 40.25% Mismatches: 101
Query Match: 22.39% Indels: 11
RESULT 1365
ID ADR66934 standard; protein; 251 AA.
DE Human prostatic carcinoma derived DNA SEQ ID 232 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Best Local Similarity: 40.25% Mismatches: 101
Query Match: 22.39% Indels: 11
RESULT 1366
ID ADR66036 standard; protein; 251 AA.
DE Human prostatic carcinoma derived protein SEQ ID 232 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Best Local Similarity: 40.25% Mismatches: 101
Query Match: 22.39% Indels: 11
RESULT 1367
ID AAR84668 standard; protein; 261 AA.
DE Prepro-hk2 kallikrein.
PN WO9530758-A1.
PD 16-NOV-1995.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITECH INC.
Best Local Similarity: 40.23% Mismatches: 112
Query Match: 22.29% Indels: 11
RESULT 1368
ID AAW10600 standard; protein; 261 AA.
DE Human prepro-Trip226-glandular kallikrein-2.
PN WO9701630-A1.
PD 16-JAN-1997.
PA (ORIN) ORION YHTYMAE OY.
Best Local Similarity: 40.23% Mismatches: 112
Query Match: 22.29% Indels: 11
RESULT 1369
ID AAU98921 standard; protein; 245 AA.
DE Human prostate specific antigen (PSA) variant.
PN WO200240059-A2.
PD 23-MAY-2002.
PA (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.
PA (MINC/) MINCHEFF M S.
PA (LOUK/) LOUKINOV D I.
PA (ZOUB/) ZOUBAK S.
Best Local Similarity: 41.38% Mismatches: 95
Query Match: 22.24% Indels: 11

RESULT 1370
ID AAY0894 standard; protein; 238 AA.
DE Chimeric serine protease FXT protein.
PN EP927764-A2.
PA (HOF) ROCHE DIAGNOSTICS GMBH. Mismatches: 95
Best Local Similarity: 40.52% Indels: 8
Query Match:
RESULT 1371
ID AAB21314 standard; protein; 255 AA.
DE Human KLK2.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 40.80% Mismatches: 108
Query Match: 22.19% Indels: 11
RESULT 1372
ID AAW06971 standard; protein; 261 AA.
DE Prostate-specific glandular kallikrein prepro-hk2.
PN WO9634964-A2.
PD 07-NOV-1996.
PA (HYBR-) HYBRITECH INC.
PA (MAYO-) MAYO FOUNDATION.
Best Local Similarity: 40.80% Mismatches: 108
Query Match: 22.19% Indels: 11
RESULT 1373
ID AAW83203 standard; protein; 261 AA.
DE Prostate-specific glandular kallikrein protein pphk2.
PN WO9846795-A1.
PD 22-OCT-1998.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (MAYO-) MAYO FOUNDATION.
Best Local Similarity: 40.80% Mismatches: 108
Query Match: 22.19% Indels: 11
RESULT 1374
ID AAW49085 standard; protein; 261 AA.
DE Wild-type human Kallikrein 2 (hk2).
PN WO9821365-A2.
PD 22-MAY-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITECH INC.
Best Local Similarity: 40.80% Mismatches: 108
Query Match: 22.19% Indels: 11
RESULT 1375
ID AAW45397 standard; protein; 261 AA.
DE Prostate-specific glandular kallikrein precursor prepro-hk2.
PN WO9802748-A1.
PD 22-JAN-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITECH INC.
Best Local Similarity: 40.80% Mismatches: 108
Query Match: 22.19% Indels: 11
RESULT 1376
ID AAW96189 standard; protein; 261 AA.
DE Prepro human Kallikrein 2 (preprohk2).
PN WO9859073-A1.
PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITECH INC.
Best Local Similarity: 40.80% Mismatches: 108
Query Match: 22.19% Indels: 11
RESULT 1377
ID AAB21318 standard; protein; 261 AA.
DE Human KLK2.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 40.80% Mismatches: 108
Query Match: 22.19% Indels: 11
ID AAU06279 standard; protein; 261 AA.

DE Human Kallikrein2 polypeptide.
PN WO200145728-A2.
PD 28-JUN-2001.
PA (EPIM-) EPIMUNE INC. Mismatches: 108
Best Local Similarity: 40.80% Indels: 11
Query Match:
RESULT 1379
ID ADB75390 standard; protein; 261 AA.
DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 108
Best Local Similarity: 40.80% Indels: 11
Query Match:
RESULT 1380
ID AAW83213 standard; protein; 237 AA.
DE Prostate-specific antigen protein hk3.
PN WO9846795-A1.
PD 22-OCT-1998.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (MAYO-) MAYO FOUNDATION.
Best Local Similarity: 41.56% Mismatches: 95
Query Match: 22.14% Indels: 11
RESULT 1381
ID AAW56086 standard; protein; 237 AA.
DE Human prostate specific antigen protein.
PN WO9810292-A1.
PD 12-MAR-1998.
PA (CENZ) CENTOCOR INC. Mismatches: 95
Best Local Similarity: 41.56% Indels: 11
Query Match: 22.14%
RESULT 1382
ID AAW96187 standard; protein; 237 AA.
DE Human prostate specific antigen (PSA).
PN WO9859073-A1.
PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (YOUNG) YOUNG C Y F.
PA (TIND) TINDALL D J.
PA (KLEE) KLEE G G.
Best Local Similarity: 41.56% Mismatches: 95
Query Match: 22.14% Indels: 11
RESULT 1383
ID AAB11041 standard; peptide; 237 AA.
DE Human prostate-specific antigen N-terminal fragment #2.
PN EP1043394-A2.
PD 11-OCT-2000.
PA (SERA-) SERATEC GES BIOTECHNOLOGIE MBH. Mismatches: 95
Best Local Similarity: 41.56% Indels: 11
Query Match: 22.14%
RESULT 1384
ID AAB19819 standard; protein; 237 AA.
DE Prostate specific antigen specific to benign prostatic hyperplasia.
PN WO200067030-A1.
PD 09-NOV-2000.
PA (HYBR-) HYBRITECH INC.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Best Local Similarity: 41.56% Mismatches: 95
Query Match: 22.14% Indels: 11
RESULT 1385
ID AAB19818 standard; protein; 237 AA.
DE Prostate specific antigen elevated in benign prostatic hyperplasia.
PN WO200066718-A1.
PD 09-NOV-2000.
PA (HYBR-) HYBRITECH INC.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Best Local Similarity: 41.56% Mismatches: 95
Query Match: 22.14% Indels: 11
RESULT 1386
ID ADA50546 standard; protein; 237 AA.
DE Human prostate specific antigen (PSA/KLK3), SEQ ID NO:1.
PN WO2003031569-A2.
PD 17-APR-2003.

PA (CENZ) CENTOCOR INC.			
Best Local Similarity: 41.56%	Mismatches: 95		
Query Match: 22.14%	Indels: 11		
RESULT 1387			
ID ADA09840 standard; protein; 237 AA.			
DE Human mature prostate specific antigen (PSA).			
PN US2003059864-A1.			
PD 27-MAR-2003.			
PA (MIKO/) MIKOLAJCZYK S D.			
PA (RITT/) RITTENHOUSE H G.			
Best Local Similarity: 41.56%	Mismatches: 95		
Query Match: 22.14%	Indels: 11		
RESULT 1388			
ID ADJ59023 standard; protein; 237 AA.			
DE Human PSA mature protein sequence.			
PN WO2003047506-A2.			
PD 12-JUN-2003.			
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.			
Best Local Similarity: 41.56%	Mismatches: 95		
Query Match: 22.14%	Indels: 11		
RESULT 1389			
ID ADF60980 standard; protein; 237 AA.			
DE Human prostate specific antigen (PSA).			
PN US2003166036-A1.			
PD 04-SEP-2003.			
PA (MIKO/) MIKOLAJCZYK S D.			
PA (RITT/) RITTENHOUSE H G.			
Best Local Similarity: 41.56%	Mismatches: 95		
Query Match: 22.14%	Indels: 11		
RESULT 1390			
ID AAP70677 standard; protein; 245 AA.			
DE Human kallikrein gene product.			
PN WO8702709-A.			
PD 07-MAY-1987.			
PA (BIOT-) BIOTECHN RES PARTN.			
PA (CALB-) CALIF BIOTECHNOL INC.			
Best Local Similarity: 39.7%	Mismatches: 99		
Query Match: 22.07%	Indels: 12		
RESULT 1391			
ID AAW45398 standard; protein; 237 AA.			
DE Prostate-specific antigen protein hK3 (PSA).			
PN WO9802748-A1.			
PD 22-JAN-1998.			
PA (MAYO-) MAYO FOUNDATION.			
PA (HYBR-) HYBRITECH INC.			
Best Local Similarity: 41.56%	Mismatches: 96		
Query Match: 22.05%	Indels: 11		
RESULT 1392			
ID ADJ59025 standard; protein; 237 AA.			
DE Human PSA mature protein sequence.			
PN WO2003047506-A2.			
PD 12-JUN-2003.			
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.			
Best Local Similarity: 41.56%	Mismatches: 95		
Query Match: 22.05%	Indels: 11		
RESULT 1393			
ID AAW06972 standard; protein; 261 AA.			
DE Kallikrein prepro-hK2v217 variant.			
PN WO9634964-A2.			
PD 07-NOV-1996.			
PA (HYBR-) HYBRITECH INC.			
PA (MAYO-) MAYO FOUNDATION.			
Best Local Similarity: 40.80%	Mismatches: 108		
Query Match: 22.05%	Indels: 11		
RESULT 1394			
ID AAW45400 standard; protein; 261 AA.			
DE Prostate-specific glandular kallikrein hK2v217.			
PN WO9802748-A1.			
PD 22-JAN-1998.			
PA (MAYO-) MAYO FOUNDATION.			
PA (HYBR-) HYBRITECH INC.			
Best Local Similarity: 40.80%	Mismatches: 108		
Query Match: 22.05%	Indels: 11		
RESULT 1395			
ID AAW59129 standard; protein; 232 AA.			
DE Homo sapiens Tub Interactor (HTI-1) protein.			
PN WO9812302-A1.			
PD 26-MAR-1998.			
PA (MILL-) MILLENNIUM PHARM INC.			
Best Local Similarity: 43.78%	Mismatches: 76		
Query Match: 22.00%	Indels: 11		
RESULT 1396			
ID AAY72523 standard; protein; 232 AA.			
DE Human prostate antigen #1.			
PN WO200104143-A2.			
PD 18-JAN-2001.			
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity: 43.78%	Mismatches: 76		
Query Match: 22.00%	Indels: 11		
RESULT 1397			
ID AAU74769 standard; protein; 232 AA.			
DE Protein sequence of prostate homologue #1.			
PN WO200200708-A2.			
PD 03-JAN-2002.			
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.			
Best Local Similarity: 43.78%	Mismatches: 76		
Query Match: 22.00%	Indels: 11		
RESULT 1398			
ID AAU74930 standard; protein; 232 AA.			
DE Amino acid sequence of prostate protein fragment #1.			
PN WO200200867-A1.			
PD 03-JAN-2002.			
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.			
Best Local Similarity: 43.78%	Mismatches: 76		
Query Match: 22.00%	Indels: 11		
RESULT 1399			
ID AAR84669 standard; protein; 244 AA.			
DE Pro-hK2 kallikrein.			
PN WO9530758-A1.			
PD 16-NOV-1995.			
PA (MAYO-) MAYO FOUNDATION.			
PA (HYBR-) HYBRITECH INC.			
Best Local Similarity: 41.18%	Mismatches: 100		
Query Match: 22.00%	Indels: 11		
RESULT 1400			
ID ADO38617 standard; protein; 261 AA.			
DE Prostate Specific Antigen (PSA).			
PN US2004058881-A1.			
PD 25-MAR-2004.			
PA (ANTH-) ANTIGEN EXPRESS INC.			
Best Local Similarity: 39.60%	Mismatches: 105		
Query Match: 22.00%	Indels: 13		
RESULT 1401			
ID ADJ59027 standard; protein; 237 AA.			
DE Human PSA analogue (Y154) mature protein sequence.			
PN WO2003047506-A2.			
PD 12-JUN-2003.			
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.			
Best Local Similarity: 41.56%	Mismatches: 96		
Query Match: 21.95%	Indels: 11		
RESULT 1402			
ID AAW83204 standard; protein; 244 AA.			
DE Prostate-specific glandular kallikrein protein phK2.			
PN WO9846795-A1.			
PD 22-OCT-1998.			
PA (BAYU) BAYLOR COLLEGE MEDICINE.			
PA (MAYO-) MAYO FOUNDATION.			
Best Local Similarity: 41.81%	Mismatches: 96		
Query Match: 21.90%	Indels: 11		
RESULT 1403			
ID AAW45396 standard; protein; 244 AA.			
DE Prostate-specific glandular kallikrein precursor pro-hK2.			
PN WO9802748-A1.			
PD 22-JAN-1998.			
PA (MAYO-) MAYO FOUNDATION.			

PA (HYBR-) HYBRITECH INC.
Best Local Similarity: 41.81% Mismatches: 96
Query Match: 21.90% Indels: 11
RESULT 1404
ID AAW96188 standard; protein; 244 AA.
DE Pro human kallikrein 2 (prohK2).
PN WO9859073-A1.
PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (YOUNG) YOUNG C Y F.
PA (TIND/) TINDALL D J.
PA (KLEE/) KLEE G G.
Best Local Similarity: 41.81% Mismatches: 96
Query Match: 21.90% Indels: 11
RESULT 1405
ID AAW03130 standard; protein; 250 AA.
DE Prostate-specific antigen.
PN WO9621042-A2.
PD 11-JUL-1996.
PA (UYBO-) UNIV BOSTON.
Best Local Similarity: 40.52% Mismatches: 96
Query Match: 21.90% Indels: 11
RESULT 1406
ID ADP27538 standard; protein; 281 AA.
DE Human kallikrein-2 (KLK-2) EHT102 protein b variant SeqID 12.
PN FR2848569-A1.
PD 18-JUN-2004.
PA (EXON-) EXONHIT THERAPEUTICS SA.
Best Local Similarity: 41.81% Mismatches: 96
Query Match: 21.90% Indels: 11
RESULT 1407
ID ADP27537 standard; protein; 297 AA.
DE Human kallikrein-2 (KLK-2) EHT102 protein a variant SeqID 11.
PN FR2848569-A1.
PD 18-JUN-2004.
PA (EXON-) EXONHIT THERAPEUTICS SA.
Best Local Similarity: 41.81% Mismatches: 96
Query Match: 21.90% Indels: 11
RESULT 1408
ID ADJ59029 standard; protein; 236 AA.
DE Human PSA analogue (h155/Y154) mature protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Best Local Similarity: 41.52% Mismatches: 96
Query Match: 21.88% Indels: 11
RESULT 1409
ID AAR77098 standard; protein; 237 AA.
DE Prostate-specific antigen.
PN WO9528498-A1.
PD 26-OCT-1995.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Best Local Similarity: 40.69% Mismatches: 96
Query Match: 21.81% Indels: 11
RESULT 1410
ID AAW63202 standard; protein; 237 AA.
DE Prostate-specific glandular kallikrein protein hk2.
PN WO9846795-A1.
PD 22-OCT-1998.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (MAYO-) MAYO FOUNDATION.
Best Local Similarity: 41.99% Mismatches: 96
Query Match: 21.81% Indels: 11
RESULT 1411
ID AAW45395 standard; protein; 237 AA.
DE Mature prostate-specific glandular kallikrein hk2.
PN WO9802748-A1.
PD 22-JAN-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITECH INC.
Best Local Similarity: 41.99% Mismatches: 96
Query Match: 21.81% Indels: 11
RESULT 1412

ID AAW96186 standard; protein; 237 AA.
DE Mature human kallikrein 2 (hk2).
PN WO9859073-A1.
PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (YOUNG) YOUNG C Y F.
PA (TIND/) TINDALL D J.
PA (KLEE/) KLEE G G.
Best Local Similarity: 41.99% Mismatches: 96
Query Match: 21.81% Indels: 11
RESULT 1413
ID ADA50561 standard; protein; 237 AA.
DE Kallikrein KLK2, SEQ ID NO:16.
PN WO2003031569-A2.
PD 17-APR-2003.
PA (CENZ) CENTOCOR INC.
Best Local Similarity: 41.99% Mismatches: 96
Query Match: 21.81% Indels: 11
RESULT 1414
ID AAR84667 standard; protein; 237 AA.
DE Mature kallikrein hk2.
PN WO9530758-A1.
PD 16-NOV-1995.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITECH INC.
Best Local Similarity: 41.99% Mismatches: 96
Query Match: 21.71% Indels: 11
RESULT 1415
ID ADI17277 standard; protein; 217 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 813.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 44.44% Mismatches: 87
Query Match: 21.66% Indels: 13
RESULT 1416
ID ADI17269 standard; protein; 217 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 805.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 44.44% Mismatches: 87
Query Match: 21.66% Indels: 13
RESULT 1417
ID ADJ63076 standard; protein; 217 AA.
DE Trypsin protein which is related to human NOVX protein - SEQ ID 67.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO) ALSOBROOK J P.
PA (TCHE) TCHERNEV V T.
PA (LIUX) LIU X.
PA (SPYT) SPYTEK K A.
PA (ZERR) ZERRHUSEN B D.
PA (PATT) PATTURAJAN M.
PA (LEPL) LEPLLEY D M.
PA (BURG) BURGESS C E.
PA (SHIM) SHIMKETS R A.
PA (GROS) GROSSE W M.
PA (SZEK) SZEKERES E S.
PA (VERN) VERNET C A M.
PA (LILL) LI L.
PA (CASM) CASMAN S J.
PA (BOLD) BOLDOG F L.
PA (GORM) GORMAN L.
PA (GANG) GANGOLLI E A.
PA (FERN) FERNANDES E R.
PA (RIEG) RIEGER D K.
PA (EDIN) EDINGER S R.
PA (GUNT) GUNTHER E.
PA (MILL) MILLET I.
PA (SCIO) SCIORE P.
PA (ELLE) ELLERMAN K.
PA (MACD) MACDOUGALL J R.

PA (SMIT/) SMITHSON G. 87
 Query Match: 44.44% Mismatches: 13
 Indels: 13
 RESULT 1418
 ID AAW83212 standard; protein; 237 AA.
 DE hK2 variant A217V.
 PN WO9846795-A1.
 PD 22-OCT-1998.
 PA (BAYO) BAYLOR COLLEGE MEDICINE.
 PA (MAYO-) MAYO FOUNDATION.
 Query Match: 41.99% Mismatches: 96
 Indels: 11
 RESULT 1419
 ID AAW9087 standard; protein; 237 AA.
 DE Mutant human Kallikrein 2 (hK2) A217V.
 PN WO9821365-A2.
 PD 22-MAY-1998.
 PA (MAYO-) MAYO FOUNDATION.
 PA (HYBR-) HYBRITECH INC.
 Query Match: 41.99% Mismatches: 96
 Indels: 11
 RESULT 1420
 ID AAW96190 standard; protein; 237 AA.
 DE Variant human Kallikrein 2 (hK2).
 PN WO9859073-A1.
 PD 30-DEC-1998.
 PA (MAYO-) MAYO FOUNDATION.
 PA (YOUNG) YOUNG C Y F.
 PA (TIND/) TINDALL D J.
 PA (KLEE/) KLEE G G.
 Query Match: 41.99% Mismatches: 96
 Indels: 11
 RESULT 1421
 ID AAW11023 standard; protein; 240 AA.
 DE Human prostate specific antigen.
 PN WO9640754-A1.
 PD 19-DEC-1996.
 PA (TEXA) UNIV TEXAS SYSTEM.
 Query Match: 41.03% Mismatches: 96
 Indels: 14
 RESULT 1422
 ID AAR84671 standard; protein; 237 AA.
 DE Mature kallikrein hK3.
 PN WO9530758-A1.
 PD 16-NOV-1995.
 PA (MAYO-) MAYO FOUNDATION.
 PA (HYBR-) HYBRITECH INC.
 Query Match: 41.13% Mismatches: 97
 Indels: 11
 RESULT 1423
 ID ABM82643 standard; protein; 227 AA.
 DE Human diagnostic and therapeutic pproteain SEQ ID NO:2892.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match: 39.59% Mismatches: 82
 Indels: 30
 RESULT 1424
 ID AAR84670 standard; protein; 238 AA.
 DE Mature kallikrein hK2.
 PN WO9530758-A1.
 PD 16-NOV-1995.
 PA (MAYO-) MAYO FOUNDATION.
 PA (HYBR-) HYBRITECH INC.
 Query Match: 40.93% Mismatches: 101
 Indels: 11
 RESULT 1425
 ID AAR94526 standard; protein; 279 AA.
 DE Korean Viper Salmoisa thrombin-like protease, Halybin.
 PN EP707067-A2.
 PD 17-APR-1996.
 PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
 Query Match: 37.66% Mismatches: 110
 Indels: 110

Query Match: 21.25% Indels: 4
 RESULT 1426
 ID AAG79000 standard; protein; 233 AA.
 DE Mamushi fibrinolytic enzyme, Brevinase.
 PN XR2001045716-A.
 PD 05-JUN-2001.
 PA (LEEJ/) LEE J W.
 PA (PARK/) PARK W.
 Query Match: 37.93% Mismatches: 92
 Indels: 11
 RESULT 1427
 ID AAM52944 standard; protein; 260 AA.
 DE Agkistrodon halyis brevicaudus thrombin-like protease, salmobin.
 PN KR98002267-A.
 PD 30-MAR-1998.
 PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.
 Query Match: 36.14% Mismatches: 106
 Indels: 12
 RESULT 1428
 ID AAB50447 standard; protein; 205 AA.
 DE Human prostate cancer-related intracellular protein #1.
 PN WO200071711-A2.
 PD 30-NOV-2000.
 PA (SAAT/) SAATCIOGLU F.
 Query Match: 44.22% Mismatches: 69
 Indels: 7
 RESULT 1429
 ID ADE78966 standard; protein; 227 AA.
 DE Human protein modification and maintenance molecule (PMMM)-4.
 PN WO2003063688-A2.
 PD 07-AUG-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match: 39.18% Mismatches: 84
 Indels: 30
 RESULT 1430
 ID ABR09589 standard; protein; 234 AA.
 DE Deinagkistrodon acutus venom thrombin-like protein (234 residue variant).
 PN CN1181421-A.
 PD 13-MAY-1998.
 PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
 Query Match: 37.65% Mismatches: 100
 Indels: 11
 RESULT 1431
 ID AAM69388 standard; protein; 205 AA.
 DE Prostate tumour specific gene clone DE13 protein.
 PN WO9837418-A2.
 PD 27-AUG-1998.
 PA (CORI-) CORIXA CORP.
 Query Match: 20.67% Mismatches: 70
 Indels: 7
 RESULT 1432
 ID AAW71872 standard; protein; 205 AA.
 DE Protein encoded by prostate tumour clone P703 splice variant DE13.
 PN WO9837093-A2.
 PD 27-AUG-1998.
 PA (CORI-) CORIXA CORP.
 Query Match: 43.72% Mismatches: 70
 Indels: 7
 RESULT 1433
 ID AAY82005 standard; protein; 205 AA.
 DE Human immunogenic prostate tumour protein sequence SEQ ID NO:176.
 PN WO200004149-A2.
 PD 27-JAN-2000.
 PA (CORI-) CORIXA CORP.
 Query Match: 43.72% Mismatches: 70
 Indels: 7
 RESULT 1434
 ID ABG94414 standard; protein; 205 AA.
 DE Human prostate tumour protein partial variant sequence #2.
 PN US2002090372-A1.
 PD 11-JUL-2002.
 PA (XUJ/) XU J.
 PA (DILL/) DILLON D C.

Best Local Similarity: 43.72% Mismatches: 70
Query Match: 20.64% Indels: 7
RESULT 1435
ID AAM01120 standard; protein; 205 AA.
DE Human prostate-specific amino acid sequence P703P-DE13.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.72% Mismatches: 70
Query Match: 20.64% Indels: 7
RESULT 1436
ID AAU69766 standard; protein; 205 AA.
DE Human prostate cDNA encoded protein #6.
PN WO200173032-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.72% Mismatches: 70
Query Match: 20.64% Indels: 7
RESULT 1437
ID AAB74803 standard; protein; 205 AA.
DE Prostate tumour antigen predicted amino acid sequence for P703P-DE13.
PN WO200125272-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.72% Mismatches: 70
Query Match: 20.64% Indels: 7
RESULT 1438
ID AAG99005 standard; protein; 205 AA.
DE Human prostate-specific amino acid sequence P703P-DE13.
PN WO200134802-A2.
PD 17-MAY-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.72% Mismatches: 70
Query Match: 20.64% Indels: 7
RESULT 1439
ID ABU71656 standard; protein; 205 AA.
DE Prostate cancer specific antigen P703P #2.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
Best Local Similarity: 43.72% Mismatches: 70
Query Match: 20.64% Indels: 7
RESULT 1440
ID AAU04964 standard; protein; 205 AA.
DE Human prostate tumour protein DE13.
PN US6262245-B1.
PD 17-JUL-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.72% Mismatches: 70
Query Match: 20.64% Indels: 7
RESULT 1441
ID ABB95225 standard; protein; 205 AA.
DE Human prostate tumour protein DE13.
PN US6262245-B1.
PD 17-JUL-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.72% Mismatches: 70
Query Match: 20.64% Indels: 7
RESULT 1442
ID ABG76668 standard; protein; 205 AA.
DE Prostate tumour protein #6.
PN US2002081580-A1.
PD 27-JUN-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
Best Local Similarity: 43.72% Mismatches: 70
Query Match: 20.64% Indels: 7
RESULT 1443
ID ABR54337 standard; protein; 205 AA.
DE Prostate tumour specific protein sequence SEQ ID 176.
PN WO200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.72% Mismatches: 70
Query Match: 20.64% Indels: 7
RESULT 1444
ID ADG26042 standard; protein; 205 AA.
DE Human prostate-specific polypeptide #6.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.72% Mismatches: 70
Query Match: 20.64% Indels: 7
RESULT 1445
ID ADK36957 standard; protein; 281 AA.
DE Novel human polypeptide seqID9039.
PN WO200216439-A2.
PD 28-FEB-2002.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 39.26% Mismatches: 91
Query Match: 20.45% Indels: 19
RESULT 1447
ID ABU92024 standard; protein; 218 AA.
DE Human protein modification and maintenance molecule-4 (PMM-4).
PN WO2003031939-A2.
PD 17-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 37.76% Mismatches: 83
Query Match: 20.43% Indels: 38
RESULT 1448
ID AAB31579 standard; peptide; 225 AA.

DE Amino acid sequence of cod trypsin isozymes.
PN WO200078332-A2.
PD 28-DEC-2000.
PA (BJAR/) BJARNASON J B. Mismatches: 92
Best Local Similarity: 44.30% Indels: 10
Query Match: 20.38%
RESULT 1449
ID ADE15982 standard; protein; 218 AA.
DE G-coupled protein receptor related polypeptide, SEQ ID NO 12.
PN WO200283841-A2.
PD 24-OCT-2002.
PA (CURA-) CURAGEN CORP. Mismatches: 83
Best Local Similarity: 37.76% Indels: 38
Query Match: 20.33%
RESULT 1450
ID ADL93921 standard; protein; 218 AA.
DE Human G-coupled protein receptor-related protein #6.
PN US2004006205-A1.
PD 08-JAN-2004.
PA (LILL/) LI L.
PA (GERL/) GERLACH V.
PA (LIUX/) LIU X.
PA (MILL/) MILLER C E.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERHUSEN B D.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (ZHON/) ZHONG H.
PA (SMIT/) SMITHSON G.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOGF L.
PA (VOSS/) VOSS E Z.
PA (VERN/) VERNET C A.
PA (MACD/) MACDOUGALL J R.
PA (RAST/) RASTELLI L.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (MEZE/) MEZES P S.
PA (FURT/) FURTA K.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (MADY/) MADIYANKAR U M.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (EDIN/) EDINGER S.
PA (MAZU/) MAZUR A.
Best Local Similarity: 37.76% Mismatches: 83
Query Match: 20.33% Indels: 38
RESULT 1451
ID AAY28641 standard; protein; 207 AA.
DE Human secreted protein from cDNA clone HKAET41.
PN WO9940183-A1.
PD 12-AUG-1999.
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 69
Best Local Similarity: 50.28% Indels: 4
Query Match: 20.23%
RESULT 1452
ID AA46773 standard; protein; 233 AA.
DE Amino acid sequence of Salmonase.
PN EP814164-A2.
PD 29-DEC-1997.
PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST. Mismatches: 95
Best Local Similarity: 36.64% Indels: 11
Query Match: 20.21%
RESULT 1453
ID AA221442 standard; protein; 226 AA.
DE Human trypsin domain consensus protein #2.
PN WO200226802-A2.
PD 04-APR-2002.
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 56
Best Local Similarity: 42.58% Indels: 65
Query Match: 20.16%
RESULT 1454

ID ABG75786 standard; protein; 226 AA.
DE Trypsin domain consensus sequence, SMART.
PN US2002165152-A1.
PD 07-NOV-2002.
PA (KAPE/) KAPPELLER-LIBERMAN R. Mismatches: 56
Best Local Similarity: 42.58% Indels: 65
Query Match: 20.16%
RESULT 1455
ID ABM83248 standard; protein; 299 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3497.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP. Mismatches: 91
Best Local Similarity: 36.07% Indels: 53
Query Match: 20.04%
RESULT 1456
ID ADA05736 standard; protein; 198 AA.
DE Human NOV18c protein SEQ ID NO:96.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP. Mismatches: 65
Best Local Similarity: 36.82% Indels: 71
Query Match: 19.97%
RESULT 1457
ID ADN62900 standard; protein; 198 AA.
DE Human NOV18c.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWU/) JI W.
PA (MILL/) MILLER C E.
PA (RST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Best Local Similarity: 36.82% Mismatches: 65
Query Match: 19.97% Indels: 71
RESULT 1458
ID ADA50560 standard; protein; 194 AA.
DE Prostate specific antigen (PSA/KLK3), SEQ ID NO:15.
PN WO2003031569-A2.
PD 17-APR-2003.
PA (CENZ-) CENTOCOR INC. Mismatches: 75
Best Local Similarity: 38.74% Indels: 36
Query Match: 19.80%
RESULT 1459

ID ADG75694 standard; protein; 215 AA.
DE Human protein modification and maintenance molecule polypeptide SeqID8.
PN WO2003083084-A2.
PD 09-OCT-2003.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 37.14% Mismatches: 77
Query Match: 19.80% Indels: 42
RESULT 1460

ID ABM92829 standard; protein; 215 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3078.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 37.14% Mismatches: 77
Query Match: 19.80% Indels: 42
RESULT 1461

ID ADA05738 standard; protein; 181 AA.
DE Human NOVI18d protein SEQ ID NO:98.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 37.39% Mismatches: 61
Query Match: 19.77% Indels: 63
RESULT 1462

ID ADNG2902 standard; protein; 181 AA.
DE Human NOVI18d.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATI/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JTWV/) JI W.
PA (MILL/) MILLER C E.
PA (RASI/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Best Local Similarity: 37.39% Mismatches: 61
Query Match: 19.77% Indels: 63
RESULT 1463

ID ABM82641 standard; protein; 222 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2890.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 36.69% Mismatches: 88
Query Match: 19.70% Indels: 36
RESULT 1464

ID AAB08510 standard; protein; 230 AA.
DE A recombinant protein C activator polypeptide.
PN WO200050612-A2.
PD 31-AUG-2000.
PA (INLI) INSTRUMENTATION LAB.
Best Local Similarity: 36.21% Mismatches: 94
Query Match: 19.68% Indels: 13
RESULT 1465

ID AAW76538 standard; protein; 231 AA.
DE A concortrix protein C activator protein fragment.
PN WO9842850-A1.
PD 01-OCT-1998.
PA (RPMS-) RPMS TECHNOLOGY LTD.
Best Local Similarity: 36.21% Mismatches: 94
Query Match: 19.68% Indels: 13
RESULT 1466

ID AAM99041 standard; protein; 246 AA.
DE Polypeptide fragment encoded by gene 179.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 41.56% Mismatches: 110
Query Match: 19.68% Indels: 6
RESULT 1467

ID ABB51196 standard; protein; 246 AA.
DE Human secreted protein encoded by gene 179 SEQ ID NO:1149.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 41.56% Mismatches: 110
Query Match: 19.68% Indels: 6
RESULT 1468

ID ABO45453 standard; protein; 246 AA.
DE Novel human secreted protein #179 fragment #1.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 41.56% Mismatches: 110
Query Match: 19.68% Indels: 6
RESULT 1469

ID ABO26933 standard; protein; 246 AA.
DE Protein associated with novel secreted protein gene 179 #1.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 41.56% Mismatches: 110
Query Match: 19.68% Indels: 6
RESULT 1470

ID ABB09590 standard; protein; 218 AA.
DE Deinagkistrodon acutus venom thrombin-like protein (218 residue variant).
PN CN1181421-A.
PD 13-MAY-1998.
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
Best Local Similarity: 36.49% Mismatches: 94
Query Match: 19.63% Indels: 9
RESULT 1471

ID ABM84665 standard; protein; 220 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4914.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 36.65% Mismatches: 82
Query Match: 19.60% Indels: 42
RESULT 1472

ID AAB08511 standard; protein; 230 AA.
DE Biosynthetic variant of protein C activator polypeptide.
PN WO200050612-A2.
PD 31-AUG-2000.
PA (INLI) INSTRUMENTATION LAB.
Best Local Similarity: 36.96% Mismatches: 97
Query Match: 19.53% Indels: 9
RESULT 1473

ID AAR20557 standard; protein; 234 AA.

DE Fibrinogenolytic protein #4 from snake venom.
PN DE4023699-A.
PD 30-JAN-1992.
PA (BADI) BASF AG.
Best Local Similarity: 36.68% Mismatches: 105
Query Match: 19.51% Indels: 4
RESULT 1474
ID AAP81333 standard; protein; 255 AA.
DE Batroxobin.
PN JP63049084-A.
PD 01-MAR-1988.
PA (YAMA/) YAMASHINA I.
Best Local Similarity: 32.92% Mismatches: 109
Query Match: 19.46% Indels: 4
RESULT 1475
ID AAR05436 standard; protein; 255 AA.
DE Batroxobin gene product.
PN JP02124092-A.
PD 11-MAY-1990.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 32.92% Mismatches: 109
Query Match: 19.46% Indels: 4
RESULT 1476
ID AAV17869 standard; protein; 255 AA.
DE Araraca batroxobin.
PN WO9929838-A1.
PD 17-JUN-1999.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Best Local Similarity: 32.92% Mismatches: 109
Query Match: 19.46% Indels: 4
RESULT 1477
ID AAE21441 standard; protein; 249 AA.
DE Human trypsin domain consensus protein #1.
PN WO200226802-A2.
PD 04-APR-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 40.32% Mismatches: 65
Query Match: 19.43% Indels: 53
RESULT 1478
ID AAM52946 standard; protein; 231 AA.
DE Batroxobin, a snake venom protease.
PN KR98002267-A.
PD 30-MAR-1998.
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.
Best Local Similarity: 34.21% Mismatches: 101
Query Match: 19.36% Indels: 4
RESULT 1479
ID AAR89042 standard; protein; 228 AA.
DE Polypeptide fragment encoded by gene 179.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 42.22% Mismatches: 100
Query Match: 19.17% Indels: 5
RESULT 1480
ID ABB51197 standard; protein; 228 AA.
DE Human secreted protein encoded by gene 179 SEQ ID NO:1150.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 42.22% Mismatches: 100
Query Match: 19.17% Indels: 5
RESULT 1481
ID ABO45454 standard; protein; 228 AA.
DE Novel human secreted protein #179 fragment #2.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 42.22% Mismatches: 100
Query Match: 19.17% Indels: 5
RESULT 1482
ID ABO26934 standard; protein; 228 AA.
DE Protein associated with novel secreted protein gene 179 #2.

PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 42.22% Mismatches: 100
Query Match: 19.17% Indels: 5
RESULT 1483
ID AAB11711 standard; protein; 264 AA.
DE Mouse serine protease BSSP5 (mBSSP5) SEQ ID NO:4.
PN WO200031243-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Best Local Similarity: 39.10% Mismatches: 102
Query Match: 19.14% Indels: 25
RESULT 1484
ID AAM52945 standard; protein; 236 AA.
DE Flaboxobin, a snake venom protease.
PN KR98002267-A.
PD 30-MAR-1998.
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.
Best Local Similarity: 36.25% Mismatches: 109
Query Match: 19.12% Indels: 8
RESULT 1485
ID AAR20556 standard; protein; 236 AA.
DE Fibrinogenolytic protein #3 from snake venom.
PN DE4023699-A.
PD 30-JAN-1992.
PA (BADI) BASF AG.
Best Local Similarity: 37.28% Mismatches: 92
Query Match: 19.02% Indels: 14
RESULT 1486
ID ABM82831 standard; protein; 233 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3080.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 36.78% Mismatches: 77
Query Match: 18.97% Indels: 42
RESULT 1487
ID AAE39993 standard; protein; 253 AA.
DE Human adipin protein #2.
PN US2003092620-A1.
PD 15-MAY-2003.
PA (GEST) GENSET SA.
Best Local Similarity: 38.00% Mismatches: 91
Query Match: 18.93% Indels: 18
RESULT 1488
ID ABG75785 standard; protein; 227 AA.
DE Trypsin domain consensus sequence, PFAM.
PN US2002165152-A1.
PD 07-NOV-2002.
PA (KAPE/) KAPPELLER-LIBERMANN R.
Best Local Similarity: 40.43% Mismatches: 60
Query Match: 18.83% Indels: 48
RESULT 1489
ID ADE58223 standard; protein; 253 AA.
DE Human Protein P00746, SEQ ID NO 4094.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
Best Local Similarity: 38.49% Mismatches: 91
Query Match: 18.83% Indels: 18
RESULT 1490
ID AAP70758 standard; protein; 269 AA.
DE Pig pancreas elastase-2.
PN JP62000276-A.
PD 06-JAN-1987.
PA (SANY) SANKYO CO LTD.
Best Local Similarity: 38.55% Mismatches: 100
Query Match: 18.78% Indels: 28
RESULT 1491
ID AAE39992 standard; protein; 253 AA.
DE Human adipin protein #1.

PN US2003092620-A1.
PD 15-MAY-2003.
PA (GEST) GENSET SA.
Best Local Similarity: 38.49% Mismatches: 92
Query Match: 18.73% Indels: 18
RESULT 1492
ID AAB11710 standard; protein; 264 AA.
DE Human serine protease BSSP5 (hbSSP5) SEQ ID NO:2.
PN WO2000031243-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Best Local Similarity: 36.84% Mismatches: 105
Query Match: 18.71% Indels: 25
RESULT 1493
ID ABR39439 standard; protein; 264 AA.
DE Human GENSET polypeptide clone name vCTRL-1.
PN WO2003014151-A2.
PD 20-FEB-2003.
PA (GEST) GENSET SA.
Best Local Similarity: 36.84% Mismatches: 105
Query Match: 18.71% Indels: 25
RESULT 1494
ID ABU09382 standard; protein; 271 AA.
DE Consensus sequence of trypsin-like domain.
PN WO2003031463-A2.
PD 17-APR-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 39.05% Mismatches: 86
Query Match: 18.68% Indels: 56
RESULT 1495
ID ABM82830 standard; protein; 212 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3079.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 36.33% Mismatches: 79
Query Match: 18.66% Indels: 45
RESULT 1496
ID ABM82644 standard; protein; 212 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2893.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 36.33% Mismatches: 79
Query Match: 18.66% Indels: 45
RESULT 1497
ID ABM81778 standard; protein; 264 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO2719, SEQ:4580.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 36.84% Mismatches: 105
Query Match: 18.66% Indels: 25
RESULT 1498
ID ADR66037 standard; protein; 213 AA.
DE Human prostatic carcinoma derived protein SEQ ID 233 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Best Local Similarity: 40.19% Mismatches: 85
Query Match: 18.64% Indels: 14
RESULT 1499
ID ADR66935 standard; protein; 213 AA.
DE Human prostatic carcinoma derived DNA SEQ ID 233 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.

PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Best Local Similarity: 40.19% Mismatches: 85
Query Match: 18.64% Indels: 14
RESULT 1500
ID ADE58221 standard; protein; 263 AA.
DE Rat Protein AAB31922, SEQ ID NO 4092.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Best Local Similarity: 37.41% Mismatches: 106
Query Match: 18.64% Indels: 22

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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 5, 2005, 22:38:43 ; Search time 40 Seconds
(without alignments)
4072.106 Million cell updates/sec

Title: US-10-015-385A-193

Perfect score: 2066
Sequence: 1 caagcaggtcatcccttg.....aggggcaaaaaaaaaa 1091

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_epool_p/US10015385/runat_05032005_173552_17285/app_query_fasta_1.1287
-DB=Issued_Patents_AA -QWMT=fascan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=dioum62 -TRANS=human40.cdi
-LIST=1500 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10015385 @CGN 1.1 46 @runat_05032005_173552_17285 -NCPUS=6 -ICPUS=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1372.5	66.4	254	4	US-09-949-016-6948
2	1371.5	66.4	249	4	US-09-949-016-8151
3	811	39.3	162	4	US-09-244-111-6
4	632.5	30.6	260	4	US-09-618-259-7
5	628.5	30.4	260	3	US-09-070-526-2
6	624.5	30.2	260	3	US-09-008-271A-7
7	622.5	30.1	260	3	US-09-025-059-3
8	622.5	30.1	260	4	US-09-618-259-8
9	618.5	29.9	250	4	US-09-205-238-427
10	618.5	29.9	282	3	US-09-025-059-1
11	602.5	29.2	288	4	US-09-386-642-13
12	598.5	29.0	289	4	US-09-386-642-14

13	597.5	28.9	248	3	US-08-944-483-24	Sequence 24, Appl
14	573	27.7	247	2	US-08-956-267A-2	Sequence 2, Appl
15	569	27.5	325	4	US-09-949-016-7713	Sequence 7713, Ap
16	568	27.5	290	4	US-09-949-016-8166	Sequence 8166, Ap
17	564.5	27.3	270	4	US-09-949-016-7712	Sequence 7712, Ap
18	564.5	27.3	293	4	US-09-509-908-2	Sequence 2, Appl
19	564	27.3	276	1	US-08-467-155A-1	Sequence 1, Appl
20	564	27.3	276	2	US-08-628-198-1	Sequence 1, Appl
21	564	27.3	276	3	US-09-201-038-1	Sequence 1, Appl
22	564	27.3	276	5	PCT-US96-07343-1	Sequence 1, Appl
23	561	27.2	244	1	US-08-361-395-1	Sequence 1, Appl
24	560	27.1	265	4	US-09-949-016-7716	Sequence 7716, Ap
25	555	26.9	253	2	US-08-557-146-2	Sequence 2, Appl
26	555	26.9	253	2	US-08-824-874-3	Sequence 3, Appl
27	555	26.9	253	2	US-09-154-344-2	Sequence 2, Appl
28	555	26.9	253	3	US-08-930-188-2	Sequence 2, Appl
29	555	26.9	253	3	US-09-210-084-3	Sequence 3, Appl
30	555	26.9	253	4	US-09-764-762-3	Sequence 3, Appl
31	555	26.9	253	5	PCT-US96-04294-2	Sequence 2, Appl
32	552	26.7	229	3	US-09-120-582-2	Sequence 2, Appl
33	547	26.5	223	1	US-08-278-091-9	Sequence 9, Appl
34	547	26.5	223	1	US-08-483-859-9	Sequence 9, Appl
35	547	26.5	223	1	US-08-472-173-9	Sequence 9, Appl
36	547	26.5	223	2	US-08-487-167-9	Sequence 9, Appl
37	547	26.5	223	2	US-08-482-816-9	Sequence 9, Appl
38	547	26.5	223	2	US-08-296-149-9	Sequence 9, Appl
39	547	26.5	223	2	US-08-801-499-9	Sequence 9, Appl
40	547	26.5	223	2	US-08-615-271-9	Sequence 9, Appl
41	547	26.5	223	3	US-09-074-660-9	Sequence 9, Appl
42	547	26.5	223	3	US-09-074-659-9	Sequence 9, Appl
43	547	26.5	223	3	US-09-106-468-9	Sequence 9, Appl
44	547	26.5	223	3	US-09-106-467-9	Sequence 9, Appl
45	547	26.5	223	3	US-09-601-318-2	Sequence 2, Appl
46	547	26.5	223	4	US-09-618-259-11	Sequence 11, Appl
47	546	26.4	244	4	US-09-027-337-4	Sequence 4, Appl
48	545	26.4	225	4	US-09-654-600A-4	Sequence 4, Appl
49	545	26.4	225	4	US-08-628-198-11	Sequence 11, Appl
50	544.5	26.4	291	1	US-08-467-155A-11	Sequence 11, Appl
51	544.5	26.4	291	2	US-08-628-198-11	Sequence 11, Appl
52	544.5	26.4	291	3	US-09-201-038-11	Sequence 11, Appl
53	544.5	26.4	291	3	PCT-US96-07343-11	Sequence 11, Appl
54	544.5	26.4	291	5	US-08-978-404B-44	Sequence 44, Appl
55	543	26.3	246	2	US-08-944-483-33	Sequence 33, Appl
56	540	26.1	224	3	US-08-978-404B-43	Sequence 43, Appl
57	539.5	25.6	225	2	US-08-557-146-12	Sequence 12, Appl
58	539.5	25.6	225	2	US-09-154-344-12	Sequence 12, Appl
59	524	25.4	232	2	US-08-978-404B-45	Sequence 45, Appl
60	520	25.2	232	1	US-08-278-091-8	Sequence 8, Appl
61	520	25.2	232	1	US-08-483-859-8	Sequence 8, Appl
62	520	25.2	232	2	US-08-472-173-8	Sequence 8, Appl
63	520	25.2	232	2	US-08-487-167-8	Sequence 8, Appl
64	520	25.2	232	2	US-08-482-816-8	Sequence 8, Appl
65	520	25.2	232	2	US-08-296-149-8	Sequence 8, Appl
66	520	25.2	232	2	US-08-801-499-8	Sequence 8, Appl
67	520	25.2	232	2	US-08-615-271-8	Sequence 8, Appl
68	520	25.2	232	3	US-09-074-660-8	Sequence 8, Appl
69	520	25.2	232	3	US-09-074-659-8	Sequence 8, Appl
70	520	25.2	232	3	US-09-106-468-8	Sequence 8, Appl
71	520	25.2	232	3	US-09-106-466A-8	Sequence 8, Appl
72	520	25.2	232	3	US-09-106-467-8	Sequence 8, Appl
73	518.5	25.1	268	2	US-08-824-874-1	Sequence 1, Appl
74	518.5	25.1	268	3	US-09-210-084-1	Sequence 1, Appl
75	518.5	25.1	268	4	US-09-764-762-1	Sequence 1, Appl
76	503	24.3	263	2	US-08-790-137-4	Sequence 4, Appl
77	503	24.3	263	2	US-08-824-874-5	Sequence 5, Appl
78	503	24.3	263	3	US-08-807-151-5	Sequence 5, Appl
79	503	24.3	263	3	US-09-210-084-5	Sequence 5, Appl
80	503	24.3	263	3	US-09-478-957-5	Sequence 5, Appl
81	503	24.3	263	4	US-09-764-762-5	Sequence 5, Appl
82	501	24.2	249	4	US-09-949-016-8770	Sequence 8770, Ap
83	498	24.1	254	3	US-09-439-313-525	Sequence 525, App
84	498	24.1	254	4	US-09-636-215-525	Sequence 525, App
85	498	24.1	254	4	US-09-685-166A-525	Sequence 525, App

86	498	24.1	254	4	US-09-679-426-525	Sequence 525, App	159	459	22.2	238	4	US-09-664-595A-15	Sequence 15, Appl
87	498	24.1	254	4	US-09-759-143-525	Sequence 525, App	160	459	22.2	262	3	US-09-025-059-4	Sequence 4, Appl
88	498	24.1	254	4	US-09-651-236-525	Sequence 525, App	161	459	22.2	262	4	US-09-755-100A-14	Sequence 14, Appl
89	497.5	24.1	281	1	US-08-467-155A-7	Sequence 7, Appl	162	458.5	22.2	261	3	US-08-768-859A-6	Sequence 6, Appl
90	497.5	24.1	281	2	US-08-628-138-7	Sequence 7, Appl	163	458.5	22.2	261	3	US-08-767-820A-6	Sequence 6, Appl
91	497.5	24.1	281	3	US-09-201-038-7	Sequence 7, Appl	164	458.5	22.2	261	3	US-08-622-046B-14	Sequence 14, Appl
92	497.5	24.1	281	5	PCT-US96-07343-7	Sequence 7, Appl	165	458.5	22.2	261	3	US-09-100-264-7	Sequence 7, Appl
93	497	24.1	258	1	US-08-744-026-3	Sequence 3, Appl	166	458.5	22.2	261	3	US-09-983-075D-7	Sequence 7, Appl
94	497	24.1	258	2	US-09-102-732-3	Sequence 3, Appl	167	458.5	22.2	261	3	US-08-843-076D-3	Sequence 3, Appl
95	497	24.1	258	3	US-09-261-767-3	Sequence 3, Appl	168	458.5	22.2	278	4	US-09-949-016-7711	Sequence 7711, Ap
96	496.5	23.0	248	1	US-08-744-026-1	Sequence 1, Appl	169	458	22.2	228	1	US-08-278-031-7	Sequence 7, Appl
97	496.5	24.0	248	2	US-09-102-732-1	Sequence 1, Appl	170	458	22.2	228	1	US-08-483-859-7	Sequence 7, Appl
98	496.5	24.0	248	3	US-09-261-767-1	Sequence 1, Appl	171	458	22.2	228	1	US-08-472-173-7	Sequence 7, Appl
99	494	23.9	254	3	US-09-436-313-523	Sequence 523, App	172	458	22.2	228	2	US-08-487-167-7	Sequence 7, Appl
100	494	23.9	254	4	US-09-636-215-523	Sequence 523, App	173	458	22.2	228	2	US-08-482-816-7	Sequence 7, Appl
101	494	23.9	254	4	US-09-685-166A-523	Sequence 523, App	174	458	22.2	228	2	US-08-296-149-7	Sequence 7, Appl
102	494	23.9	254	4	US-09-679-426-523	Sequence 523, App	175	458	22.2	228	2	US-08-801-439-7	Sequence 7, Appl
103	494	23.9	254	4	US-09-759-143-523	Sequence 523, App	176	458	22.2	228	2	US-08-615-271-7	Sequence 7, Appl
104	494	23.9	254	4	US-09-651-236-523	Sequence 523, App	177	458	22.2	228	3	US-09-074-660-7	Sequence 7, Appl
105	493	23.9	262	2	US-08-790-137-1	Sequence 1, Appl	178	458	22.2	228	3	US-09-074-659-7	Sequence 7, Appl
106	493	23.9	262	2	US-08-137-3	Sequence 4, Appl	179	458	22.2	228	3	US-09-106-468-7	Sequence 7, Appl
107	493	23.9	262	2	US-08-681-151-4	Sequence 4, Appl	180	458	22.2	228	3	US-09-106-466A-7	Sequence 7, Appl
108	493	23.9	262	2	US-08-824-874-4	Sequence 4, Appl	181	458	22.2	228	3	US-09-106-467-7	Sequence 7, Appl
109	493	23.9	262	3	US-08-807-151-4	Sequence 4, Appl	182	457.5	22.1	237	3	US-08-768-859A-1	Sequence 1, Appl
110	493	23.9	262	3	US-09-210-084-4	Sequence 4, Appl	183	457.5	22.1	237	3	US-08-767-820A-1	Sequence 7, Appl
111	493	23.9	262	3	US-09-478-957-4	Sequence 4, Appl	184	457.5	22.1	237	3	US-08-622-046B-7	Sequence 7, Appl
112	493	23.9	262	4	US-09-764-762-4	Sequence 4, Appl	185	457.5	22.1	237	3	US-08-944-483-38	Sequence 38, Appl
113	492	23.8	225	2	US-09-027-337-5	Sequence 5, Appl	186	457.5	22.1	237	3	US-09-100-264-3	Sequence 3, Appl
114	492	23.8	225	4	US-09-644-600-5	Sequence 5, Appl	187	457.5	22.1	237	4	US-09-303-339-2	Sequence 2, Appl
115	492	23.8	225	4	US-09-654-600A-5	Sequence 5, Appl	188	457.5	22.1	237	4	US-08-843-076D-7	Sequence 7, Appl
116	492	23.8	262	1	US-08-744-026-4	Sequence 4, Appl	189	457.5	22.1	237	4	US-09-303-208-1	Sequence 1, Appl
117	492	23.8	262	2	US-09-102-732-4	Sequence 4, Appl	190	455.5	22.0	237	1	US-08-096-946-11	Sequence 11, Appl
118	492	23.8	262	3	US-09-261-767-4	Sequence 4, Appl	191	455.5	22.0	237	5	PCT-US94-07329-11	Sequence 11, Appl
119	491	23.8	221	4	US-09-959-392-33	Sequence 33, Appl	192	455.5	22.0	237	5	PCT-US95-06157-1	Sequence 1, Appl
120	490	23.7	224	3	US-08-944-483-34	Sequence 34, Appl	193	455.5	22.0	261	3	US-08-768-859A-19	Sequence 19, Appl
121	487.5	23.6	449	4	US-09-636-215-617	Sequence 617, App	194	455.5	22.0	261	3	US-08-767-820A-19	Sequence 19, Appl
122	487.5	23.6	449	4	US-09-685-166A-617	Sequence 617, App	195	455.5	22.0	261	3	US-08-622-046B-3	Sequence 3, Appl
123	487.5	23.6	449	4	US-09-679-426-617	Sequence 617, App	196	454.5	22.0	232	2	US-08-897-340-31	Sequence 31, Appl
124	487.5	23.6	449	4	US-09-759-143-617	Sequence 617, App	197	454.5	22.0	232	2	US-09-252-329-31	Sequence 31, Appl
125	487.5	23.6	449	4	US-09-651-236-617	Sequence 617, App	198	454.5	22.0	244	5	PCT-US95-06157-10	Sequence 10, Appl
126	487	23.6	224	2	US-08-766-982-13	Sequence 13, Appl	199	454.5	21.9	238	5	PCT-US95-06157-8	Sequence 8, Appl
127	487	23.6	224	3	US-08-944-483-36	Sequence 36, Appl	200	452.5	21.9	244	3	US-08-768-859A-10	Sequence 10, Appl
128	487	23.6	224	3	US-09-296-219-13	Sequence 13, Appl	201	452.5	21.9	244	3	US-08-767-820A-10	Sequence 10, Appl
129	478.5	23.2	375	4	US-09-755-100A-11	Sequence 11, Appl	202	452.5	21.9	244	3	US-08-622-046B-16	Sequence 16, Appl
130	478	23.1	220	3	US-08-944-483-35	Sequence 35, Appl	203	452.5	21.9	244	3	US-09-100-264-5	Sequence 5, Appl
131	472.5	22.9	220	3	US-09-439-313-327	Sequence 327, App	204	452.5	21.9	244	4	US-08-843-076D-5	Sequence 5, Appl
132	472.5	22.9	220	3	US-09-352-616A-327	Sequence 327, App	205	450.5	21.8	237	2	US-08-844-024-2	Sequence 2, Appl
133	472.5	22.9	220	4	US-09-232-149A-327	Sequence 327, App	206	450.5	21.8	237	2	US-08-718-547-2	Sequence 2, Appl
134	472.5	22.9	220	4	US-09-636-215-327	Sequence 327, App	207	450.5	21.8	237	3	US-08-768-859A-16	Sequence 16, Appl
135	472.5	22.9	220	4	US-09-685-166A-327	Sequence 327, App	208	450.5	21.8	237	3	US-08-767-820A-16	Sequence 16, Appl
136	472.5	22.9	220	4	US-09-688-489-327	Sequence 327, App	209	450.5	21.8	237	3	US-08-622-046B-12	Sequence 12, Appl
137	472.5	22.9	220	4	US-09-679-426-327	Sequence 327, App	210	450.5	21.8	237	3	US-08-944-483-37	Sequence 37, Appl
138	472.5	22.9	220	4	US-09-759-143-327	Sequence 327, App	211	450.5	21.8	237	3	US-09-100-264-1	Sequence 1, Appl
139	472.5	22.9	220	4	US-09-651-236-327	Sequence 327, App	212	450.5	21.8	237	4	US-08-843-076D-1	Sequence 1, Appl
140	472.5	22.8	262	4	US-08-618-259-9	Sequence 9, Appl	213	450.5	21.8	238	3	US-08-768-859A-8	Sequence 8, Appl
141	470.5	22.8	261	1	US-08-744-026-5	Sequence 5, Appl	214	450.5	21.8	238	3	US-08-767-820A-8	Sequence 8, Appl
142	470.5	22.8	261	2	US-09-102-732-5	Sequence 5, Appl	215	450	21.8	260	3	US-08-983-075D-9	Sequence 9, Appl
143	470.5	22.8	261	3	US-09-083-521-6	Sequence 6, Appl	216	449.5	21.8	244	3	US-08-622-046B-5	Sequence 5, Appl
144	470.5	22.8	261	3	US-09-261-767-5	Sequence 5, Appl	217	448.5	21.7	237	1	US-08-096-946-10	Sequence 10, Appl
145	470.5	22.8	261	4	US-09-413-049-1	Sequence 1, Appl	218	448.5	21.7	237	5	PCT-US94-07329-10	Sequence 10, Appl
146	470.5	22.8	261	4	US-09-907-402-1	Sequence 1, Appl	219	448.5	21.7	237	5	PCT-US95-06157-16	Sequence 16, Appl
147	470.5	22.8	261	4	US-09-618-259-10	Sequence 10, Appl	220	447.5	21.7	237	3	US-08-768-859A-21	Sequence 21, Appl
148	470	22.7	238	3	US-08-944-483-39	Sequence 39, Appl	221	447.5	21.7	237	3	US-08-767-820A-21	Sequence 21, Appl
149	469.5	22.7	271	1	US-08-467-155A-10	Sequence 10, Appl	222	447.5	21.7	237	3	US-08-622-046B-1	Sequence 1, Appl
150	469.5	22.7	271	2	US-08-628-138-10	Sequence 10, Appl	223	447.5	21.7	237	3	US-09-100-264-12	Sequence 12, Appl
151	469.5	22.7	271	3	US-09-201-038-10	Sequence 10, Appl	224	447.5	21.7	237	4	US-08-843-076D-8	Sequence 8, Appl
152	469.5	22.7	271	5	PCT-US96-07343-10	Sequence 10, Appl	225	445	21.5	240	1	US-08-472-228A-1	Sequence 1, Appl
153	469	22.7	284	4	US-09-386-642-54	Sequence 54, Appl	226	445	21.5	240	5	PCT-US96-09303-1	Sequence 1, Appl
154	464.5	22.5	286	1	US-08-467-155A-9	Sequence 9, Appl	227	445	21.5	240	5	US-08-467-155A-8	Sequence 8, Appl
155	464.5	22.5	286	2	US-08-628-138-9	Sequence 9, Appl	228	430	20.8	299	2	US-08-628-138-8	Sequence 8, Appl
156	464.5	22.5	286	3	US-09-201-038-9	Sequence 9, Appl	229	430	20.8	299	2	US-09-201-038-8	Sequence 8, Appl
157	464.5	22.5	286	5	PCT-US96-07343-9	Sequence 9, Appl	230	430	20.8	299	5	US-08-628-138-8	Sequence 8, Appl
158	460.5	22.3	261	5	PCT-US95-06157-6	Sequence 6, Appl	231	430	20.8	299	5	PCT-US96-07343-8	Sequence 8, Appl

232	426.5	20.6	205	3	US-09-020-956-176	Sequence 176, App	Sequence 176, App	305	362.5	17.5	242	3	US-09-004-731-36	Sequence 36, Appl
233	426.5	20.6	205	3	US-09-030-607-176	Sequence 176, App	Sequence 176, App	306	362.5	17.5	242	3	US-08-749-699-36	Sequence 36, Appl
234	426.5	20.6	205	3	US-09-439-313-176	Sequence 176, App	Sequence 176, App	307	362.5	17.5	242	4	US-09-004-729-36	Sequence 36, Appl
235	426.5	20.6	205	3	US-09-352-616A-176	Sequence 176, App	Sequence 176, App	308	362.5	17.5	319	4	US-09-386-642-11	Sequence 11, Appl
236	426.5	20.6	205	4	US-09-233-149A-176	Sequence 176, App	Sequence 176, App	309	362.5	17.5	328	4	US-09-386-642-11	Sequence 12, Appl
237	426.5	20.6	205	4	US-09-159-812-176	Sequence 176, App	Sequence 176, App	310	358.5	17.4	232	4	US-09-959-392-31	Sequence 31, Appl
238	426.5	20.6	205	4	US-09-636-215-176	Sequence 176, App	Sequence 176, App	311	358	17.3	812	4	US-09-991-761A-7	Sequence 7, Appl
239	426.5	20.6	205	4	US-09-683-166A-176	Sequence 176, App	Sequence 176, App	312	357.5	17.3	822	3	US-08-906-769-81	Sequence 81, Appl
240	426.5	20.6	205	4	US-09-115-453-176	Sequence 176, App	Sequence 176, App	313	357.5	17.3	232	3	US-08-906-769-81	Sequence 81, Appl
241	426.5	20.6	205	4	US-09-688-489-176	Sequence 176, App	Sequence 176, App	314	357.5	17.3	232	3	US-08-906-616-81	Sequence 81, Appl
242	426.5	20.6	205	4	US-09-679-436-176	Sequence 176, App	Sequence 176, App	315	357.5	17.3	232	3	US-08-817-795-81	Sequence 81, Appl
243	426.5	20.6	205	4	US-09-759-143-176	Sequence 176, App	Sequence 176, App	316	357.5	17.3	232	3	US-08-639-075A-81	Sequence 81, Appl
244	426.5	20.6	205	4	US-09-651-236-176	Sequence 176, App	Sequence 176, App	317	357.5	17.3	232	3	US-09-012-431-81	Sequence 81, Appl
245	418	20.2	207	4	US-09-244-111-4	Sequence 4, Appl	Sequence 4, Appl	318	357.5	17.3	232	3	US-09-012-692-81	Sequence 81, Appl
246	417.5	20.2	233	2	US-08-738-413B-9	Sequence 9, Appl	Sequence 9, Appl	319	357.5	17.3	232	3	US-08-906-613-81	Sequence 81, Appl
247	406.5	19.7	231	4	US-09-402-515A-16	Sequence 16, Appl	Sequence 16, Appl	320	357	17.3	268	4	US-09-949-016-10712	Sequence 10712, A
248	406.5	19.7	246	4	US-09-205-258-1149	Sequence 1149, Ap	Sequence 1149, Ap	321	356.5	17.3	248	3	US-08-944-483-63	Sequence 63, Appl
249	404	19.6	234	1	US-08-684-862-6	Sequence 6, Appl	Sequence 6, Appl	322	355.5	17.2	148	4	US-09-618-259-2	Sequence 2, Appl
250	396	19.2	228	4	US-09-205-258-1150	Sequence 1150, Ap	Sequence 1150, Ap	323	355.5	17.2	231	2	US-09-027-337-6	Sequence 6, Appl
251	393	19.0	236	1	US-08-684-862-5	Sequence 5, Appl	Sequence 5, Appl	324	355.5	17.2	231	4	US-09-644-600-6	Sequence 6, Appl
252	390	18.9	236	2	US-08-738-413B-10	Sequence 10, Appl	Sequence 10, Appl	325	355.5	17.2	231	4	US-09-654-600A-6	Sequence 6, Appl
253	387	18.7	232	2	US-08-738-413B-11	Sequence 11, Appl	Sequence 11, Appl	326	355.5	17.2	276	2	US-09-016-366A-15	Sequence 15, Appl
254	387	18.7	253	6	5223425-8	Patent No. 5223425	Patent No. 5223425	327	355.5	17.2	276	2	US-08-978-404B-21	Sequence 21, Appl
255	387	18.7	253	6	5223425-8	Patent No. 5223425	Patent No. 5223425	328	354.5	17.2	461	6	5270178-2	Patent No. 5270178
256	385.5	18.7	267	4	US-09-949-016-9575	Sequence 9575, Ap	Sequence 9575, Ap	329	354.5	17.2	461	6	5270178-2	Patent No. 5270178
257	385	18.6	250	6	5223425-4	Patent No. 5223425	Patent No. 5223425	330	354	17.1	229	2	US-08-557-146-13	Sequence 13, Appl
258	385	18.6	250	6	5223425-4	Patent No. 5223425	Patent No. 5223425	331	354	17.1	229	2	US-09-154-344-13	Sequence 13, Appl
259	377.5	18.3	154	3	US-09-261-416-5	Sequence 5, Appl	Sequence 5, Appl	332	354	17.1	461	6	5270178-17	Patent No. 5270178
260	374.5	18.1	238	6	5223425-5	Patent No. 5223425	Patent No. 5223425	333	354	17.1	461	6	5270178-18	Patent No. 5270178
261	374.5	18.1	238	6	5223425-5	Patent No. 5223425	Patent No. 5223425	334	354	17.1	461	6	5270178-17	Patent No. 5270178
262	374.5	18.1	259	6	5223425-2	Patent No. 5223425	Patent No. 5223425	335	354	17.1	461	6	5270178-18	Patent No. 5270178
263	374.5	18.1	259	6	5223425-2	Patent No. 5223425	Patent No. 5223425	336	353.5	17.1	230	3	US-08-944-483-62	Sequence 62, Appl
264	374	18.1	260	6	5223425-10	Patent No. 5223425	Patent No. 5223425	337	353.5	17.1	270	2	US-08-978-404B-8	Sequence 8, Appl
265	374	18.1	260	6	5223425-10	Patent No. 5223425	Patent No. 5223425	338	353.5	17.1	460	6	5270178-15	Patent No. 5270178
266	370.5	17.9	228	3	US-08-944-483-44	Sequence 44, Appl	Sequence 44, Appl	339	353.5	17.1	460	6	5270178-15	Patent No. 5270178
267	370	17.9	418	4	US-09-370-838-62	Sequence 62, Appl	Sequence 62, Appl	340	353	17.1	274	2	US-08-978-404B-5	Sequence 5, Appl
268	370	17.9	418	4	US-09-854-133-62	Sequence 62, Appl	Sequence 62, Appl	341	351.5	17.0	814	1	US-08-750-711-1	Sequence 1, Appl
269	368	17.8	299	3	US-08-944-483-66	Sequence 66, Appl	Sequence 66, Appl	342	351.5	17.0	1019	1	US-08-296-014A-4	Sequence 4, Appl
270	368	17.8	418	1	US-08-508-448C-25	Sequence 25, Appl	Sequence 25, Appl	343	351.5	17.0	1019	2	US-08-596-405-4	Sequence 4, Appl
271	368	17.8	418	4	US-09-370-838-82	Sequence 82, Appl	Sequence 82, Appl	344	351.5	17.0	1019	2	US-08-877-620-4	Sequence 4, Appl
272	368	17.8	418	4	US-09-370-838-83	Sequence 83, Appl	Sequence 83, Appl	345	351.5	17.0	1019	4	US-09-287-368-4	Sequence 4, Appl
273	368	17.8	418	4	US-09-854-133-82	Sequence 82, Appl	Sequence 82, Appl	346	351.5	17.0	1019	4	US-09-626-795-4	Sequence 4, Appl
274	368	17.8	418	4	US-09-854-133-83	Sequence 83, Appl	Sequence 83, Appl	347	351.5	17.0	1083	1	US-08-296-014A-2	Sequence 2, Appl
275	367	17.8	234	2	US-08-738-413B-12	Sequence 12, Appl	Sequence 12, Appl	348	351.5	17.0	1083	2	US-08-596-405-2	Sequence 2, Appl
276	366.5	17.7	400	3	US-09-518-046-20	Sequence 20, Appl	Sequence 20, Appl	349	351.5	17.0	1083	2	US-08-877-620-2	Sequence 2, Appl
277	366.5	17.7	400	3	US-09-004-731-30	Sequence 30, Appl	Sequence 30, Appl	350	351.5	17.0	1083	4	US-09-287-368-2	Sequence 2, Appl
278	366.5	17.7	400	3	US-09-004-731-33	Sequence 33, Appl	Sequence 33, Appl	351	351.5	17.0	1083	4	US-09-626-795-2	Sequence 2, Appl
279	366.5	17.7	400	3	US-08-749-699-33	Sequence 30, Appl	Sequence 30, Appl	352	349.5	16.9	166	4	US-08-636-215-838	Sequence 838, App
280	366.5	17.7	400	3	US-08-749-699-33	Sequence 33, Appl	Sequence 33, Appl	353	349.5	16.9	166	4	US-09-685-166A-838	Sequence 838, App
281	366.5	17.7	400	4	US-09-004-729-30	Sequence 30, Appl	Sequence 30, Appl	354	349.5	16.9	166	4	US-09-679-426-838	Sequence 838, App
282	366.5	17.7	400	4	US-09-004-729-30	Sequence 33, Appl	Sequence 33, Appl	355	349.5	16.9	166	4	US-09-759-143-838	Sequence 838, App
283	366	17.7	232	1	US-08-508-448C-19	Sequence 19, Appl	Sequence 19, Appl	356	349.5	16.9	166	4	US-09-651-236-838	Sequence 838, App
284	365.5	17.7	245	3	US-08-906-769-121	Sequence 121, App	Sequence 121, App	357	349	16.9	159	3	US-09-020-956-172	Sequence 172, App
285	365.5	17.7	245	3	US-08-906-616-121	Sequence 121, App	Sequence 121, App	358	349	16.9	159	3	US-08-030-607-172	Sequence 172, App
286	365.5	17.7	245	3	US-08-639-075A-121	Sequence 121, App	Sequence 121, App	359	349	16.9	159	3	US-09-439-313-172	Sequence 172, App
287	365.5	17.7	245	3	US-09-012-692-121	Sequence 121, App	Sequence 121, App	360	349	16.9	159	3	US-09-352-616A-172	Sequence 172, App
288	365.5	17.7	245	3	US-08-906-613-121	Sequence 121, App	Sequence 121, App	361	349	16.9	159	4	US-09-232-149A-172	Sequence 172, App
289	365.5	17.7	245	3	US-08-906-613-121	Sequence 121, App	Sequence 121, App	362	349	16.9	159	4	US-09-159-812-172	Sequence 172, App
290	364.5	17.6	312	4	US-09-023-942A-4	Sequence 4, Appl	Sequence 4, Appl	363	349	16.9	159	4	US-09-636-215-172	Sequence 172, App
291	363.5	17.6	314	3	US-09-008-271A-3	Sequence 3, Appl	Sequence 3, Appl	364	349	16.9	159	4	US-08-685-166A-172	Sequence 172, App
292	363.5	17.6	314	4	US-09-023-942A-6	Sequence 6, Appl	Sequence 6, Appl	365	349	16.9	159	4	US-09-115-453-172	Sequence 172, App
293	363.5	17.6	314	4	US-09-907-794A-257	Sequence 257, App	Sequence 257, App	366	349	16.9	159	4	US-09-688-489-172	Sequence 172, App
294	363.5	17.6	314	4	US-09-905-125A-257	Sequence 257, App	Sequence 257, App	367	349	16.9	159	4	US-09-679-426-172	Sequence 172, App
295	363.5	17.6	314	4	US-09-902-770A-257	Sequence 257, App	Sequence 257, App	368	349	16.9	159	4	US-09-759-143-172	Sequence 172, App
296	363.5	17.6	314	4	US-09-906-700A-257	Sequence 257, App	Sequence 257, App	369	349	16.9	159	4	US-09-651-236-172	Sequence 172, App
297	363.5	17.6	314	4	US-09-903-603A-257	Sequence 257, App	Sequence 257, App	370	348	16.8	461	6	5460953-3	Patent No. 5460953
298	363.5	17.6	314	4	US-09-904-920A-257	Sequence 257, App	Sequence 257, App	371	348	16.8	461	6	5460953-3	Patent No. 5460953
299	363.5	17.6	314	4	US-09-909-064A-257	Sequence 257, App	Sequence 257, App	372	347	16.8	262	1	US-07-720-189-1	Sequence 1, Appl
300	363.5	17.6	314	4	US-09-905-381A-257	Sequence 257, App	Sequence 257, App	373	347	16.8	284	4	US-09-387-375-7	Sequence 7, Appl
301	363.5	17.6	314	4	US-09-906-618-257	Sequence 257, App	Sequence 257, App	374	347	16.8	284	4	US-10-041-400A-7	Sequence 7, Appl
302	363.5	17.6	387	3	US-09-032-215-3	Sequence 8, Appl	Sequence 8, Appl	375	347	16.8	284	4	US-10-042-091A-7	Sequence 7, Appl
303	363.5	17.6	236	1	US-08-684-862-4	Sequence 13, Appl	Sequence 13, Appl	376	347	16.8	306	4	US-09-386-642-53	Sequence 53, Appl
304	363	17.6	236	1	US-08-684-862-4	Sequence 4, Appl	Sequence 4, Appl	377	347	16.8	356	4	US-09-054-272-18	Sequence 18, Appl

378	347	16.8	409	3	US-09-065-872-2	Sequence 2, Appli	451	340.5	16.5	230	1	US-08-266-407A-47	Sequence 47, Appl
379	347	16.8	409	4	US-03-667-570A-2	Sequence 2, Appli	452	340.5	16.5	230	2	US-08-892-544-47	Sequence 47, Appl
380	347	16.8	410	3	US-09-065-872-1	Sequence 1, Appli	453	340.5	16.5	230	2	US-08-766-982-12	Sequence 12, Appl
381	347	16.8	410	4	US-09-067-570A-1	Sequence 1, Appli	454	340.5	16.5	230	3	US-08-944-483-53	Sequence 53, Appl
382	347	16.8	419	1	US-08-295-411-1	Sequence 1, Appli	455	340.5	16.5	230	3	US-09-296-219-12	Sequence 12, Appl
383	347	16.8	419	2	US-08-955-471-1	Sequence 1, Appli	456	340.5	16.5	244	4	US-09-601-318-4	Sequence 4, Appli
384	347	16.8	419	4	US-09-667-570A-3	Sequence 3, Appli	457	340.5	16.5	244	4	US-09-601-318-5	Sequence 5, Appli
385	347	16.8	419	4	US-10-182-263-1	Sequence 1, Appli	458	340.5	16.5	244	4	US-09-601-318-6	Sequence 6, Appli
386	347	16.8	419	5	PCT-US92-1042-1	Sequence 1, Appli	459	340.5	16.5	244	4	US-09-601-318-7	Sequence 7, Appli
387	347	16.8	460	2	US-08-756-506-2	Sequence 2, Appli	460	340.5	16.5	245	4	US-09-079-970A-6	Sequence 1, Appli
388	347	16.8	460	2	US-08-756-506-4	Sequence 4, Appli	461	340.5	16.5	245	4	US-09-016-366A-23	Sequence 23, Appl
389	347	16.8	461	4	US-10-182-263-2	Sequence 2, Appli	462	340.5	16.5	267	2	US-08-978-404B-18	Sequence 18, Appl
390	347	16.8	461	4	US-09-054-272-32	Sequence 32, Appl	463	340.5	16.5	267	2	US-09-917-254-101	Sequence 101, App
391	347	16.8	461	4	US-09-949-016-5921	Sequence 5921, Ap	464	340.5	16.5	267	3	US-08-705-875A-6	Sequence 6, Appli
392	347	16.8	461	6	5225337-2	Patent No. 5225337	465	340.5	16.5	300	3	US-09-242-999-6	Sequence 6, Appli
393	347	16.8	461	6	5225337-2	Patent No. 5225337	466	340.5	16.5	300	4	US-09-851-588-6	Sequence 2, Appli
394	347	16.8	485	4	US-09-949-016-10882	Sequence 10882, A	467	340.5	16.5	406	4	US-09-851-588-6	Sequence 2, Appli
395	346.5	16.8	791	1	US-08-643-219-1	Sequence 1, Appli	468	340.5	16.5	423	4	US-09-656-002-2	Sequence 2, Appli
396	346.5	16.8	791	3	US-08-851-350-1	Sequence 1, Appli	469	340.5	16.5	435	3	US-09-008-271A-6	Sequence 6, Appli
397	346	16.7	234	3	US-08-944-483-46	Sequence 46, Appl	470	340.5	16.5	435	4	US-09-607-745-2	Sequence 8, Appli
398	346	16.7	241	3	US-08-944-483-59	Sequence 59, Appl	471	340.5	16.5	437	4	US-09-851-588-8	Sequence 3, Appli
399	346	16.7	419	4	US-10-182-263-5	Sequence 5, Appli	472	340	16.5	419	4	US-10-182-263-3	Sequence 2, Appli
400	346	16.7	419	4	US-10-182-263-6	Sequence 6, Appli	473	339.5	16.4	253	3	US-09-578-303-4	Sequence 2, Appli
401	345.5	16.7	248	3	US-08-906-769-111	Sequence 111, App	474	339.5	16.4	258	1	US-07-990-301A-2	Sequence 8, Appli
402	345.5	16.7	248	3	US-08-906-616-111	Sequence 111, App	475	339.5	16.4	333	4	US-08-991-761A-8	Sequence 2, Appli
403	345.5	16.7	248	3	US-08-817-795-111	Sequence 111, App	476	339	16.4	419	4	US-10-182-263-4	Sequence 4, Appli
404	345.5	16.7	248	3	US-08-633-075A-111	Sequence 111, App	477	339	16.4	461	3	US-08-742-877-2	Sequence 2, Appli
405	345.5	16.7	248	3	US-09-012-692-111	Sequence 111, App	478	339	16.4	461	3	US-09-053-871A-21	Sequence 21, Appl
406	345.5	16.7	248	3	US-08-906-613-111	Sequence 111, App	479	339	16.4	461	6	US-10-133-907-5	Sequence 5, Appli
407	345.5	16.7	248	3	PCT-US95-14442A-111	Sequence 111, App	480	339	16.4	461	6	5521070-2	Patent No. 5521070
408	345.5	16.7	248	5	US-09-016-366A-21	Sequence 21, Appl	481	339	16.4	461	6	5521070-2	Patent No. 5521070
409	344	16.7	274	2	US-08-978-404B-16	Sequence 16, Appl	482	339	16.4	480	4	US-09-949-016-11123	Sequence 11123, A
410	344	16.7	274	2	US-08-978-404B-16	Sequence 16, Appl	483	339	16.4	481	4	US-09-949-016-9238	Sequence 9238, Ap
411	343.5	16.6	273	2	US-08-978-404B-3	Sequence 3, Appli	484	339	16.4	481	4	US-09-949-016-9239	Sequence 9239, Ap
412	343.5	16.6	460	6	5270178-13	Sequence 3, Appli	485	339	16.4	637	4	US-09-949-016-11538	Sequence 11538, A
413	343.5	16.6	460	6	5270178-14	Sequence 14, Appl	486	339	16.4	637	4	US-09-949-016-11539	Sequence 11539, A
414	343.5	16.6	460	6	5270178-16	Sequence 16, Appl	487	338.5	16.4	230	1	US-08-379-621-2	Sequence 2, Appli
415	343.5	16.6	460	6	5270178-13	Sequence 13, Appl	488	338.5	16.4	230	1	US-08-147-000B-2	Sequence 2, Appli
416	343.5	16.6	460	6	5270178-14	Sequence 14, Appl	489	338.5	16.4	230	1	US-08-889-078-2	Sequence 2, Appli
417	343.5	16.6	460	6	5270178-16	Sequence 16, Appl	490	338.5	16.4	261	6	5270178-5	Patent No. 5270178
418	342.5	16.6	248	3	US-09-032-215-37	Sequence 37, Appl	491	338.5	16.4	261	6	5270178-5	Patent No. 5270178
419	342.5	16.6	249	3	US-09-079-970A-5	Sequence 5, Appli	492	338.5	16.4	308	3	US-08-705-875A-10	Sequence 10, Appl
420	342.5	16.6	273	2	US-08-978-404B-6	Sequence 6, Appli	493	338.5	16.4	308	4	US-08-242-999-10	Sequence 10, Appl
421	342.5	16.6	546	6	5200340-6	Patent No. 5200340	494	338	16.4	250	3	US-08-944-483-51	Sequence 51, Appl
422	342.5	16.6	546	6	5200340-6	Patent No. 5200340	495	337.5	16.3	267	3	US-09-949-016-10711	Sequence 10711, A
423	342.5	16.6	713	4	US-09-949-016-9983	Sequence 9983, Ap	496	337	16.3	235	3	US-08-944-483-48	Sequence 48, Appl
424	342.5	16.6	790	2	US-08-463-486-54	Sequence 54, Appl	497	337	16.3	812	1	US-08-451-932-1	Sequence 1, Appli
425	342.5	16.6	790	2	US-08-469-658-54	Sequence 54, Appl	498	337	16.3	812	1	US-08-452-260-1	Sequence 1, Appli
426	342.5	16.6	791	2	US-09-131-995-1	Sequence 1, Appli	499	337	16.3	812	2	US-08-326-785-1	Sequence 1, Appli
427	342.5	16.6	791	2	US-08-832-087B-1	Sequence 1, Appli	500	337	16.3	812	2	US-08-612-788-1	Sequence 1, Appli
428	342.5	16.6	791	3	US-09-132-154-1	Sequence 1, Appli	501	337	16.3	812	2	US-08-605-598B-1	Sequence 1, Appli
429	342.5	16.6	791	4	US-08-991-761A-6	Sequence 6, Appli	502	337	16.3	812	2	US-08-429-743-1	Sequence 1, Appli
430	342.5	16.6	791	4	US-08-921-287A-1	Sequence 1, Appli	503	337	16.3	812	2	US-08-866-735-1	Sequence 1, Appli
431	342.5	16.6	810	1	US-07-854-603-2	Sequence 2, Appli	504	337	16.3	812	2	US-09-066-028-1	Sequence 1, Appli
432	342.5	16.6	810	1	US-08-147-000B-29	Sequence 29, Appl	505	337	16.3	812	3	US-09-132-012-3	Sequence 3, Appli
433	342.5	16.6	810	3	US-09-086-514-1	Sequence 1, Appli	506	337	16.3	812	4	US-09-335-325-1	Sequence 12, Appl
434	342.5	16.6	810	4	US-09-192-012-5	Sequence 5, Appli	507	337	16.3	812	4	US-08-991-761A-12	Sequence 12, Appl
435	342.5	16.6	810	4	US-09-403-736-1	Sequence 1, Appli	508	337	16.3	812	5	PCT-US95-05107-1	Sequence 1, Appli
436	342.5	16.6	810	4	US-09-701-265-1	Sequence 1, Appli	509	337	16.3	415	1	US-08-073-531B-1	Sequence 1, Appli
437	342.5	16.6	810	6	5200340-8	Patent No. 5200340	510	336	16.3	415	2	US-08-766-288-1	Sequence 1, Appli
438	342.5	16.6	810	6	5200340-8	Patent No. 5200340	511	336	16.3	415	2	US-08-991-761A-13	Sequence 13, Appl
439	342	16.6	234	1	US-08-684-862-3	Sequence 3, Appli	512	336	16.2	790	4	US-08-387-375-9	Sequence 9, Appli
440	342	16.6	273	2	US-09-016-366A-19	Sequence 19, Appl	513	334.5	16.3	316	4	US-09-387-375-9	Sequence 9, Appli
441	342	16.6	273	2	US-08-978-404B-14	Sequence 14, Appl	514	334.5	16.2	316	4	US-10-041-400A-9	Sequence 9, Appli
442	341.5	16.5	156	3	US-09-261-416-6	Sequence 6, Appli	515	334.5	16.2	316	4	US-10-042-091A-9	Sequence 9, Appli
443	341.5	16.5	261	6	5270178-19	Patent No. 5270178	516	334.5	16.2	446	4	US-10-177-661-4	Sequence 4, Appli
444	341.5	16.5	261	6	5270178-20	Patent No. 5270178	517	334.5	16.2	477	4	US-10-177-661-2	Sequence 2, Appli
445	341.5	16.5	261	6	5270178-19	Patent No. 5270178	518	334.5	16.2	562	4	US-09-879-792-12	Sequence 12, Appl
446	341.5	16.5	261	6	5270178-20	Patent No. 5270178	519	333.5	16.1	290	4	US-09-386-653A-7	Sequence 7, Appli
447	341	16.5	261	6	5270178-21	Patent No. 5270178	520	333.5	16.1	302	3	US-09-220-731-26	Sequence 26, Appl
448	341	16.5	261	6	5270178-21	Patent No. 5270178	521	333.5	16.1	302	4	US-09-242-999-22	Sequence 22, Appl
449	341	16.5	415	4	US-09-118-748-2	Sequence 2, Appli	522	333	16.1	415	1	US-08-295-411-2	Sequence 2, Appli
450	340.5	16.5	230	1	US-08-456-840-47	Sequence 47, Appl	523	333	16.1	415	2	US-08-955-471-2	Sequence 2, Appli

524	333	16.1	415	5	PCT-US92-10242-2	Sequence 2, Appli	597	324.5	15.7	461	4	US-09-949-016-8839	Sequence 8839, Ap
525	332.5	16.1	638	2	US-08-681-151-3	Sequence 3, Appli	598	324.5	15.7	466	1	US-07-882-202A-4	Sequence 4, Appli
526	332.5	16.1	810	4	US-08-991-761A-11	Sequence 11, Appl	599	324.5	15.7	466	1	US-08-021-615A-4	Sequence 4, Appli
527	331	16.0	295	3	US-08-338-368-2	Sequence 2, Appli	600	324.5	15.7	466	1	US-08-321-777-4	Sequence 4, Appli
528	331	16.0	579	1	US-08-295-411-4	Sequence 4, Appli	601	324.5	15.7	466	1	US-09-009-217-14	Sequence 14, Appl
529	331	16.0	579	2	US-08-955-471-4	Sequence 4, Appli	602	324.5	15.7	466	3	US-09-009-656-14	Sequence 14, Appl
530	331	16.0	579	3	US-09-117-708-14	Sequence 14, Appl	603	324.5	15.7	466	5	PCT-US93-04493-4	Sequence 4, Appli
531	331	16.0	579	5	PCT-US92-10242-4	Sequence 4, Appli	604	324.5	15.7	483	4	US-09-949-016-9523	Sequence 9523, Ap
532	331	16.0	615	1	US-07-998-972A-3	Sequence 3, Appli	605	323.5	15.7	275	2	US-09-016-366A-17	Sequence 17, Appl
533	331	16.0	615	1	US-08-463-953-3	Sequence 3, Appli	606	323.5	15.7	275	2	US-08-978-404B-12	Sequence 12, Appl
534	331	16.0	615	1	US-08-462-261-3	Sequence 3, Appli	607	322.5	15.6	255	2	US-09-027-337-7	Sequence 7, Appli
535	331	16.0	615	5	PCT-US92-11357-3	Sequence 3, Appli	608	322.5	15.6	255	4	US-09-644-600-7	Sequence 7, Appli
536	331	16.0	622	3	US-08-952-967-8	Sequence 8, Appli	609	322.5	15.6	255	4	US-09-654-600A-7	Sequence 7, Appli
537	331	16.0	622	4	US-09-054-272-42	Sequence 42, Appl	610	322.5	15.6	560	4	US-09-912-559-4	Sequence 4, Appli
538	330.5	16.0	560	4	US-09-949-016-6458	Sequence 6458, Ap	611	322	15.6	207	4	US-10-000-483-54	Sequence 54, Appl
539	330.5	16.0	560	4	US-09-912-559-3	Sequence 3, Appli	612	321.5	15.6	418	4	US-10-177-661-6	Sequence 6, Appli
540	330	16.0	221	3	US-08-944-483-54	Sequence 54, Appl	613	321.5	15.6	809	4	US-08-991-761A-9	Sequence 9, Appli
541	330	16.0	222	1	US-08-456-840-46	Sequence 46, Appl	614	321	15.5	248	2	US-08-851-974-3	Sequence 3, Appli
542	330	16.0	222	1	US-08-266-407A-46	Sequence 46, Appl	615	321	15.5	248	2	US-09-213-390-3	Sequence 3, Appli
543	330	16.0	222	1	US-08-892-544-46	Sequence 46, Appl	616	321	15.5	269	2	US-08-978-404B-10	Sequence 10, Appl
544	330	16.0	222	6	5223425-6	Patent No. 5223425	617	321	15.5	300	1	US-08-148-910-1	Sequence 1, Appli
545	330	16.0	222	6	5223425-6	Patent No. 5223425	618	321	15.5	300	1	US-08-448-937A-1	Sequence 1, Appli
546	329.5	15.9	230	4	US-09-601-318-3	Sequence 3, Appli	619	321	15.5	315	4	US-09-386-653A-9	Sequence 9, Appli
547	329.5	15.9	283	4	US-09-244-111-2	Sequence 2, Appli	620	321	15.5	655	1	US-08-148-910-12	Sequence 12, Appl
548	329.5	15.9	285	4	US-09-023-942A-26	Sequence 26, Appl	621	321	15.5	655	1	US-08-448-937A-12	Sequence 12, Appl
549	329.5	15.9	376	2	US-08-558-269-10	Sequence 10, Appl	622	320.5	15.5	254	3	US-08-944-483-50	Sequence 50, Appl
550	329.5	15.9	376	3	US-09-410-882-10	Sequence 10, Appl	623	319.5	15.5	240	1	US-08-278-091-11	Sequence 11, Appl
551	329	15.9	259	3	US-08-944-483-52	Sequence 52, Appl	624	319.5	15.5	240	1	US-08-483-853-11	Sequence 11, Appl
552	328.5	15.9	238	3	US-08-944-483-64	Sequence 64, Appl	625	319.5	15.5	240	1	US-08-472-173-11	Sequence 11, Appl
553	328.5	15.9	338	4	US-08-991-761A-10	Sequence 10, Appl	626	319.5	15.5	240	2	US-08-487-167-11	Sequence 11, Appl
554	328	15.9	255	1	US-08-650-129-5	Sequence 5, Appli	627	319.5	15.5	240	2	US-08-482-816-11	Sequence 11, Appl
555	328	15.9	255	3	US-08-984-417-5	Sequence 5, Appli	628	319.5	15.5	240	2	US-08-296-149-11	Sequence 11, Appl
556	328	15.9	699	4	US-09-949-016-6138	Sequence 6138, Ap	629	319.5	15.5	240	2	US-08-801-499-11	Sequence 11, Appl
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559	327.5	15.9	154	3	US-09-261-416-7	Sequence 7, Appli	632	319.5	15.5	240	3	US-09-074-669-11	Sequence 11, Appl
560	327	15.8	241	3	US-08-944-483-60	Sequence 60, Appl	633	319.5	15.5	240	3	US-09-106-468-11	Sequence 11, Appl
561	326.5	15.8	144	4	US-09-618-259-1	Sequence 1, Appli	634	319.5	15.5	240	3	US-09-106-466A-11	Sequence 11, Appl
562	325.5	15.8	261	3	US-08-163-919A-2	Sequence 2, Appli	635	319.5	15.5	240	3	US-09-106-467-11	Sequence 11, Appl
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565	325.5	15.8	492	1	US-08-469-486-2	Sequence 2, Appli	638	317.5	15.4	245	3	US-08-944-483-69	Sequence 69, Appl
566	325.5	15.8	492	2	US-08-469-658-2	Sequence 2, Appli	639	317	15.3	232	3	US-08-944-483-45	Sequence 45, Appl
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568	325	15.7	226	3	US-08-984-417-4	Sequence 4, Appli	641	316.5	15.3	226	1	US-07-929-198-2	Sequence 2, Appli
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571	324.5	15.7	228	1	US-08-472-173-10	Sequence 10, Appl	644	316.5	15.3	226	2	US-09-154-344-15	Sequence 15, Appl
572	324.5	15.7	228	2	US-08-487-167-10	Sequence 10, Appl	645	316.5	15.3	226	3	US-08-944-483-43	Sequence 43, Appl
573	324.5	15.7	228	2	US-08-816-16-10	Sequence 10, Appl	646	316	15.3	246	3	US-08-906-769-127	Sequence 127, App
574	324.5	15.7	228	2	US-08-296-149-10	Sequence 10, Appl	647	316	15.3	246	3	US-08-906-616-127	Sequence 127, App
575	324.5	15.7	228	2	US-08-801-499-10	Sequence 10, Appl	648	316	15.3	246	3	US-08-639-075A-127	Sequence 127, App
576	324.5	15.7	228	2	US-08-615-271-10	Sequence 10, Appl	649	316	15.3	246	3	US-09-012-431-127	Sequence 127, App
577	324.5	15.7	228	3	US-09-074-660-10	Sequence 10, Appl	650	316	15.3	246	3	US-09-012-692-127	Sequence 127, App
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579	324.5	15.7	228	3	US-09-106-468-10	Sequence 10, Appl	652	316	15.3	259	4	US-10-165-442-4	Sequence 4, Appli
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581	324.5	15.7	228	3	US-09-106-467-10	Sequence 10, Appl	654	315.5	15.3	292	4	US-09-578-303-5	Sequence 5, Appli
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585	324.5	15.7	406	4	US-09-782-587B-1	Sequence 1, Appli	658	315.5	15.3	487	1	US-08-469-486-53	Sequence 53, Appl
586	324.5	15.7	406	4	US-09-782-587B-3	Sequence 3, Appli	659	315.5	15.3	487	2	US-08-469-658-53	Sequence 53, Appl
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588	324.5	15.7	444	1	US-08-475-845-2	Sequence 2, Appli	661	315	15.2	691	4	US-09-949-016-7775	Sequence 7775, Ap
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590	324.5	15.7	444	2	US-08-660-289-2	Sequence 2, Appli	663	314	15.2	855	4	US-09-644-600-2	Sequence 2, Appli
591	324.5	15.7	444	2	US-08-537-807-2	Sequence 2, Appli	664	314	15.2	855	4	US-09-654-600A-2	Sequence 2, Appli
592	324.5	15.7	444	2	US-08-871-003-2	Sequence 2, Appli	665	313.5	15.2	226	1	US-07-929-198-4	Sequence 4, Appli
593	324.5	15.7	444	3	US-08-464-233-2	Sequence 2, Appli	666	312.5	15.1	242	4	US-09-959-392-34	Sequence 34, Appl
594	324.5	15.7	444	3	US-08-189-607-2	Sequence 2, Appli	667	312	15.1	248	3	US-08-944-483-71	Sequence 71, Appl
595	324.5	15.7	444	3	US-09-378-907-2	Sequence 2, Appli	668	311.5	15.1	251	3	US-08-944-483-47	Sequence 47, Appl
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674	311	15.1	812	4	US-09-192-012-9	Sequence 2, Appli	747	304	14.7	378	3	US-09-553-498-10	Sequence 10, Appli
675	311	15.1	1042	4	US-09-959-392-2	Sequence 2, Appli	748	304	14.7	378	4	US-09-618-869-10	Sequence 10, Appli
676	310.5	15.0	247	2	US-08-978-404B-47	Sequence 47, Appli	749	304	14.7	433	4	US-09-949-016-8220	Sequence 8220, Ap
677	310.5	15.0	314	4	US-09-636-382A-2	Sequence 2, Appli	750	304	14.7	472	2	US-08-811-949-63	Sequence 63, Appli
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680	309.5	15.0	492	4	US-09-879-752-14	Sequence 14, Appli	753	304	14.7	527	5	PCT-US91-01025A-2	Sequence 2, Appli
681	309.5	15.0	492	4	US-09-679-426-895	Sequence 895, App	754	304	14.7	527	6	5185259-8	Patent No. 5185259
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684	308.5	14.9	243	3	US-08-944-483-70	Sequence 70, Appli	757	304	14.7	562	2	US-08-560-098A-50	Sequence 50, Appli
685	308.5	14.9	317	4	US-09-386-629-7	Sequence 7, Appli	758	304	14.7	562	4	US-08-883-795A-38	Sequence 38, Appli
686	308.5	14.9	317	4	US-09-907-794A-263	Sequence 263, App	759	304	14.7	562	4	US-09-703-695A-4	Sequence 4, Appli
687	308.5	14.9	317	4	US-09-905-125A-263	Sequence 263, App	760	304	14.7	562	4	US-10-443-701-4	Sequence 4, Appli
688	308.5	14.9	317	4	US-09-902-775A-263	Sequence 263, App	761	304	14.7	562	6	5185259-3	Patent No. 5185259
689	308.5	14.9	317	4	US-09-906-700-263	Sequence 263, App	762	304	14.7	562	6	5200340-2	Patent No. 5200340
690	308.5	14.9	317	4	US-09-903-603A-263	Sequence 263, App	763	304	14.7	562	6	524676-5	Patent No. 524676
691	308.5	14.9	317	4	US-09-904-920A-263	Sequence 263, App	764	304	14.7	562	6	5344773-2	Patent No. 5344773
692	308.5	14.9	317	4	US-09-908-084-263	Sequence 263, App	765	304	14.7	562	6	5185259-3	Patent No. 5185259
693	308.5	14.9	317	4	US-09-905-381A-263	Sequence 263, App	766	304	14.7	562	6	5200340-2	Patent No. 5200340
694	308.5	14.9	317	4	US-09-906-618-263	Sequence 263, App	767	304	14.7	562	6	524676-5	Patent No. 524676
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698	308	14.9	417	4	US-09-820-002-4	Sequence 4, Appli	771	303.5	14.7	278	3	US-09-330-945-4	Sequence 4, Appli
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705	307	14.9	268	3	US-09-153-304-2	Sequence 2, Appli	778	303	14.7	255	4	US-10-114-454-14	Sequence 14, Appli
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716	305	14.8	247	4	US-09-949-016-6457	Sequence 6457, Ap	789	302	14.6	527	4	US-09-600-985-3	Sequence 3, Appli
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726	304.5	14.7	393	4	US-09-759-143-934	Sequence 934, App	799	297	14.4	252	3	US-08-944-483-72	Sequence 8, Appli
727	304.5	14.7	492	3	US-09-342-749-2	Sequence 2, Appli	800	297	14.4	253	2	US-09-027-337-8	Sequence 8, Appli
728	304.5	14.7	492	4	US-09-691-840-2	Sequence 2, Appli	801	297	14.4	253	4	US-09-644-600-8	Sequence 8, Appli
729	304.5	14.7	492	4	US-09-759-143-932	Sequence 932, App	802	297	14.4	253	4	US-09-654-600A-8	Sequence 8, Appli
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817	296.5	14.4	224	2	US-08-615-271-12	Sequence 12, Appl	890	286.5	13.9	228	4	US-09-004-729-10	Sequence 10, Appl
818	296.5	14.4	224	3	US-09-074-660-12	Sequence 12, Appl	891	284.5	13.8	225	3	US-09-004-731-13	Sequence 13, Appl
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821	296.5	14.4	224	3	US-09-106-468-12	Sequence 12, Appl	894	284.5	13.8	255	3	US-08-906-769-83	Sequence 83, Appl
822	296.5	14.4	224	3	US-09-106-467-12	Sequence 12, Appl	895	284.5	13.8	255	3	US-08-906-616-83	Sequence 83, Appl
823	296.5	14.4	254	2	US-08-560-098A-49	Sequence 49, Appl	896	284.5	13.8	255	3	US-08-817-795-83	Sequence 83, Appl
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825	296.5	14.4	306	2	US-08-560-098A-45	Sequence 45, Appl	898	284.5	13.8	255	3	US-09-012-431-83	Sequence 83, Appl
826	296.5	14.4	331	2	US-08-560-098A-46	Sequence 46, Appl	899	284.5	13.8	255	3	US-09-012-692-83	Sequence 83, Appl
827	296.5	14.4	365	1	US-08-093-741-83	Sequence 83, Appl	900	284.5	13.8	255	3	US-08-906-613-83	Sequence 83, Appl
828	296.5	14.4	365	1	US-08-720-012-83	Sequence 83, Appl	901	284.5	13.8	255	5	PCT-US95-1442A-83	Sequence 83, Appl
829	296.5	14.4	393	3	US-08-967-024C-24	Sequence 24, Appl	902	283.5	13.7	268	3	US-09-032-215-42	Sequence 42, Appl
830	296.5	14.4	393	3	US-08-967-024C-25	Sequence 25, Appl	903	282.5	13.7	144	4	US-09-618-259-4	Sequence 4, Appl
831	296.5	14.4	403	4	US-09-880-503-6	Sequence 6, Appl	904	282	13.6	244	3	US-08-944-483-74	Sequence 74, Appl
832	296.5	14.4	411	1	US-08-087-163-1	Sequence 1, Appl	905	279	13.5	488	4	US-09-367-777-44	Sequence 44, Appl
833	296.5	14.4	411	1	US-08-286-748B-18	Sequence 18, Appl	906	279	13.5	488	4	US-09-367-791A-27	Sequence 27, Appl
834	296.5	14.4	411	1	US-08-153-799-18	Sequence 18, Appl	907	279	13.5	902	4	US-09-644-600-10	Sequence 10, Appl
835	296.5	14.4	411	2	US-08-560-098A-48	Sequence 48, Appl	908	279	13.5	902	4	US-09-654-600A-10	Sequence 10, Appl
836	296.5	14.4	411	4	US-09-880-503-3	Sequence 3, Appl	909	278	13.5	306	1	US-08-330-978-1	Sequence 1, Appl
837	296.5	14.4	430	6	5219569-2	Patent No. 5219569	910	278	13.5	306	1	US-08-474-042-1	Sequence 1, Appl
838	296.5	14.4	430	6	5219569-2	Patent No. 5219569	911	278	13.5	306	1	US-08-484-558-1	Sequence 1, Appl
839	296.5	14.4	431	4	US-09-101-272G-1	Sequence 1, Appl	912	278	13.5	306	1	US-08-774-592-1	Sequence 1, Appl
840	296.5	14.4	431	6	5188829-1	Patent No. 5188829	913	278	13.5	437	1	US-08-487-037-2	Sequence 2, Appl
841	296.5	14.4	431	6	5188829-1	Patent No. 5188829	914	278	13.5	448	1	US-08-295-411-3	Sequence 3, Appl
842	296.5	14.4	432	2	US-08-560-098A-47	Sequence 47, Appl	915	278	13.5	448	1	US-08-955-471-3	Sequence 3, Appl
843	296	14.3	269	4	US-09-715-994-2	Sequence 2, Appl	916	278	13.5	448	5	PCT-US92-10068-1	Sequence 1, Appl
844	295.5	14.3	283	3	US-08-807-151-1	Sequence 1, Appl	917	278	13.5	448	5	PCT-US92-10242-3	Sequence 3, Appl
845	295.5	14.3	283	3	US-09-478-957-1	Sequence 1, Appl	918	278	13.5	448	1	US-08-487-037-1	Sequence 1, Appl
846	295.5	14.3	454	3	US-09-518-046-2	Sequence 2, Appl	919	278	13.5	488	1	US-08-487-037-1	Sequence 1, Appl
847	294	14.2	256	3	US-09-032-215-32	Sequence 32, Appl	920	277.5	13.4	496	4	US-09-943-016-9524	Sequence 9524, Ap
848	293.5	14.2	239	3	US-08-944-483-61	Sequence 61, Appl	921	276	13.4	254	1	US-08-330-978-3	Sequence 3, Appl
849	293.5	14.2	411	4	US-09-403-736-2	Sequence 2, Appl	922	276	13.4	254	1	US-08-474-042-3	Sequence 3, Appl
850	293.5	14.2	430	1	US-07-942-157A-3	Sequence 3, Appl	923	276	13.4	254	1	US-08-484-558-3	Sequence 3, Appl
851	292	14.1	235	2	US-08-557-146-14	Sequence 14, Appl	924	276	13.4	254	1	US-08-774-592-3	Sequence 3, Appl
852	292	14.1	235	2	US-09-154-344-14	Sequence 14, Appl	925	274.5	13.3	211	3	US-09-220-731-25	Sequence 25, Appl
853	292	14.1	235	3	US-08-944-483-42	Sequence 42, Appl	926	274.5	13.3	211	4	US-09-242-999-20	Sequence 20, Appl
854	292	14.1	237	3	US-09-004-731-22	Sequence 22, Appl	927	274	13.3	241	1	US-08-330-978-4	Sequence 4, Appl
855	292	14.1	237	3	US-08-749-699-22	Sequence 22, Appl	928	274	13.3	241	1	US-08-474-042-4	Sequence 4, Appl
856	292	14.1	237	4	US-09-004-729-22	Sequence 22, Appl	929	274	13.3	241	1	US-08-484-558-4	Sequence 4, Appl
857	292	14.1	256	3	US-08-906-769-89	Sequence 89, Appl	930	274	13.3	241	1	US-08-774-592-4	Sequence 4, Appl
858	292	14.1	256	3	US-08-906-616-89	Sequence 89, Appl	931	273	13.2	251	3	US-08-944-483-28	Sequence 28, Appl
859	292	14.1	256	3	US-08-817-795-89	Sequence 89, Appl	932	272	13.2	253	3	US-08-906-769-131	Sequence 131, App
860	292	14.1	256	3	US-08-639-075A-89	Sequence 89, Appl	933	272	13.2	253	3	US-08-906-616-131	Sequence 131, App
861	292	14.1	256	3	US-09-012-431-89	Sequence 89, Appl	934	272	13.2	253	3	US-08-639-075A-131	Sequence 131, App
862	292	14.1	256	3	US-09-012-692-89	Sequence 89, Appl	935	272	13.2	253	3	US-09-012-431-131	Sequence 131, App
863	292	14.1	256	3	US-08-906-613-89	Sequence 89, Appl	936	272	13.2	253	3	US-09-012-692-131	Sequence 131, App
864	292	14.1	256	5	PCT-US95-1442A-89	Sequence 89, Appl	937	272	13.2	253	3	US-08-906-613-131	Sequence 131, App
865	292	14.1	414	4	US-09-270-767-46426	Sequence 46426, A	938	271.5	13.1	256	4	US-08-395-456C-23	Sequence 23, Appl
866	291.5	14.1	242	3	US-08-944-483-57	Sequence 57, Appl	939	271.5	13.1	256	4	US-08-487-453A-23	Sequence 23, Appl
867	291.5	14.1	253	3	US-08-944-483-73	Sequence 73, Appl	940	270.5	13.1	256	2	US-08-230-428B-4	Sequence 4, Appl
868	291	14.1	416	2	US-09-000-846-2	Sequence 2, Appl	941	270	13.1	437	1	US-08-487-037-3	Sequence 3, Appl
869	290	14.0	235	3	US-08-807-151-3	Sequence 3, Appl	942	267.5	12.9	266	3	US-09-004-731-24	Sequence 24, Appl
870	290	14.0	235	3	US-09-478-957-3	Sequence 3, Appl	943	267.5	12.9	266	3	US-08-749-699-24	Sequence 24, Appl
871	289	14.0	223	1	US-07-956-848A-41	Sequence 41, Appl	944	267.5	12.9	266	4	US-09-004-729-24	Sequence 24, Appl
872	289	14.0	223	1	US-08-471-956-41	Sequence 41, Appl	945	266.5	12.9	352	4	US-09-943-016-6271	Sequence 6271, Ap
873	289	14.0	583	4	US-09-976-594-837	Sequence 837, App	946	266	12.9	197	1	US-08-456-840-48	Sequence 48, Appl
874	288.5	14.0	255	3	US-08-906-769-91	Sequence 91, Appl	947	265.5	12.9	197	1	US-08-266-407A-48	Sequence 48, Appl
875	288.5	14.0	255	3	US-08-906-616-91	Sequence 91, Appl	948	265.5	12.9	197	1	US-08-892-544-48	Sequence 48, Appl
876	288.5	14.0	255	3	US-08-817-795-91	Sequence 91, Appl	949	265.5	12.9	197	2	US-08-491-204A-18	Sequence 18, Appl
877	288.5	14.0	255	3	US-08-639-075A-91	Sequence 91, Appl	950	264.5	12.8	248	2	US-08-236-130-2	Sequence 2, Appl
878	288.5	14.0	255	3	US-09-012-431-91	Sequence 91, Appl	951	264.5	12.8	248	2	US-08-921-426-4	Sequence 4, Appl
879	288.5	14.0	255	3	US-09-012-692-91	Sequence 91, Appl	952	264.5	12.8	248	2	US-08-815-915-4	Sequence 4, Appl
880	288.5	14.0	255	3	US-08-906-613-91	Sequence 91, Appl	953	264.5	12.8	248	3	PCT-US95-07743-4	Sequence 4, Appl
881	288.5	14.0	255	5	PCT-US95-1442A-91	Sequence 91, Appl	954	264.5	12.8	249	5	US-09-578-303-2	Sequence 2, Appl
882	288	13.9	268	1	US-08-270-584A-2	Sequence 2, Appl	955	264.5	12.8	251	4	US-09-943-016-6112	Sequence 6112, Ap
883	288	13.9	268	3	US-08-765-192-2	Sequence 2, Appl	956	264.5	12.8	251	4	US-09-943-016-9690	Sequence 9690, Ap
884	288	13.9	268	3	US-09-199-793-2	Sequence 2, Appl	957	264.5	12.8	250	3	US-08-944-483-68	Sequence 68, Appl
885	287	13.9	227	3	US-08-944-483-40	Sequence 40, Appl	958	264	12.8	252	3	US-08-906-769-103	Sequence 103, App
886	287	13.9	407	3	US-09-734-675-4	Sequence 4, Appl	959	263	12.7	252	3	US-08-906-616-103	Sequence 103, App
887	286.5	13.9	218	3	US-09-578-303-3	Sequence 3, Appl	960	263	12.7	252	3	US-08-817-795-103	Sequence 103, App
888	286.5	13.9	228	3	US-09-004-731-10	Sequence 10, Appl	961	263	12.7	252	3		

962	263	12.7	252	3	US-08-639-075A-103	Sequence 103, App	1035	227	11.0	258	4	US-09-023-942A-8	Sequence 8, Appli
963	263	12.7	252	3	US-09-012-431-103	Sequence 103, App	1036	227	11.0	259	3	US-08-906-769-190	Sequence 190, App
964	263	12.7	252	3	US-09-012-692-103	Sequence 103, App	1037	227	11.0	259	3	US-08-906-616-190	Sequence 190, App
965	263	12.7	252	3	US-08-906-613-103	Sequence 103, App	1038	227	11.0	259	3	US-08-639-075A-190	Sequence 190, App
966	263	12.7	252	5	PCT-US95-14442A-103	Sequence 9, Appli	1039	227	11.0	259	3	US-09-004-731-85	Sequence 85, Appl
967	262.5	12.7	222	1	US-07-969-931-9	Sequence 9, Appli	1040	227	11.0	259	3	US-09-012-431-190	Sequence 190, App
968	262.5	12.7	222	1	US-07-855-417A-9	Sequence 32, Appli	1041	227	11.0	259	3	US-08-749-699-85	Sequence 85, Appl
969	262.5	12.7	225	3	US-08-944-483-32	Sequence 27, Appli	1042	227	11.0	259	3	US-09-012-692-190	Sequence 190, App
970	262.5	12.7	233	3	US-09-004-731-27	Sequence 27, Appli	1043	227	11.0	259	3	US-08-906-613-190	Sequence 190, App
971	262.5	12.7	233	3	US-08-749-699-27	Sequence 27, Appli	1044	227	11.0	259	3	US-09-004-729-85	Sequence 85, Appl
972	262.5	12.7	233	3	US-09-004-729-27	Sequence 27, Appli	1045	227	11.0	259	3	US-08-906-613-190	Sequence 190, App
973	258.5	12.5	255	4	US-09-270-767-44361	Sequence 44361, A	1046	226.5	11.0	273	3	US-08-700-519U-18	Sequence 18, Appl
974	257.5	12.5	224	1	US-08-553-516-2	Sequence 2, Appli	1047	226.5	11.0	273	3	US-08-700-519U-18	Sequence 18, Appl
975	256	12.4	267	3	US-08-906-769-145	Sequence 145, App	1048	226	10.9	215	6	5180819-2	Patent No. 5180819
976	256	12.4	267	3	US-08-906-616-145	Sequence 145, App	1049	226	10.9	215	6	5180819-2	Patent No. 5180819
977	256	12.4	267	3	US-08-639-075A-145	Sequence 145, App	1050	226	10.9	697	3	US-08-460-890A-50	Sequence 50, Appl
978	256	12.4	267	3	US-09-004-731-67	Sequence 67, Appl	1051	226	10.9	697	3	US-08-167-641C-50	Sequence 50, Appl
979	256	12.4	267	3	US-09-012-431-145	Sequence 145, App	1052	226	10.9	697	3	US-08-460-971A-50	Sequence 50, Appl
980	256	12.4	267	3	US-08-749-699-67	Sequence 67, Appl	1053	226	10.9	697	3	US-08-460-971A-50	Sequence 50, Appl
981	256	12.4	267	3	US-09-012-692-145	Sequence 145, App	1054	226	10.9	697	3	US-08-460-971A-50	Sequence 50, Appl
982	256	12.4	267	3	US-08-906-613-145	Sequence 145, App	1055	226	10.9	697	3	US-08-460-971A-50	Sequence 50, Appl
983	256	12.4	267	3	US-09-004-729-67	Sequence 67, Appli	1056	226	10.9	697	3	US-08-460-971A-50	Sequence 50, Appl
984	256	12.4	405	3	US-09-734-675-2	Sequence 2, Appli	1057	226	10.9	723	3	US-07-838-410-1	Sequence 1, Appli
985	254	12.3	242	3	US-09-004-731-41	Sequence 41, Appl	1058	226	10.9	723	3	US-08-290-937B-1	Sequence 2, Appli
986	254	12.3	242	3	US-08-749-699-41	Sequence 41, Appl	1059	226	10.9	723	3	US-08-290-937B-1	Sequence 2, Appli
987	254	12.3	242	3	US-09-004-729-41	Sequence 41, Appl	1060	226	10.9	723	3	US-08-290-937B-1	Sequence 2, Appli
988	253	12.2	242	4	US-09-328-925-12	Sequence 12, Appl	1061	226	10.9	723	3	US-08-290-937B-1	Sequence 2, Appli
989	253	12.2	231	4	US-08-395-456C-25	Sequence 25, Appl	1062	226	10.9	723	3	US-08-290-937B-1	Sequence 2, Appli
990	252.5	12.2	242	3	US-09-032-215-47	Sequence 47, Appli	1063	226	10.9	723	3	US-08-290-937B-1	Sequence 2, Appli
991	252.5	12.2	221	2	US-08-925-708-1	Sequence 1, Appli	1064	226	10.9	723	3	US-08-290-937B-1	Sequence 2, Appli
992	252.5	12.2	239	3	US-09-004-731-44	Sequence 44, Appl	1065	226	10.9	728	4	US-08-605-221-2	Sequence 2, Appli
993	252.5	12.2	239	3	US-08-749-699-44	Sequence 44, Appl	1066	226	10.9	728	4	US-08-605-221-2	Sequence 2, Appli
994	252.5	12.2	239	4	US-09-004-729-44	Sequence 44, Appl	1067	223.5	10.8	385	4	US-09-163-951-16	Sequence 16, Appl
995	252.5	12.2	247	3	US-08-944-483-49	Sequence 49, Appl	1068	223.5	10.8	385	4	US-09-163-951-16	Sequence 16, Appl
996	252	12.2	229	4	US-08-395-456C-27	Sequence 27, Appl	1069	223	10.8	723	3	US-08-030-410-3	Sequence 3, Appli
997	251	12.1	229	2	US-08-394-600B-20	Sequence 20, Appl	1070	222	10.7	723	3	US-08-906-769-149	Sequence 149, App
998	251	12.1	229	4	US-08-395-456C-20	Sequence 20, Appl	1071	222	10.7	723	3	US-08-906-769-149	Sequence 149, App
999	251	12.1	229	4	US-08-487-453A-20	Sequence 20, Appl	1072	222	10.7	213	3	US-08-639-075A-149	Sequence 149, App
1000	251	12.1	229	5	PCT-US95-02513-20	Sequence 20, Appl	1073	222	10.7	213	3	US-09-012-431-149	Sequence 149, App
1001	251	12.1	716	2	US-08-766-982-1	Sequence 1, Appli	1074	222	10.7	213	3	US-09-012-431-149	Sequence 149, App
1002	251	12.1	716	2	US-08-766-982-1	Sequence 1, Appli	1075	222	10.7	213	3	US-08-906-613-149	Sequence 149, App
1003	248.5	12.0	717	3	US-09-296-219-1	Sequence 6, Appli	1076	222	10.7	213	3	US-08-944-483-56	Sequence 56, Appl
1004	248.5	12.0	729	4	US-09-601-040A-6	Sequence 6, Appli	1077	220	10.6	278	4	US-08-270-767-32807	Sequence 32807, A
1005	247.5	12.0	717	4	US-09-601-040A-2	Sequence 2, Appli	1078	220	10.6	457	4	US-08-270-767-32807	Sequence 32807, A
1006	247.5	12.0	729	4	US-09-601-040A-8	Sequence 8, Appli	1079	219	10.6	223	1	US-08-483-859-13	Sequence 13, Appl
1007	247.5	12.0	729	4	US-08-944-483-30	Sequence 30, Appl	1080	219	10.6	223	1	US-08-483-859-13	Sequence 13, Appl
1008	245.5	11.9	711	1	US-08-184-012C-8	Sequence 8, Appli	1081	219	10.6	223	1	US-08-483-859-13	Sequence 13, Appl
1009	245.5	11.9	711	1	US-08-334-177-2	Sequence 2, Appli	1082	219	10.6	223	1	US-08-483-859-13	Sequence 13, Appl
1010	245.5	11.9	711	1	US-08-666-082B-1	Sequence 1, Appli	1083	219	10.6	223	1	US-08-483-859-13	Sequence 13, Appl
1011	245.5	11.9	711	2	US-08-766-982-2	Sequence 2, Appli	1084	219	10.6	223	1	US-08-483-859-13	Sequence 13, Appl
1012	245.5	11.9	711	2	US-09-296-219-2	Sequence 2, Appli	1085	219	10.6	223	1	US-08-483-859-13	Sequence 13, Appl
1013	245.5	11.9	711	4	US-09-600-991-20	Sequence 20, Appl	1086	219	10.6	223	1	US-08-483-859-13	Sequence 13, Appl
1014	245.5	11.9	711	4	US-09-601-040A-12	Sequence 12, Appl	1087	219	10.6	223	1	US-08-483-859-13	Sequence 13, Appl
1015	245.5	11.9	711	4	PCT-US95-016-6981	Sequence 6981, Ap	1088	219	10.6	223	1	US-08-483-859-13	Sequence 13, Appl
1016	245.5	11.9	711	5	PCT-US95-13830-2	Sequence 2, Appli	1089	219	10.6	223	1	US-08-483-859-13	Sequence 13, Appl
1017	245	11.9	226	4	US-09-601-040A-28	Sequence 28, Appl	1090	219	10.6	223	1	US-08-483-859-13	Sequence 13, Appl
1018	245	11.9	228	2	US-08-766-982-11	Sequence 11, Appl	1091	219	10.6	223	1	US-08-483-859-13	Sequence 13, Appl
1019	245	11.9	228	2	US-08-944-483-55	Sequence 55, Appl	1092	216	10.5	185	3	US-08-906-616-141	Sequence 141, App
1020	245	11.9	228	3	US-09-296-219-11	Sequence 11, Appl	1093	216	10.5	185	3	US-08-906-616-141	Sequence 141, App
1021	244.5	11.8	304	3	US-09-088-651-2	Sequence 2, Appli	1094	216	10.5	185	3	US-08-906-616-141	Sequence 141, App
1022	242	11.7	214	6	5180819-3	Patent No. 5180819	1095	216	10.5	185	3	US-08-906-616-141	Sequence 141, App
1023	242	11.7	214	6	5180819-3	Patent No. 5180819	1096	216	10.5	185	3	US-08-906-616-141	Sequence 141, App
1024	242	11.7	214	6	5180819-3	Patent No. 5180819	1097	216	10.5	185	3	US-08-906-616-141	Sequence 141, App
1025	240	11.6	161	3	US-09-261-416-2	Sequence 2, Appli	1098	215.5	10.4	238	3	US-08-944-483-31	Sequence 31, Appl
1026	234	11.3	158	3	US-09-518-045-22	Sequence 22, Appl	1099	215.5	10.4	238	3	US-08-944-483-31	Sequence 31, Appl
1027	232.5	11.3	185	3	US-08-705-875A-5	Sequence 5, Appli	1100	215.5	10.4	238	3	US-08-944-483-31	Sequence 31, Appl
1028	232.5	11.3	185	3	US-09-220-731-22	Sequence 22, Appl	1101	211	10.2	223	1	US-08-485-455D-17	Sequence 17, Appl
1029	232.5	11.3	185	3	US-09-242-999-5	Sequence 5, Appli	1102	211	10.2	223	1	US-08-485-455D-17	Sequence 17, Appl
1030	231.5	11.2	219	2	US-08-925-708-2	Sequence 2, Appli	1103	211	10.2	223	1	US-08-485-455D-17	Sequence 17, Appl
1031	231	11.2	242	3	US-08-944-483-29	Sequence 29, Appl	1104	211	10.2	223	1	US-08-485-455D-17	Sequence 17, Appl
1032	228.5	11.1	287	4	US-09-270-767-33263	Sequence 33263, A	1105	211	10.2	223	5	PCT-US95-14442A-17	Sequence 17, Appl
1033	228.5	11.1	287	4	US-09-270-767-48480	Sequence 48480, A	1106	211	10.2	223	5	PCT-US95-14442A-17	Sequence 17, Appl
1034	227.5	11.0	267	2	US-08-978-404B-46	Sequence 46, Appl	1107	211	10.2	224	3	US-08-906-769-17	Sequence 17, Appl

1108	211	10.2	224	3	US-08-906-616-17	Sequence 17, Appl	1181	168	8.1	141	3	US-09-012-692-135	Sequence 135, App
1109	211	10.2	224	3	US-08-639-075A-17	Sequence 17, Appl	1182	168	8.1	141	3	US-08-906-613-135	Sequence 135, App
1110	211	10.2	224	3	US-09-012-431-17	Sequence 17, Appl	1183	166.5	8.1	178	3	US-08-705-875A-8	Sequence 8, Appl
1111	211	10.2	224	3	US-09-012-692-17	Sequence 17, Appl	1184	166.5	8.1	178	3	US-09-220-731-23	Sequence 23, Appl
1112	211	10.2	224	3	US-08-906-613-17	Sequence 17, Appl	1185	166.5	8.1	178	4	US-09-242-999-8	Sequence 8, Appl
1113	211	10.2	235	4	US-09-796-110-2	Sequence 2, Appl	1186	166.5	8.1	243	4	US-09-270-767-44348	Sequence 44348, A
1114	210.5	10.2	222	4	US-09-270-767-62005	Sequence 62005, A	1187	166	8.0	769	4	US-09-949-016-11019	Sequence 11019, A
1115	206	10.0	164	3	US-09-518-046-25	Sequence 25, Appl	1188	165	8.0	198	3	US-08-906-769-133	Sequence 133, App
1116	206	10.0	250	4	US-09-270-767-33709	Sequence 33709, A	1189	165	8.0	198	3	US-08-906-616-133	Sequence 133, App
1117	204.5	9.9	157	3	US-09-518-046-23	Sequence 23, Appl	1190	165	8.0	198	3	US-08-639-075A-133	Sequence 133, App
1118	204.5	9.9	178	3	US-08-906-769-107	Sequence 107, App	1191	165	8.0	198	3	US-09-012-431-133	Sequence 133, App
1119	204.5	9.9	178	3	US-08-906-616-107	Sequence 107, App	1192	165	8.0	198	3	US-09-012-692-133	Sequence 133, App
1120	204.5	9.9	178	3	US-08-817-795-107	Sequence 107, App	1193	165	8.0	198	3	US-08-906-613-133	Sequence 133, App
1121	204.5	9.9	178	3	US-08-639-075A-107	Sequence 107, App	1194	163	7.9	190	2	US-08-845-998-4	Sequence 4, Appl
1122	204.5	9.9	178	3	US-09-012-431-107	Sequence 107, App	1195	163	7.9	190	3	US-09-206-537-4	Sequence 4, Appl
1123	204.5	9.9	178	3	US-09-012-692-107	Sequence 107, App	1196	163	7.9	190	3	US-09-430-854-4	Sequence 24, Appl
1124	204.5	9.9	178	3	US-08-906-613-107	Sequence 107, App	1197	160.5	7.8	178	3	US-09-220-731-24	Sequence 24, Appl
1125	204.5	9.9	178	5	PCT-US95-14442A-107	Sequence 107, App	1198	160.5	7.8	178	4	US-09-242-999-24	Sequence 24, Appl
1126	200.5	9.7	159	3	US-09-518-046-24	Sequence 24, Appl	1199	160	7.7	97	4	US-09-270-767-31931	Sequence 31931, A
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1128	199.5	9.7	254	3	US-08-906-769-139	Sequence 129, App	1201	159	7.7	190	2	US-08-845-998-6	Sequence 6, Appl
1129	199.5	9.7	254	3	US-08-906-616-129	Sequence 129, App	1202	159	7.7	190	3	US-09-206-537-6	Sequence 6, Appl
1130	199.5	9.7	254	3	US-08-639-075A-129	Sequence 129, App	1203	159	7.7	190	3	US-09-430-854-6	Sequence 6, Appl
1131	198.5	9.7	254	3	US-09-012-431-129	Sequence 129, App	1204	159	7.8	421	4	US-09-252-991A-32326	Sequence 32326, A
1132	199.5	9.7	254	3	US-09-012-692-129	Sequence 129, App	1205	158.5	7.7	163	4	US-09-270-767-60652	Sequence 60652, A
1133	199.5	9.7	254	3	US-08-906-613-129	Sequence 129, App	1206	158.5	7.7	286	4	US-09-270-767-45162	Sequence 45162, A
1134	196.5	9.5	141	4	US-09-949-016-7265	Sequence 7265, Ap	1207	158	7.6	357	4	US-09-270-767-43564	Sequence 43564, A
1135	195	9.4	326	3	US-09-411-977-3	Sequence 3, Appl	1208	158	7.6	357	4	US-09-270-767-58936	Sequence 58936, A
1136	195	9.4	326	4	US-10-057-951-3	Sequence 3, Appl	1209	157.5	7.6	764	2	US-08-177-109A-2	Sequence 2, Appl
1137	192.5	9.3	260	3	US-08-906-769-139	Sequence 139, App	1210	157.5	7.6	764	2	US-08-687-706-2	Sequence 2, Appl
1138	192.5	9.3	260	3	US-08-906-616-139	Sequence 139, App	1211	157.5	7.6	798	4	US-09-949-016-11021	Sequence 11021, A
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1140	192.5	9.3	260	3	US-09-012-431-139	Sequence 139, App	1213	156.5	7.6	276	4	US-09-270-767-32048	Sequence 32048, A
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1142	192.5	9.3	260	3	US-08-906-613-139	Sequence 139, App	1215	156	7.6	112	4	US-09-270-767-33319	Sequence 33319, A
1143	191	9.2	74	4	US-09-205-258-1151	Sequence 1151, Ap	1216	156	7.6	112	4	US-09-270-767-48536	Sequence 48536, A
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1145	191	9.2	138	6	5200340-4	Patent No. 5200340	1218	154.5	7.5	204	3	US-08-906-616-147	Sequence 147, App
1146	190	9.2	90	4	US-09-270-767-57991	Sequence 57991, A	1219	154.5	7.5	204	3	US-08-639-075A-147	Sequence 147, App
1147	187.5	9.1	271	3	US-09-578-303-6	Sequence 6, Appl	1220	154.5	7.5	204	3	US-09-013-431-147	Sequence 147, App
1148	187	9.1	312	4	US-09-636-382A-15	Sequence 15, Appl	1221	154.5	7.5	204	3	US-09-012-692-147	Sequence 147, App
1149	186.5	9.0	570	4	US-10-067-422-9	Sequence 9, Appl	1222	154.5	7.5	204	3	US-08-906-613-147	Sequence 147, App
1150	186	9.0	159	4	US-09-618-259-5	Sequence 5, Appl	1223	154	7.5	589	4	US-09-252-991A-18210	Sequence 18210, A
1151	183	8.9	313	4	US-09-270-767-44375	Sequence 123, App	1224	153.5	7.4	151	4	US-09-270-767-33178	Sequence 33178, A
1152	182	8.8	145	3	US-08-906-769-123	Sequence 123, App	1225	153.5	7.4	151	4	US-09-270-767-48395	Sequence 48395, A
1153	182	8.8	145	3	US-08-906-616-123	Sequence 123, App	1226	153.5	7.5	3122	4	US-10-237-551-201	Sequence 201, App
1154	182	8.8	145	3	US-08-639-075A-123	Sequence 123, App	1227	153.5	7.5	3122	4	US-10-237-551-250	Sequence 250, App
1155	182	8.8	145	3	US-09-012-692-123	Sequence 123, App	1228	152.5	7.4	139	4	US-09-270-767-33648	Sequence 33648, A
1156	182	8.8	145	3	US-08-906-613-123	Sequence 123, App	1229	152.5	7.4	200	3	US-09-008-271A-5	Sequence 5, Appl
1157	182	8.8	346	4	US-09-949-016-9000	Sequence 9000, Ap	1230	151.5	7.4	425	4	US-09-252-991A-31834	Sequence 31834, A
1158	181	8.8	118	4	US-09-621-976-5522	Sequence 5522, Ap	1231	151	7.4	308	4	US-09-252-991A-27249	Sequence 27249, A
1159	181	8.8	133	4	US-09-949-016-7471	Sequence 7471, Ap	1232	151	7.4	328	4	US-09-253-991A-24003	Sequence 24003, A
1160	180	8.7	144	3	US-09-012-431-123	Sequence 123, App	1233	150.5	7.3	79	4	US-09-270-767-33666	Sequence 33666, A
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1163	178.5	8.6	164	3	US-09-030-607-178	Sequence 178, App	1236	150	7.4	595	4	US-09-854-133-187	Sequence 187, App
1164	178.5	8.6	164	3	US-09-439-313-178	Sequence 178, App	1237	150	7.3	2508	4	US-09-627-650B-7	Sequence 7, Appl
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1166	178.5	8.6	164	4	US-09-232-149A-178	Sequence 178, App	1239	150	7.3	2544	4	US-09-627-650B-3	Sequence 3, Appl
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1168	178.5	8.6	164	4	US-09-636-215-178	Sequence 178, App	1241	150	7.3	2601	4	US-09-627-650B-9	Sequence 9, Appl
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1170	178.5	8.6	164	4	US-09-115-453-178	Sequence 178, App	1243	149	7.2	77	3	US-09-439-313-329	Sequence 329, App
1171	178.5	8.6	164	4	US-09-688-489-178	Sequence 178, App	1244	149	7.2	77	3	US-09-352-616A-329	Sequence 329, App
1172	178.5	8.6	164	4	US-09-679-426-178	Sequence 178, App	1245	149	7.2	77	4	US-09-232-149A-329	Sequence 329, App
1173	178.5	8.6	164	4	US-09-759-143-178	Sequence 178, App	1246	149	7.2	77	4	US-09-636-215-329	Sequence 329, App
1174	178.5	8.6	164	4	US-09-651-236-178	Sequence 178, App	1247	149	7.2	77	4	US-09-685-166A-329	Sequence 329, App
1175	175.5	8.5	481	4	US-09-949-016-9748	Sequence 9748, Ap	1248	149	7.2	77	4	US-09-688-489-329	Sequence 329, App
1176	173.5	8.4	218	4	US-09-270-767-44299	Sequence 44299, A	1249	149	7.2	77	4	US-09-679-426-329	Sequence 329, App
1177	168	8.1	141	3	US-08-906-769-135	Sequence 135, App	1250	149	7.2	77	4	US-09-759-143-329	Sequence 329, App
1178	168	8.1	141	3	US-08-906-616-135	Sequence 135, App	1251	149	7.2	77	4	US-09-651-236-329	Sequence 329, App
1179	168	8.1	141	3	US-08-639-075A-135	Sequence 135, App	1252	149	7.3	419	4	US-09-252-991A-32949	Sequence 32949, A
1180	168	8.1	141	3	US-09-012-431-135	Sequence 135, App	1253	148	7.2	693	4	US-09-252-991A-26071	Sequence 26071, A

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c1255	145	7.1	416	4	US-09-252-991A-30923	Sequence 30923, A	1328	135.5	6.6	794	4	US-09-252-991A-28569	Sequence 28569, A
c1256	145	7.1	783	4	US-09-252-991A-18035	Sequence 18035, A	1329	135.5	6.6	801	1	US-07-906-349A-6	Sequence 6, Appl
c1257	144.5	7.0	971	4	US-09-252-991A-31830	Sequence 31830, A	1330	135.5	6.6	1034	4	US-09-252-991A-28921	Sequence 28921, A
c1258	144	7.0	339	4	US-09-252-991A-25235	Sequence 25235, A	c1331	135	6.6	416	4	US-09-252-991A-32875	Sequence 32875, A
c1259	143.5	6.9	72	3	US-08-908-769-87	Sequence 87, Appl	c1332	135	6.6	480	4	US-08-252-991A-26799	Sequence 26799, A
c1260	143.5	6.9	72	3	US-08-906-616-87	Sequence 87, Appl	c1333	135	6.6	511	4	US-09-252-991A-26078	Sequence 26078, A
c1261	143.5	6.9	72	3	US-08-817-795-87	Sequence 87, Appl	c1334	135	6.6	1000	4	US-09-252-991A-31361	Sequence 31361, A
c1262	143.5	6.9	72	3	US-08-639-075A-87	Sequence 87, Appl	1335	135	6.5	1128	4	US-09-627-063B-11	Sequence 11, Appl
c1263	143.5	6.9	72	3	US-09-012-431-87	Sequence 87, Appl	1336	135	6.5	1128	4	US-09-436-063C-11	Sequence 11, Appl
c1264	143.5	6.9	72	3	US-09-012-692-87	Sequence 87, Appl	c1337	134.5	6.6	310	4	US-09-252-991A-19986	Sequence 19986, A
c1265	143.5	6.9	72	3	US-08-906-613-87	Sequence 87, Appl	c1338	134.5	6.6	420	4	US-09-252-991A-23621	Sequence 23621, A
c1266	143.5	6.9	72	3	PCT-US95-14442A-87	Sequence 87, Appl	c1339	134.5	6.6	441	4	US-09-252-991A-18870	Sequence 18870, A
c1267	143.5	6.9	635	4	US-09-252-991A-31646	Sequence 31646, A	1340	134.5	6.5	595	4	US-09-252-991A-18995	Sequence 18995, A
c1268	143.5	6.9	772	4	US-09-252-991A-30446	Sequence 30446, A	c1341	134.5	6.5	622	4	US-09-270-767-42577	Sequence 42577, A
c1269	143	7.0	697	4	US-09-252-991A-24009	Sequence 24009, A	c1342	134.5	6.6	1041	4	US-09-252-991A-29266	Sequence 29266, A
c1270	142.5	6.9	208	3	US-08-906-769-151	Sequence 151, App	c1343	134.5	6.6	1246	4	US-09-252-991A-23140	Sequence 23140, A
c1271	142.5	6.9	208	3	US-08-906-616-151	Sequence 151, App	c1344	134	6.6	192	4	US-09-252-991A-18154	Sequence 18154, A
c1272	142.5	6.9	208	3	US-08-639-075A-151	Sequence 151, App	c1345	134	6.6	218	4	US-09-252-991A-20606	Sequence 20606, A
c1273	142.5	6.9	208	3	US-09-012-431-151	Sequence 151, App	1346	134	6.5	251	4	US-09-252-991A-20606	Sequence 20606, A
c1274	142.5	6.9	208	3	US-09-012-692-151	Sequence 151, App	c1347	134	6.6	290	4	US-09-252-991A-27441	Sequence 27441, A
c1275	142.5	6.9	208	3	US-08-906-613-151	Sequence 151, App	1348	134	6.5	328	4	US-09-252-991A-21969	Sequence 21969, A
c1276	142.5	6.9	239	4	US-09-252-991A-21250	Sequence 21250, A	c1349	134	6.6	342	4	US-09-252-991A-23038	Sequence 23038, A
c1277	142.5	6.9	798	4	US-09-252-991A-23774	Sequence 23774, A	c1350	134	6.6	352	4	US-09-252-991A-17906	Sequence 17906, A
c1278	142	6.9	257	4	US-09-252-991A-32137	Sequence 32137, A	1351	134	6.5	611	4	US-09-252-991A-32402	Sequence 32402, A
c1279	142	6.9	666	4	US-09-248-796A-15507	Sequence 15507, A	c1352	134	6.5	615	4	US-09-252-991A-26695	Sequence 26695, A
c1280	141.5	6.8	85	4	US-09-270-767-33231	Sequence 33231, A	c1353	134	6.6	707	4	US-09-252-991A-24045	Sequence 24045, A
c1281	141.5	6.8	85	4	US-09-270-767-48448	Sequence 48448, A	1354	134	6.5	726	4	US-09-252-991A-20675	Sequence 20675, A
c1282	141.5	6.8	802	4	US-09-823-240A-2	Sequence 2, Appl	c1355	134	6.6	748	4	US-09-252-991A-18427	Sequence 18427, A
c1283	141	6.9	406	4	US-09-252-991A-24973	Sequence 24973, A	c1356	134	6.5	793	4	US-09-270-767-42801	Sequence 42801, A
c1284	141	6.9	450	4	US-09-252-991A-16659	Sequence 16659, A	c1357	133.5	6.6	2294	4	US-09-252-991A-17231	Sequence 17231, A
c1285	140.5	6.8	278	4	US-09-602-777A-76	Sequence 76, Appl	c1358	133.5	6.6	351	4	US-09-252-991A-18476	Sequence 18476, A
c1286	140.5	6.8	1400	3	US-08-630-915A-37	Sequence 37, Appl	c1359	133.5	6.6	457	4	US-09-252-991A-25131	Sequence 25131, A
c1287	140.5	6.8	1400	3	US-09-879-957-37	Sequence 37, Appl	c1360	133.5	6.6	552	3	US-09-219-849-7	Sequence 7, Appl
c1288	140	6.9	334	4	US-09-252-991A-27154	Sequence 27154, A	1361	133.5	6.5	699	4	US-10-237-551-143	Sequence 143, App
c1289	139.5	6.9	633	1	US-08-642-255-73	Sequence 73, Appl	1362	133.5	6.5	699	4	US-10-237-551-254	Sequence 254, App
c1290	139	6.7	87	3	US-08-906-769-161	Sequence 161, App	1363	133	6.4	320	4	US-09-252-991A-24634	Sequence 24634, A
c1291	139	6.7	87	3	US-08-639-075A-161	Sequence 161, App	c1364	133	6.5	410	4	US-09-252-991A-25451	Sequence 25451, A
c1292	139	6.7	87	3	US-08-906-616-161	Sequence 161, App	c1365	133	6.5	497	4	US-09-252-991A-17412	Sequence 17412, A
c1293	139	6.7	87	3	US-09-012-431-161	Sequence 161, App	c1366	133	6.5	587	4	US-09-252-991A-25368	Sequence 25368, A
c1294	139	6.7	87	3	US-09-012-692-161	Sequence 161, App	1367	132.5	6.4	226	4	US-09-252-991A-20432	Sequence 20432, A
c1295	139	6.7	87	3	US-08-906-613-161	Sequence 161, App	1368	132.5	6.4	263	4	US-09-252-991A-16906	Sequence 16906, A
c1296	139	6.7	89	3	US-08-906-769-165	Sequence 165, App	1369	132.5	6.4	326	4	US-09-538-082-1019	Sequence 1019, Ap
c1297	139	6.7	89	3	US-08-906-616-165	Sequence 165, App	1370	132.5	6.4	339	4	US-09-252-991A-22531	Sequence 22531, A
c1298	139	6.7	89	3	US-08-639-075A-165	Sequence 165, App	1371	132.5	6.4	343	4	US-09-949-016-11007	Sequence 11007, A
c1299	139	6.7	89	3	US-09-012-431-165	Sequence 165, App	1372	132.5	6.4	371	4	US-09-252-991A-32348	Sequence 32348, A
c1300	139	6.7	89	3	US-09-012-692-165	Sequence 165, App	c1373	132.5	6.5	654	4	US-09-252-991A-25801	Sequence 25801, A
c1301	139	6.7	89	3	US-08-906-613-165	Sequence 165, App	c1374	132.5	6.5	700	4	US-09-252-991A-23746	Sequence 23746, A
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c1303	139	6.8	553	4	US-09-060-854B-2	Sequence 2, Appl	1376	132.5	6.4	1652	4	US-09-627-650B-1	Sequence 1, Appl
c1304	139	6.7	1497	4	US-09-060-854B-2	Sequence 2, Appl	1377	132.5	6.4	1652	4	US-09-436-063C-1	Sequence 1, Appl
c1305	139	6.7	1497	4	US-09-529-904-3	Sequence 3, Appl	1378	132.5	6.4	2732	4	US-09-086-436-30	Sequence 30, Appl
c1306	138.5	6.8	957	4	US-09-252-991A-20408	Sequence 20408, A	c1379	132	6.5	335	4	US-09-252-991A-24899	Sequence 24899, A
c1307	138	6.7	361	4	US-09-252-991A-24085	Sequence 24085, A	c1380	132	6.5	479	4	US-09-252-991A-32994	Sequence 32994, A
c1308	138	6.8	492	4	US-08-468-996-11	Sequence 11, Appl	1381	132	6.4	507	4	US-09-252-991A-31473	Sequence 31473, A
c1309	138	6.8	519	4	US-09-252-991A-32180	Sequence 32180, A	1382	132	6.4	520	4	US-09-252-991A-29451	Sequence 29451, A
c1310	137.5	6.7	605	4	US-09-976-594-616	Sequence 616, App	c1383	132	6.5	569	4	US-09-252-991A-25582	Sequence 25582, A
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c1314	137.5	6.8	1078	3	US-09-548-608-21	Sequence 21, Appl	1387	131.5	6.4	246	4	US-09-252-991A-25102	Sequence 25102, A
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RESULT 2
US-09-949-016-8151
; Sequence 8151, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 8151
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8151

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Score: 1371.50 Matches: 249
Percent Similarity: 99.60% Conservative: 0
Best Local Similarity: 99.60% Mismatches: 0
Query Match: 66.38% Indels: 1
DB: 4 Gaps: 1

US-10-015-385A-193 (1-1091) x US-09-949-016-8151 (1-249)

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; Sequence 6, Application US/09244111
; Patent No. 656498
; GENERAL INFORMATION:
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; APPLICANT: Ni, et al.
; TITLE OF INVENTION: Human Serine Protease and Serpin Polypeptides
; FILE REFERENCES: PF391
; CURRENT APPLICATION NUMBER: US/09/244,111
; CURRENT FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 60/073,961
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 6
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-244-111-6

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US-10-015-385A-193 (1-1091) x US-09-244-111-6 (1-162)

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US-09-618-259-7
; Sequence 7, Application US/09618259
; Patent No. 6642013
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
; FILE REFERENCE: D6020C1P2
; CURRENT APPLICATION NUMBER: US/09/618,259
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 7
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of TADG-14 protein
US-09-618-259-7

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Best Local Similarity:	48.08%	Mismatches:
Query Match:	30.61%	Indels:
DB:	4	Gaps:

US-10-015-385A-193 (1-1091) x US-09-618-259-7 (1-260)

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RESULT 5

US-09-070-526-2
; Sequence 2, Application US/09070526
; Patent No. 6100059
; GENERAL INFORMATION:
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: CLINKENBEARD, HELEN
; APPLICANT: BURGESS, NICOLA
; TITLE OF INVENTION: No. 6100059el Compounds
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,526
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711952.3
; FILING DATE: 9-JUN-1997
; APPLICATION NUMBER: EP 97309646.4
; FILING DATE: 1-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-30353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-070-526-2

Alignment Scores:
Pred. No.: 6,53e-42 Length: 260
Score: 628.50 Matches: 124
Percent Similarity: 57.98% Conservative: 25
Best Local Similarity: 48.25% Mismatches: 95
Query Match: 30.42% Indels: 13
DB: 3 Gaps: 4

US-10-015-385A-193 (1-1091) x US-09-070-526-2 (1-260)

Qy 88 CCCTTTTCCCCAGACTTTGGAAAGTGCACCCACCATGGGGTCTCAGATCTTTTGTCTCTG 147
Db 6 ProArgAlaAlaLysThrTrp-----MetPheLeuLeuLeu 17
Qy 148 -----TGTGTTCTTTGGGCTCAGCCAGGAGCCACCGAAGATTTTCAATGGCACT 198
Db 18 LeuGlyGlyAlaTrpAlaGlyHisSerArgAlaGlnGluAspLysValLeuGlyGlyHis 37
Qy 199 GAGTGTGGGCTTAACCTACAGCCCTGAGCGGTGGGGTGTGGAGGAGCCAGCGCTGGC 258
Db 38 GluCysGlnProHisSerGlnProTrpGlnAlaLeuPheGlnGlyGlnLeuLeu 57
Qy 259 TGGCGGGGTGTCTTATTGACACAGAGTGGGTCTCTACAGCGGTCTACTGACGGGAGC 318
Db 58 CysGlyGlyValLeuValGlyGlyAsnTrpValLeuThrAlaAlaHisCysLysLysPro 77
Qy 319 AGGTACTGGGTGGCGCTGGGGAAACACAGCTCAGCCAGCTGCGAGTGGAGCCGAGCATC 378
Db 78 LysTyrThrValArgLeuGlyAspHisSerLeuGlnAsnLysAspGlyProGluGlnGlu 97
Qy 379 CGGCACAGCGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGGCTCGACG---AGCCAC 435
Db 98 IleProValValGlnSerIleProHisProCysTyrAsnSerSerAspValGluAspHis 117
Qy 436 GAGCAGACCTCCGGCTGCTCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 495
Db 118 AsnHisAspLeuMetLeuLeuGlnLeuArgAspGlnAlaSerLeuGlySerLysValLys 137
Qy 496 CCCTTGGCGCTGCCAATGACTGTGCAACCGCTGGCAGCGAGTCCAGCTGCGAGTGG 555
Db 138 ProIleSerLeuAlaAspHisCysThrGlnProGlyGlnLysCysThrValSerGlyTrp 157
Qy 556 GGCATCACCAACCCAGGAGACCCATTCCTCCGATCTGCTCCAGTGTCTCAACCTCTCC 615
Db 158 GlyThrValThrSerProArgGluAsnPheProAspThrLeuAsnCysAlaGluValLys 177
Qy 616 ATCGTCTCCCATGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 675
Db 178 IlePheProGlnLysLysCysGluAspAlaTyrProGlyGlnIleThrAspGlyMetVal 197
Qy 676 TGTGAGCGCGCTCCCGGCGCAGATCCCTCCAGGAGTGTGCTGGGGGCTGTGGGGGCTGT 735
Db 198 CysAlaGlySerSerLysGlyAlaAspThrCysGlnGlyAspSerGlyGlyProLeuVal 217
Qy 736 TGTGGGGAGTCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 795
Db 218 CysAspGlyAlaLeuGlnGlyIleThrSerTrpGlySer---AppProCysGlyArgSer 236
Qy 796 GGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGG 846
Db 237 AspLysProGlyValTyrThrAsnIleCysArgTyrLeuAspTrpIleLys 253

RESULT 6

US-09-008-271A-7
; Sequence 7, Application US/09008271A
; Patent No. 6203979

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi

TITLE OF INVENTION: HUMAN PROTEASE MOLECULES

NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/008, 271A
  FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: <Unknown>
  FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
  NAME: Mohan-Peterson, Sheela
  REGISTRATION NUMBER: 41,201
  REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 650-845-0555
  TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
  LENGTH: 260 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  IMMEDIATE SOURCE:
  LIBRARY: COLNOT27
  CLONE: 1798496
SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
US-09-008-271A-7

Alignment Scores:
Pred. No.: 1,368-41 Length: 260
Score: 624.50 Matches: 124
Percent Similarity: 57.69% Conservative: 26
Best Local Similarity: 47.69% Mismatches: 97
Query Match: 30.23% Indels: 13
DB: 3 Gaps: 4

US-10-015-385A-193 (1-1091) x US-09-008-271A-7 (1-260)
QY 88 CCTTTTCCCGCAGACTTTGGAAGTGACCCACCACCTGGGGCTCAGCATCTTTTGTCTCTG 147
DB 6 ProArgAlaAlaLysThrTrp-----MetPheLeuLeuLeu 17
QY 148 -----TGTGTCTTCTGGGCTCAGCCAGGACGACCCAGCAAGATTTTCAATGGCACT 198
DB 18 LeuGlyGlyAlaTrpAlaGlyHisSerArgAlaGlnGluAspLysValLeuGlyHis 37
QY 199 GAGTGTGGCGTAACATCAGCGCTGGCAGGTGGGGCTGTTTGGGGACACGCTGGCG 258
DB 38 GluCysGlnProHisSerGlnProTrpGlnAlaAlaLeuSerGlnGlyGlnGlnLeu 57
QY 259 TCGGGGGTGTCTTATTACACAGGTGGGTCTCAGCGGCTCAGTGGAGCGGCAGC 318
DB 58 CysGlyGlyValLeuValGlyAlaSerTrpValLeuThrAlaAlaHisCysLysPro 77
QY 319 AGGTACTGGCTGGCTGGGGAACACAGCTCAGCTCAGCTGACCGACGACGAGATC 378
DB 78 LysTyrThrValArgLeuGlyAspHisSerLeuGlnAsnLysAspGlyProGluGlnGlu 97
QY 379 CGGCACAGCGGTTCTGTGTGACCATCCCGCTACCTGGGAGCTCGACG---AGCCAC 435
DB 98 IleProValValGlnSerIleProHisProCysTyrAsnSerSerAspValGluAspHis 117
QY 436 GAGCAGGACCTCGGCTGTGGCTGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTCAA 495
DB 118 AnHisAspLeuMetLeuGlnLeuArgAspGlnAlaSerLeuGlySerLysValLys 137
QY 496 CCCCTGGCCCTGCCCAATGACTGTGCAACCGCTGCGACCGAGTGCCAGCTCTCAGCTGG 555
DB 138 ProIleSerLeuAlaAspHisCysThrGlnProGlyGlnLysCysThrValSerGlyTrp 157
QY 556 GGCATCACCAACCAACCCAGGAACCCATTCCTCCGGATCTGCTCCAGTGGCTCAACCTTCC 615
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Db 158 GlyThrValThrSerProArgGluAsnPheProAspThrLeuAsnCysAlaGluValLys 177
QY 616 ATCGTCTCCCATGCCACCTGCGCATGGTGTGTATCCCGGAGAAATCACGAGCAACATGGTG 675
DB 178 IlePheProGlnLysCysGluAspAlaTyrProGlyGlnIleThrAspGlyMetVal 197
QY 676 TGTGACAGCGGGCTCCCGGGCAGGATGCTCCAGGCTGATCTGGGGGCCCCCTGGTG 735
DB 198 CysAlaGlySerSerLysGlyAlaAspThrCysGlnGlyAspSerGlyGlyProLeuVal 217
QY 736 TGTGGGGAGTCTTCAAGTCTGTGCTCTGGGGTCTGTGGGCGCTGTGGACCAAGAT 795
DB 218 CysAspGlyAlaLeuGlnGlyIleThrSerTrpGlySer---AspProCysGlyArgSer 236
QY 796 GGCATCCCTGGAGTCTACACCTATATTTTCAAGTATGTGAGATCGGATCGGATGATCATG 855
DB 237 AspLysProGlyValThrAsnIleCysArgTyrLeuAspTrpIleLysLysIleIle 256

RESULT 7
US-09-025-059-3
; Sequence 3, Application US/09025059
; Patent No. 6075136
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,059
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0481 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1020091
US-09-025-059-3

Alignment Scores:
Pred. No.: 1,968-41 Length: 260
Score: 622.50 Matches: 121
Percent Similarity: 60.32% Conservative: 28
Best Local Similarity: 48.99% Mismatches: 93
Query Match: 30.13% Indels: 5
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QY 778 GGGCCCTGTGACAGATGGCATCCCTGGAGTCTACACCTATATTGCAAGTATGTGGAC 837
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Db 222 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTyrValAsp 241
|||||

QY 838 TGGATCCGGATGATCATGAGGAACAAC 864
|||||
Db 242 TrpIleGlnGluThrMetLysAsnAen 250
|||||

RESULT 10

US-09-025-059-1
; Sequence 1, Application US/09025059
; Patent No. 6075136
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,059
; FILING DATE:

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0481 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:

INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 282 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGTU10
; CLONE: 2723646
US-09-025-059-1

Alignment Scores:
Pred. No.: 4,15e-41 Length: 282
Score: 618.50 Matches: 120
Percent Similarity: 62.25% Conservative: 35
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
DB: 3 Gaps: 4

US-10-015-385A-193 (1-1091) x US-09-025-059-1 (1-282)

QY 127 CTCAGCATCTTTTGTCTCTGTGTCTTGGGCTCAGCCAGGCACACCGAAGATT 186
|||||
Db 36 LeuGlnLeuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGluThr---ArgIle 54
|||||
QY 187 TTCATAGGCATGAGTGTGGGCTAACTCACAGCGTGGCAGGTGGGCTGTTTGAAGGC 246
|||||

Db 55 IleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGluLys 74
QY 247 ACCAGCCTCGGCTCGGGGGTGTCTTATTGACACACAGGTGGTCTCTCACAGCGGCTCAC 306
|||||
Db 75 ThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAlaHis 94
|||||
QY 307 TGCAGCGGACAGAGTACTGGGTGCGCTGGGGGAACACAGCCTCAGCCAGCTGAGTGG 366
|||||
Db 95 CysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGly 114
|||||
QY 367 ACCAGCAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCC-- 423
|||||
Db 115 CysGlnGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerIle 134
|||||
QY 424 --TCGACGACGACGACGACGACCTCGGCTGTGGGGCTGCGCTGCGGCTGCGGCTA 480
|||||
Db 135 ProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSerIle 154
|||||
QY 481 ACCAGCAGCGTTCAACCCCTGCGCTGCGCAATGACTGTGCAACCGCTGGCAGCGAGTGC 540
|||||
Db 155 ThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCys 174
|||||
QY 541 CACGTCTCAGCTGGGCGCATCACCAACCCAGCAACCCATTCGCGGATCTGCTCCAG 600
|||||
Db 175 LeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeuArg 194
|||||
QY 601 TGCCTCAACCTCTCATCGTCTCCCATGCCACCTCGCTGCTGTGTATCTCCGGGAGATC 660
|||||
Db 195 CysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIle 214
|||||
QY 661 ACAGCACAACATGGTGTGTGCAAGGC---GGCCTCCCGGGGAGGATGCTGCCAGGTGAT 717
|||||
Db 215 ThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGlyAsp 234
|||||
QY 718 TCTGGGGCCCTGTGTGTGGGGAGTCTCTCAAGTCTGTGTCTCTGGGGGTCTGTG 777
|||||
Db 235 SerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln--- 253
|||||
QY 778 GGGCCCTGTGACAGATGGCATCCCTGGAGTCTACACCTATATTGCAAGTATGTGGAC 837
|||||
Db 254 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTyrValAsp 273
|||||
QY 838 TGGATCCGGATGATCATGAGGAACAAC 864
|||||
Db 274 TrpIleGlnGluThrMetLysAsnAsn 282
|||||

RESULT 11

US-09-386-642-13
; Sequence 13, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-13

Alignment Scores:
Pred. No.: 7,79e-40 Length: 288
Score: 602.50 Matches: 116
Percent Similarity: 60.35% Conservative: 21

Best Local Similarity: 51.10% Mismatches: 87
Query Match: 29.16% Indels: 3
DB: 4 Gaps: 3

US-10-015-385A-193 (1-1091) x US-09-386-642-13 (1-288)

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QY 181 AAGATTTCATGGCACTGAGTGT---GGGCGTAACACACAGCCGTCGGCAGGTGGGGCTG 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 51 LysIleValGlyGlyTyrAsnCysLeuGluProHisSerGlnProTrpGlnAlaLeu 70
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 238 TTTGAGGCAACAGCAGCTGCGCTGCGGGGTGCTTATTGACACAGGTGGGTCTCTACA 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 71 PheGlnGlyGlnLeuLeuLeuLeuLeuValGlyValGlyAsnTrpValLeuThr 90
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 298 GCGGCTCACTGCGGCGGAGGAGTACTGGGTGCGCTGGGGGAACACAGCCTCAGCCAG 357
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 91 AlaAlaHisCysLysLysProLysTyrThrValArgLeuGlyAspHisSerLeuGlnAsn 110
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 358 CTCGACTGACAGCAGATCCGGCAGCGGCTCTCTGTGACCCATCCCGGCTACCTG 417
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 111 LysAspGlyProGluGlnGlnIleProValValGlnSerIleProHisProCysTyrAsn 130
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 418 GGAGCTCGACG---AGCCAGCAGCAGCAGCTCCGCTGCTGCGGTGCGCTGCCCTG 474
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 131 SerSerAspValGluAspHisAsnHisAspLeuMetLeuLeuGlnLeuArgAspGlnAla 150
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 475 GCGGTAAACAGCAGCGGTTCAACCCCTGCGCCCTGCGCAATGACTGTGCAACCGCTGCCACC 534
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 151 SerLeuGlySerLysValLysProLysLeuAlaAspHisCysThrGlnProGlyGln 170
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 535 GAGTCCAGCTCTAGGCTGGGGGATCACCACACCGAACCACCGAACCATTCCCGGATCTG 594
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 171 LysCysThrValSerGlyTrpGlyThrValThrSerProArgGluAsnPheProAspThr 190
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 595 CTCAGTGCCTCAACCTCTCCATGCTCTCCCATGCCACCTGCGCATGCTGTGTATCCCGG 654
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 191 LeuAsnCysAlaGluValLysIlePheProGlnLysLysCysGluAspAlaTyrProGly 210
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 655 AGAATCAGCAGCAACATGCTGTGTGCGGCGCGCTCCGCGGCGAGTGCCTGCCAGGCT 714
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 211 GlnIleThrAspGlyMetValCysAlaGlySerSerLysGlyAlaAspThrCysGlnGly 230
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 715 GATTCTGGGGCCCTGCTGTGTGTGGGGAGTCTTCAAGTCTGTGTGTCTGCGGGTCT 774
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 231 AspSerGlyGlyProLeuValCysAspGlyAlaLeuGlnGlyIleThrSerTrpGlySer 250
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 775 GTGGGGCCCTGTGGACAGATGGCATCCCTGAGTCTACACCTATATTGCAAGTATGTG 834
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 251 ---AspProCysGlyArgSerAspLysProGlyValTyrThrAsnIleCysArgTyrLeu 269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 835 GACTGATCCGGATCATGATCATG 855
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 270 AspTrpIleLysIleIle 276
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 12

US-09-386-642-14

; Sequence 14, Application US/09386642

; Patent No. 6420157

; GENERAL INFORMATION:

; APPLICANT: Darrow, Andrew

; APPLICANT: Qi, Jensen

; APPLICANT: Andrade-Gordon, Patricia

; TITLE OF INVENTION: Zymogen Activation System

; FILE REFERENCE: ORT-1028

; CURRENT APPLICATION NUMBER: US/09/386,642

; CURRENT FILING DATE: 1999-08-31

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 289

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-14

Alignment Scores:

Pred. No.: 1,62e-39 Length: 289
Score: 598.50 Matches: 114
Percent Similarity: 63.79% Conservative: 34
Best local Similarity: 49.14% Mismatches: 79
Query Match: 28.97% Indels: 5
DB: 4 Gaps: 4

US-10-015-385A-193 (1-1091) x US-09-386-642-14 (1-289)

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QY 181 AAGATTTCATGGCACTGAGTGT---GGGCGTAACACACAGCCGTCGGCAGGTGGGGCTG 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 51 LysIleValGlyGlyTyrAsnCysLeuGluLysHisSerGlnProTrpGlnAlaLeu 70
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 238 TTTGAGGCAACAGCAGCTGCGCTGCGGGGTGCTTATTGACACAGGTGGGTCTCTACA 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 71 PheGluLysThrArgLeuLeuLeuLeuLeuLeuAlaThrLeuIleAlaProArgTrpLeuThr 90
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 298 GCGGCTCACTGCGGCGGAGGAGTACTGGGTGCGCTGGGGGAACACAGCCTCAGCCAG 357
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 91 AlaAlaHisCysLysLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLys 110
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 358 CTCGACTGAGCAGCAGATCCGGCAGCAGCGGCTTCTGTGACCCATCCCGGCTACCTG 417
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 111 GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn 130
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 418 GGAGCC-----TCGACGAGCCACGAGCAGCAGCTCCCGGCTGCTGCGGCTGCCCTGCC 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 131 AsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerPro 150
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 472 GTCCCGTAAACAGCAGCGGTTCACCCCTGCGCCCTGCCATGACTGTGTGCAACCGTGGC 531
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 151 ValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGly 170
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 532 ACCGAGTGCACGCTCTCAGGCTGGGGCATCACCAACCCACCGAACCATTCCCGGAT 591
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 171 ThrSerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHis 190
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 592 CTGCTCCAGTGCCTCAACCTCTCCATGCTCTCCCATGCCACCTGCCATGGTGTGTATCCC 651
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DB 191 ThrLeuArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTyrPro 210
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QY 652 GGGAGAATCAGCAGCAACATGCTGTGTGTCAGGC---GGGCTCCCGGGCAGGATGCCTGC 708
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DB 211 GlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCys 230
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QY 709 CAGGCTGATTCTGGGGGCCCTGCTGTGTGGGGAGTCTTCAAGGCTGTGTCTCTGG 768
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DB 231 GlnGlyAspSerGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrp 250
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QY 769 GGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTGCAAG 828
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DB 251 GlyGln---AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLys 269
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QY 829 TATGTGGATGATCCGGATGATCATGAGGAACAAC 864
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DB 270 TyrValAspTrpIleGlnGluThrMetLysAsnAsn 281
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RESULT 13

US-08-944-483-24

; Sequence 24, Application US/08944483

; Patent No. 6232456

; GENERAL INFORMATION:

; APPLICANT: COHEN, MAURICE

; APPLICANT: COLPITTS, TRACEY L.

; APPLICANT: FRIEDMAN, PAULA N.

; APPLICANT: GRANADOS, EDWARD N.

; APPLICANT: KLASS, MICHAEL R.

; APPLICANT: RUSSELL, JOHN C.

Db 311 ValCysArgTyrThrAsnTrpIleGln 319

Search completed: March 5, 2005, 23:08:24
Job time : 54 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 5, 2005, 23:00:19 ; Search time 49 Seconds
(without alignments)
4284.591 Million cell updates/sec

Title: us-10-015-385A-193

Perfect score: 2066

Sequence: 1 caagcaggtcatcccttgg.....aggggcacaaaaaaaaa 1091

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Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 1500 summaries

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Database :

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2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	622.5	30.1	260	2	I56559
2	569.5	27.6	248	2	S55066
3	567	27.4	248	2	S55067
4	561	27.2	231	1	TRPQTR
5	555	26.9	243	2	A35871
6	555	26.9	253	2	A53968
7	533	26.8	246	2	B25528
8	552	26.7	229	1	TRBOTR
9	550	26.6	247	2	S13813
10	546	26.4	247	1	TRDQ
11	545	26.4	246	1	TRDSC
12	544.5	26.4	247	2	A27547
13	543	26.3	246	1	TRRT1
14	540	26.1	238	2	S31779

15	533.5	25.8	247	2	S05494	trypsin (EC 3.4.21
16	532	25.8	246	1	TRRT2	trypsin (EC 3.4.21
17	527.5	25.5	261	2	A31136	tissue kallikrein
18	524	25.4	232	1	KQPG	tissue kallikrein
19	520.5	25.2	261	2	A25606	tissue kallikrein
20	519	25.1	246	2	JQ1471	trypsin (EC 3.4.21
21	518	25.1	246	2	JQ1472	trypsin (EC 3.4.21
22	518	25.1	246	2	A34079	tissue kallikrein
23	513.5	24.9	231	2	S31778	trypsin (EC 3.4.21
24	513.5	24.9	239	2	A27207	tissue kallikrein
25	511.5	24.8	261	2	S45303	tissue kallikrein
26	510.5	24.7	261	1	NGMSG	7S nerve growth fa
27	508	24.6	242	2	S31776	trypsin (EC 3.4.21
28	508	24.6	242	2	S31775	trypsin (EC 3.4.21
29	503	24.3	260	2	A37938	tissue kallikrein
30	503	24.3	263	2	S15686	tissue kallikrein
31	502	24.3	259	2	B31136	tissue kallikrein
32	501	24.2	247	1	B25852	trypsin (EC 3.4.21
33	499.5	24.2	241	2	S39048	trypsin (EC 3.4.21
34	496.5	24.0	261	1	TRMSM5	tissue kallikrein
35	496	24.0	242	2	S49489	trypsin (EC 3.4.21
36	495.5	24.0	257	2	S33772	tissue kallikrein
37	495.5	24.0	261	2	S01971	tissue kallikrein
38	494.5	23.9	247	1	A25852	trypsin (EC 3.4.21
39	493	23.9	262	1	KQHU	tissue kallikrein
40	491.5	23.8	240	2	S39047	trypsin (EC 3.4.21
41	491	23.8	256	1	NGMSA	7S nerve growth fa
42	490.5	23.7	229	1	TRDFS	trypsin (EC 3.4.21
43	490.5	23.7	261	2	A41020	tissue kallikrein
44	489	23.7	244	2	A44284	tissue kallikrein
45	488	23.6	265	1	KQRTP	tissue kallikrein
46	485.5	23.5	261	2	JE0236	tissue kallikrein
47	485	23.5	304	2	S33496	trypsin (EC 3.4.21
48	484.5	23.5	259	2	A29746	tissue kallikrein
49	481.5	23.3	250	2	T01779	trypsin (EC 3.4.21
50	481.5	23.3	261	2	A29745	tissue kallikrein
51	479	23.2	261	1	S35711	semenogelase (EC 3
52	477.5	23.1	261	1	KQMS1	tissue kallikrein
53	476	23.0	259	2	I38363	trypsin (EC 3.4.21
54	470.5	22.8	261	1	A32297	semenogelase (EC 3
55	469.5	22.7	261	2	A24378	tissue kallikrein
56	468	22.7	259	1	KQRTTN	tonin (EC 3.4.21.-
57	467.5	22.6	261	1	EGMSB	tissue kallikrein
58	467	22.6	247	2	S12764	trypsin (EC 3.4.21
59	461.5	22.3	259	2	D23863	tissue kallikrein
60	458.5	22.2	250	2	S31384	trypsin (EC 3.4.21
61	458.5	22.2	261	2	A29586	tissue kallikrein
62	450	21.8	258	2	A57290	venom plasminogen
63	437.5	21.2	257	1	JC2479	venombin B (EC 3.4
64	436.5	21.1	250	2	S15685	kallikrein, glandu
65	432	20.9	236	1	A32121	snake venom factor
66	431.5	20.9	261	2	A28062	gamma-renin (EC 3.
67	431	20.9	262	1	JC4803	venombin A (EC 3.4
68	427	20.7	233	1	JG0169	venombin A (EC 3.4
69	417	20.2	236	1	B32121	snake venom factor
70	411.5	19.9	228	1	S35689	venombin A (EC 3.4
71	408	19.7	235	1	S65621	venombin AB (EC 3.
72	406.5	19.7	231	2	A60468	venombin A (EC 3.4
73	402	19.5	255	1	A28169	venombin A (EC 3.4
74	395	19.1	236	1	A41456	venombin A (EC 3.4
75	388	18.8	232	1	A54361	venombin A (EC 3.4
76	388	18.8	269	2	A26823	pancreatic elastas
77	386.5	18.7	1524	2	T30337	polypotein - Afri
78	385.5	18.7	188	2	B32340	tissue kallikrein
79	385.5	18.7	264	2	I38136	chymotrypsin-like
80	385	18.6	263	1	I55608	complement factor
81	382	18.5	246	1	DBHU	complement factor
82	378	18.3	225	2	S45356	probable serine pr
83	376	18.2	343	1	A57014	proctasin (EC 3.4.
84	374.5	18.1	259	1	WMMS28	complement factor
85	371	18.0	234	1	S20407	venombin A (EC 3.4
86	371	18.0	263	2	A21195	chymotrypsin (EC 3
87	371	18.0	271	1	ELRT2	pancreatic elastas

88	370.5	17.9	638	1	KOHUP	plasma kallikrein	161	327	15.8	244	2	S72219	chymotrypsin B - A
89	366	17.7	258	1	S36783	venombin A (EC 3.4	162	327	15.8	259	2	S68424	allergen Der f III
90	364	17.6	156	2	B23863	tissue kallikrein	163	326.5	15.8	248	1	PMSC2	granzyme C (EC 3.4
91	362.5	17.5	246	2	S64707	chymase (EC 3.4.21	164	326.5	15.8	266	1	ELPG	pancreatic elastase
92	359.5	17.4	277	2	S35340	trypsin (EC 3.4.21	165	326	15.8	248	2	S33755	granzyme-like prote
93	359.5	17.4	1019	2	A38738	coagulation factor	166	325.5	15.8	492	1	KFHU7	coagulation factor
94	359	17.4	443	2	I46932	coagulation factor	167	324.5	15.7	476	1	EXBO	coagulation factor
95	358.5	17.4	263	2	A31299	chymotrypsin (EC 3	168	324	15.7	274	2	A45754	trypsin (EC 3.4.2
96	358	17.3	812	1	PLBO	plasma (EC 3.4.21	169	324	15.7	465	2	A45754	coagulation factor
97	357	17.3	262	1	A31372	granzyme A (EC 3.4	170	324	15.7	459	2	J00419	enteropeptidase (E
98	357	17.3	271	2	S29239	chymotrypsin (EC 3	171	322	15.6	265	2	A56318	chymotrypsin (EC 3
99	355.5	17.2	276	2	A38654	mast cell proteina	172	322	15.6	460	2	B61545	plasmin (EC 3.4.21
100	354.5	17.2	263	2	S47537	chymotrypsin (EC 3	173	321.5	15.6	251	2	JC2125	chymase (EC 3.4.21
101	354	17.1	260	2	A45061	granzyme A (EC 3.4	174	321.5	15.6	436	2	JX0172	acrosin (EC 3.4.21
102	354	17.1	271	2	A25528	pancreatic elastase	175	321	15.5	226	1	KCUF	brachyurin (EC 3.4
103	353.5	17.1	270	2	S56160	mast cell trypsinase	176	321	15.5	226	2	S69370	chymase - bovine
104	353	17.0	274	2	JC4171	trypsinase (EC 3.4.2	177	321	15.5	247	2	S64708	chymase (EC 3.4.21
105	352	17.0	461	1	JX0210	protein C (activat	178	321	15.5	248	2	A43520	natural killer cel
106	351	17.0	459	1	KXBO	protein C (activat	179	321	15.5	269	2	B32410	mastocytoma protei
107	349.5	16.9	266	2	B26823	pancreatic elastase	180	321	15.5	655	1	A46688	hepatocyte growth
108	348	16.8	267	2	A40006	trypsin (EC 3.4.21	181	320.5	15.5	247	1	PMSC1	granzyme B (EC 3.4
109	347	16.8	461	1	KXHU	protein C (activat	182	320	15.5	431	2	S47538	acrosin (EC 3.4.21
110	346.5	16.8	244	2	S26042	chymase (EC 3.4.21	183	319.5	15.5	559	1	A29941	t-plasminogen acti
111	346.5	16.8	461	1	S18994	protein C (activat	184	319	15.4	1034	1	A53663	enteropeptidase (E
112	344	16.7	275	2	B35863	trypsinase (EC 3.4.2	185	318	15.4	271	2	I46580	factor IX - pig (f
113	343.5	16.6	273	2	A47246	trypsinase (EC 3.4.2	186	318	15.4	274	2	I47078	coagulation factor
114	343.5	16.6	274	2	S35339	trypsin (EC 3.4.21	187	318	15.4	618	2	A35827	thrombin (EC 3.4.2
115	343.5	16.6	558	2	JC5878	plasma hyaluronan-	188	317.5	15.4	245	1	KVBOB	chymotrypsin (EC 3
116	343	16.6	275	2	A32410	trypsinase (EC 3.4.2	189	317.5	15.4	246	2	A32692	cytotoxic T-lympho
117	342.5	16.6	437	2	S18407	acrosin (EC 3.4.21	190	317	15.3	249	2	A56634	granzyme M (EC 3.4
118	342.5	16.6	810	1	PLHU	plasmin (EC 3.4.21	191	316.5	15.3	246	1	A46504	chymase (EC 3.4.21
119	342	16.6	275	2	C35863	trypsinase (EC 3.4.2	192	316.5	15.3	433	1	JN0560	u-plasminogen acti
120	342	16.6	275	2	A35863	trypsinase (EC 3.4.2	193	316	15.3	482	1	EXRT	coagulation factor
121	341.5	16.5	258	2	I58220	trypsinase 2 - rat	194	315.5	15.3	254	1	TRWV3Y	trypsin-like prote
122	340.5	16.5	246	2	B38678	mast cell proteina	195	315.5	15.3	266	1	ELRT1	pancreatic elastase
123	339.5	16.4	258	2	A45161	serine proteinase	196	315.5	15.3	392	1	A30100	serine proteinase
124	339.5	16.4	267	4	A56615	probable pancreati	197	315	15.2	248	2	S43259	trypsin-like prote
125	339	16.4	257	2	B45061	granzyme A (EC 3.4	198	315	15.2	275	2	S40005	trypsin (EC 3.4.21
126	339	16.4	461	1	KPHU	coagulation factor	199	315	15.2	617	2	S10511	thrombin (EC 3.4.2
127	339	16.4	625	1	KFHU1	coagulation factor	200	315	15.2	686	1	A59271	Ra-reactive factor
128	338	16.4	625	1	TBBO	thrombin (EC 3.4.2	201	314	15.2	418	2	A37344	acrosin (EC 3.4.21
129	337.5	16.3	238	1	TRWV5Y	trypsin-like prote	202	313	15.2	613	2	S15468	complement C3b/C4b
130	337.5	16.3	264	2	S65562	granzyme 3 (EC 3.4	203	313	15.2	855	2	JC7731	membrane-bound arg
131	337	16.3	434	1	A35005	u-plasminogen acti	204	312.5	15.1	274	2	S40004	trypsin-related pr
132	337	16.3	812	1	PLMS	plasmin (EC 3.4.21	205	312.5	15.1	615	1	KFHU12	coagulation factor
133	336.5	16.3	251	2	T10262	mast cell serine p	206	311.5	15.1	761	2	JC5759	brain-specific ser
134	336.5	16.3	251	2	PC1235	29K serine protein	207	311	15.1	261	1	S40162	cathepsin G (EC 3.
135	336.5	16.3	638	1	KQMSPL	plasma kallikrein	208	311	15.1	421	2	S29599	acrosin (EC 3.4.21
136	336	16.3	416	1	KFBO	coagulation factor	209	311	15.1	559	1	A35029	t-plasminogen acti
137	336	16.3	790	1	PLFG	plasmin (EC 3.4.21	210	311	15.1	1035	1	A43090	enteropeptidase (E
138	335.5	16.2	258	4	S70439	pancreatic elastase	211	310.5	15.0	247	1	PRRTG	factor IX - rabbit
139	334	16.2	245	1	KYBOA	chymotrypsin (EC 3	212	310	15.0	275	2	I46712	oviductin (EC 3.4.
140	333.5	16.1	263	1	KYRTB	chymotrypsin (EC 3	213	308.5	14.9	1004	2	T30338	hepsin (EC 3.4.21
141	333	16.1	285	2	I48144	coagulation factor	214	308	14.9	417	1	S00845	serine proteinase
142	333	16.1	810	2	I46260	plasmin (EC 3.4.21	215	307	14.9	250	2	S55493	chymotrypsin (EC 3
143	332.5	16.1	638	1	KQRTPL	plasma kallikrein	216	307	14.9	259	1	S49129	limulus clotring e
144	332.5	16.1	810	2	B30848	trypsin (EC 3.4.21	217	306.5	14.8	375	1	A23689	thrombin (EC 3.4.2
145	331.5	16.0	256	1	TRFF	trypsin-like prote	218	305.5	14.8	236	2	I42696	hypothetical prote
146	331.5	16.0	275	2	S40007	trypsin (EC 3.4.21	219	305	14.8	196	2	T08808	granzyme B (EC 3.4
147	331	16.0	622	1	TBHU	thrombin (EC 3.4.2	220	305	14.8	281	1	A61021	tissue kallikrein
148	330.5	16.0	237	2	S68702	chymase (EC 3.4.2	221	304	14.7	149	1	KQMSM	thrombin (EC 3.4.2
149	330.5	16.0	247	1	JYHUCM	plasma hyaluronan-	222	304	14.7	268	2	C42696	pancreatic elastase
150	330.5	16.0	560	1	JC4795	coagulation factor	223	304	14.7	268	2	S68825	t-plasminogen acti
151	330	16.0	282	2	I84621	apoptein(a) (EC	224	304	14.7	562	1	UKHT	chymase (EC 3.4.21
152	330	16.0	4548	1	S00657	myonase (EC 3.4.-	225	303.5	14.7	244	2	A46721	coagulation factor
153	329.5	15.9	226	2	JEO151	pancreatic elastase	226	303.5	14.7	309	2	B49878	cathepsin G (EC 3.
154	329.5	15.9	269	2	C26823	apolipoprotein(a)	227	303	14.7	255	2	A27122	mast cell proteina
155	329.5	15.9	1420	2	A32869	serine proteinase	228	302.5	14.6	244	2	A34910	trypsin-related pr
156	328.5	15.9	455	2	A61545	plasmin (EC 3.4.21	229	302.5	14.6	273	2	S40003	low-density lipopr
157	328.5	15.9	786	1	A47547	serine proteinase	230	302.5	14.6	1113	2	JEO315	pancreatic elastase
158	328	15.9	452	1	A30351	coagulation factor	231	302	14.6	268	2	S68826	trypsin homolog -
159	328	15.9	699	1	I54763	Ra-reactive factor	232	302	14.6	281	2	T13596	t-plasminogen acti
160	327.5	15.9	266	2	S54146	trypsin (EC 3.4.21	233	302	14.6	394	2	J50600	

234	302	14.6	477	1	A34369	t-plasminogen acti	307	247	12.0	243	2	A56338	venom proteinase (
235	302	14.6	477	2	JS0598	t-plasminogen acti	308	245.5	11.9	711	1	A47136	macrophage-stimula
236	301	14.6	431	2	JS0599	t-plasminogen acti	309	243.5	11.8	705	1	CIHURB	complement-stimula
237	301	14.6	442	1	UKPG	u-plasminogen acti	310	239.5	11.6	265	2	I48679	neutrophil elastase
238	300	14.5	245	2	A48598	kallikrein-like ae	311	237.5	11.5	232	2	S32398	serine proteinase
239	300	14.5	433	1	UKWS	u-plasminogen acti	312	237	11.5	716	1	JCS061	macrophage-stimula
240	299.5	14.5	235	2	A42696	thrombin (EC 3.4.2	313	235.5	11.4	198	2	S06176	cytotoxic T-lympho
241	299.5	14.5	246	2	A38678	mast cell proteina	314	235	11.4	96	2	A05308	tissue kallikrein
242	299.5	14.5	258	1	A44184	chymotrypsin (EC 3	315	235	11.4	230	2	A27802	hypodermis C (EC 3
243	299	14.5	260	2	S26043	chymase (EC 3.4.21	316	234.5	11.4	219	1	TRPGA2	azurocidin - pig
244	299	14.5	421	1	S11674	acrosin (EC 3.4.21	317	234	11.3	230	2	I48685	mast cell proteina
245	298.5	14.4	191	2	S54115	complement factor	318	227.5	11.0	267	1	ELHUL	leukocyte elastase
246	298.5	14.4	249	1	A35842	chymase (EC 3.4.21	319	227.5	11.0	272	2	JC4170	trypsin-like prote
247	298.5	14.4	270	2	B29934	pancreatic elastase	320	227	11.0	259	1	TRSMG	trypsin (EC 3.4.21
248	298.5	14.4	407	1	KFB07	coagulation factor	321	226	10.9	728	1	JH0579	hepatocyte growth
249	297	14.4	237	1	TRCY1	trypsin (EC 3.4.21	322	225	10.9	548	2	D82175	probable trypsin V
250	297	14.4	477	2	JS0597	t-plasminogen acti	323	217.5	10.5	710	1	I51283	hepatocyte growth
251	296.5	14.4	248	1	S01007	granzyme F (EC 3.4	324	216	10.5	728	1	A35644	hepatocyte growth
252	295.5	14.3	239	2	G42696	thrombin (EC 3.4.2	325	216	10.5	728	1	A60185	hepatocyte growth
253	294	14.2	247	2	S23504	chymase (EC 3.4.21	326	204.5	9.9	177	2	S23505	chymase (EC 3.4.21
254	294	14.2	303	2	T13598	trypsin homolog -	327	201.5	9.8	248	2	S49323	chymotrypsin (EC 3
255	293.5	14.2	431	1	UKHU	u-plasminogen acti	328	201	9.7	214	2	S17680	fibrinolytic prote
256	293	14.2	234	2	F42696	thrombin (EC 3.4.2	329	197.5	9.6	213	2	S17537	fibrinolytic prote
257	293	14.2	247	2	S59135	mast cell proteina	330	192.5	9.3	763	2	I50807	complement factor
258	293	14.2	265	2	A38894	serine proteinase	331	189.5	9.2	94	2	PC2013	tissue kallikrein
259	293	14.2	265	2	JS0260	serine proteinase	332	182	8.8	104	2	S15395	tissue kallikrein-
260	293	14.2	433	1	UKBAY	u-plasminogen acti	333	182	8.8	348	1	HPHUR	haptoglobin-relate
261	292.5	14.2	236	2	A28566	T-cell suppressor	334	180.5	8.7	377	2	C88710	protein C43G2.5 [i
262	291.5	14.1	216	1	KYVH20	chymotrypsin (EC 3	335	180	8.7	258	2	G02959	haptoglobin - rhes
263	291	14.1	271	2	S41308	serine proteinase	336	179.5	8.7	149	2	S35208	serine proteinase
264	291	14.1	415	1	A43170	acrosin (EC 3.4.21	337	177	8.6	347	1	HPHU1	haptoglobin precur
265	290.5	14.1	420	2	A55283	acrosin (EC 3.4.21	338	177	8.6	406	1	HPHU2	haptoglobin precur
266	289.5	14.0	248	2	A33412	cytotoxic T-lympho	339	176.5	8.5	760	1	C2MS	classical compleme
267	289	14.0	583	2	A29154	complement factor	340	176	8.5	735	2	T35778	probable fusidic a
268	288.5	14.0	270	2	A29934	pancreatic elastase	341	175.5	8.5	330	2	B82415	probable serine pr
269	288.5	14.0	1047	2	A55617	masquerade precurs	342	174	8.4	161	2	I48158	coagulation factor
270	288	13.9	268	2	QJ1473	pancreatic elastase	343	172	8.3	346	2	I36942	haptoglobin - chlm
271	287.5	13.9	235	2	H42696	thrombin (EC 3.4.2	344	171	8.3	159	2	S35202	proteinase 2 - buf
272	287.5	13.9	603	2	S28941	coagulation factor	345	171	8.3	258	2	I36945	haptoglobin Hp - c
273	286.5	13.9	218	1	KYVH2C	chymotrypsin (EC 3	346	171	8.3	345	2	I36941	haptoglobin - chlm
274	286	13.8	254	2	S35585	chymotrypsin-like	347	170	8.2	347	2	G00006	haptoglobin - blac
275	285.5	13.8	235	2	D42696	thrombin (EC 3.4.2	348	169	8.2	329	1	HPDG	haptoglobin precur
276	282.5	13.7	331	2	T27906	hypothetical prote	349	168	8.1	66	2	I52972	kallikrein - mouse
277	282	13.6	416	1	S33777	hepsin (EC 3.4.21	350	168	8.1	154	2	S35207	proteinase 7 - buf
278	280.5	13.6	366	2	JE0105	testicular serine	351	166	8.0	258	2	I36947	haptoglobin Hpp -
279	280	13.6	254	2	S65465	trypsin-like prote	352	166	8.0	349	2	I36944	haptoglobin - chlm
280	280	13.6	430	1	A24702	serine proteinase	353	166	8.0	752	1	C2HU	complement C2 prec
281	278.5	13.5	432	1	S18932	u-plasminogen acti	354	165	8.0	161	2	I62744	coagulation factor
282	278.5	13.5	593	2	S45281	coagulation factor	355	165	8.0	347	1	HPMS	haptoglobin precur
283	278	13.5	488	1	EXHU	coagulation factor	356	161.5	7.9	660	1	Q0BE3	BHLFI protein - hu
284	277.5	13.4	266	2	JC4850	trypsin-like prote	357	159.5	7.7	152	2	S35209	serine proteinase
285	275.5	13.3	240	1	CPBOA3	procarboxypeptidas	358	159.5	7.7	805	2	T25795	hypothetical prote
286	275.5	13.3	265	2	T15451	hypothetical prote	359	159	7.7	126	2	A23473	chymotrypsin-like
287	275	13.3	237	2	S53378	serine proteinase	360	158.5	7.7	264	2	A28942	pancreatic elastase
288	275	13.3	688	1	CIHUS	complement subcomp	361	157.5	7.6	764	1	BBHU	complement factor
289	274.5	13.3	695	1	S05008	complement subcomp	362	157	7.6	407	2	C70816	hypothetical prote
290	273	13.2	247	2	S45113	granzyme-like prot	363	154.5	7.5	747	2	I51579	hypothetical prote
291	272	13.2	475	1	EXCH	coagulation factor	364	153.5	7.4	761	1	BWMS	complement factor
292	271.5	13.1	256	1	PRHU3	proteinase 3 (EC 3	365	152.5	7.4	159	2	I84615	coagulation factor
293	271	13.1	2616	2	A57096	nuclei protein prec	366	152	7.4	181	2	T08805	hypothetical prote
294	270	13.1	694	2	JC5554	complement subcomp	367	151.5	7.3	152	2	S35203	serine proteinase
295	269.5	13.0	248	2	S33756	granzyme-like prot	368	148	7.2	81	2	A18966	tissue kallikrein
296	264.5	12.8	251	1	TRHUAZ	azurocidin precurs	369	147.5	7.2	825	2	JC4163	DNA-binding protei
297	264.5	12.8	256	2	T10109	trypsin (EC 3.4.21	370	145.5	7.0	82	2	T46510	hypothetical prote
298	264.5	12.8	264	2	S32794	trypsin-like prote	371	143.5	6.9	1357	2	T29265	hypothetical prote
299	259	12.5	248	2	S01006	cytotoxic T-lympho	372	142	7.0	673	1	C8EO6C	collagen alpha 1(I
300	258.5	12.5	282	2	A36172	procytotoxic T-lym	373	140.5	6.8	1560	2	T00080	hypothetical prote
301	258.5	12.5	285	2	T35195	probable serine pr	374	139.5	6.8	639	2	G02919	transcription fact
302	257.5	12.5	254	2	S49328	trypsin-like prote	375	139.5	6.8	1952	2	T48814	hypothetical prote
303	256	12.4	403	2	C82228	probable trypsin V	376	139	6.7	1087	2	T31100	probable potassium
304	255	12.3	367	2	JE0104	testicular serine	377	138.5	6.7	158	2	S35201	serine proteinase
305	252	12.2	400	1	A48050	coagulation factor	378	138	6.7	153	2	S35204	proteinase 4 - buf
306	251	12.1	716	1	A40332	macrophage-stimula	379	138	6.7	383	2	S32975	gene BCRF2 protein

380	137.5	6.7	660	1	QBEB3	BHLF1 protein - hu	453	124.5	6.0	464	2	S22697	extensin - Volvox
381	137	6.6	743	2	S34853	probable fusidic a	c 454	124.5	6.1	671	1	CGRT1S	collagen alpha 1(I)
382	136.5	6.6	152	2	S35206	serine proteinase	455	124.5	6.0	1691	1	S22917	collagen alpha 5(I)
383	135.5	6.6	46	2	I49416	glandular kallikre	c 456	124	6.1	677	2	S23296	collagen alpha 2(I)
384	135.5	6.6	1794	2	T38459	hypothetical diver	457	124	6.0	708	1	QBEB8	UL80 protein - hum
c 385	135	6.6	460	2	T33110	hypothetical prote	458	124	6.0	759	2	T44142	collagen alpha 1(I)
c 386	135	6.6	1027	2	S28774	collagen alpha cha	c 459	124	6.1	1024	2	S18251	collagen alpha 1(X)
c 387	135	6.6	1049	1	CGB078	collagen alpha 1(I)	460	124	6.0	3020	2	A43932	mucin 2 precursor,
c 388	134	6.6	435	2	T15143	hypothetical prote	461	123.5	6.0	137	2	S55364	mucin 2 precursor,
c 389	133.5	6.5	639	2	C43674	US4 protein - huma	462	123.5	6.0	151	2	S35205	serine proteinase,
390	132.5	6.4	292	2	S24169	mucin - rat	463	123.5	6.0	574	2	T43556	proteinase 5 - buf
391	132.5	6.4	326	2	S34427	tristetraproline p	464	123.5	6.0	715	2	T43556	WisKott-Aldrich sy
c 392	132.5	6.5	640	2	T08179	LRG5 protein - Chl	c 465	123.5	6.0	715	2	G86239	protein F20B24.6 I
c 393	132.5	6.5	1042	1	CGCH1S	collagen alpha 1(I)	c 466	123.5	6.1	1486	1	B40333	collagen alpha 1(I)
c 394	132.5	6.5	3436	2	S55659	tegument protein 6	c 467	123.5	6.0	1492	2	A40333	collagen alpha 1(I)
c 395	132.5	6.4	3570	2	T45025	mucin MUC5B, trach	468	123.5	6.0	2715	2	T13049	eyelid - fruit fly
396	132	6.4	347	1	HPRT	haptoglobin precu	c 469	123	6.0	2944	2	A54849	collagen alpha 1(I)
397	132	6.4	2332	2	T34434	hypothetical prote	c 470	123	6.0	375	1	A45225	pulmonary surfact
398	131	6.3	839	2	T04859	hypothetical prote	c 471	123	6.0	635	2	A57131	collagen alpha 2(I)
c 399	131	6.3	1151	2	T18535	extensin homolog F	c 472	123	6.0	688	2	A53330	collagen alpha 2(I)
c 400	130	6.3	396	1	KX802	high molecular mas	c 473	123	6.0	1100	2	JC8033	leukocyte formin p
c 401	130	6.4	438	2	S53787	plasma protein 2 -	c 474	123	6.0	1418	2	T45467	collagen alpha 1(I)
c 402	130	6.3	573	2	A35333	collagen alpha cha	c 475	122.5	5.9	1464	1	CGHUIS	collagen alpha 1(I)
c 403	130	6.3	775	1	EDBE11	cell surface glyco	c 476	122.5	5.9	75	2	A37002	immediate-early pr
c 404	130	6.4	1466	1	CGHU1L	collagen alpha 1(I)	c 477	122.5	6.0	684	2	S18166	collagen alpha 1(I)
c 405	129.5	6.3	817	2	S51342	immediate-early pr	c 478	122.5	5.9	1091	2	S33596	collagen alpha 2(I)
c 406	129.5	6.3	1585	2	T31611	verprolin - yeast	c 479	122	5.9	3164	1	WNBEH6	protein-tyrosine k
c 407	129	6.3	308	2	T37286	hypothetical prote	c 480	122	5.9	931	2	S13580	collagen alpha 1(I)
c 408	129	6.2	721	2	E70766	collagen 40 - Caen	c 481	122	5.9	1049	1	CGBOVS	collagen alpha 1(I)
c 409	129	6.2	3530	2	A59266	hypothetical prote	c 482	122	5.9	1188	2	S49915	collagen alpha 1(I)
c 410	128.5	6.2	320	2	JC1255	unconventional myo	c 483	122	5.9	1520	2	T00273	extensin-like prot
c 411	128.5	6.2	1006	2	G86292	TIS11 protein - ra	c 484	122	5.9	1575	2	S68448	hypothetical prote
c 412	128	6.2	256	2	A60533	hypothetical prote	c 485	121.5	5.9	1744	2	S40991	synaptotagmin, 170K
c 413	128	6.2	296	2	A31219	tumor-associated a	c 486	121.5	5.9	435	2	T15143	collagen alpha 1(I)
c 414	128	6.2	301	2	T21314	collagen 1 - Caeno	c 487	121.5	5.9	610	2	S35049	hypothetical prote
c 415	128	6.2	649	1	T46500	hypothetical prote	c 488	121.5	5.9	825	1	EDBEXD	immediate-early pr
c 416	128	6.3	1546	1	CGHU2E	hypothetical prote	c 489	121	5.9	1487	1	CGHUGC	collagen alpha 1(I)
c 417	128	6.2	2142	2	B35098	collagen alpha 2(X)	c 490	121	5.9	363	2	T16755	collagen alpha 1(X)
c 418	127.5	6.2	69	2	S28195	MHC class III hiet	c 491	121	5.9	620	2	S06733	hydroxyproline-ric
c 419	127.5	6.2	72	2	S28196	tissue kallikrein	c 492	121	5.9	680	2	S31216	collagen alpha 1(X)
c 420	127.5	6.3	431	2	S09824	hypothetical prote	c 493	121	5.9	780	2	T00366	hypothetical prote
c 421	127.5	6.2	507	2	T47468	antifreeze glycope	c 494	121	5.9	862	2	T46289	hypothetical prote
c 422	127.5	6.2	1433	2	A46053	bullous pemphigoid	c 495	121	5.9	1142	2	JX0369	collagen alpha 1(X)
c 423	127	6.1	548	2	S52735	CW17R protein - mo	c 496	121	5.9	1373	1	A43291	collagen alpha 2(I)
c 424	127	6.1	754	2	A55267	collagen alpha 5(I)	c 497	120.5	5.9	1487	1	EDBEF6	155K transcription
c 425	127	6.1	805	2	T49385	hypothetical prote	c 498	120.5	5.9	329	2	T32783	hypothetical prote
c 426	127	6.2	1414	1	S23809	collagen alpha 2(I)	c 499	120.5	5.8	635	2	T75477	hypothetical prote
c 427	127	6.2	1453	2	S21626	collagen alpha 1(I)	c 500	120.5	5.8	666	2	B70803	hypothetical prote
c 428	126.5	6.2	290	2	T23416	hypothetical prote	c 501	120.5	5.9	963	2	T19140	hypothetical prote
c 429	126.5	6.2	488	2	A27353	collagen alpha 1(I)	c 502	120.5	5.9	1106	2	JQ0405	hypothetical 119.5
c 430	126.5	6.1	522	2	S41819	collagen alpha 1(I)	c 503	120.5	5.9	1733	1	B45344	probable nuclear a
c 431	126.5	6.1	839	2	F75518	nucleoporin p62 -	c 504	120	5.8	1896	1	RNPF2L	DNA-directed RNA p
c 432	126.5	6.1	1201	2	CGH441	hypothetical prote	c 505	120	5.9	490	2	T09084	phosphatidylinosit
c 433	126.5	6.2	1806	1	CGHU1E	unknown protein [i	c 506	120	5.8	779	1	CGBOIS	collagen alpha 1(I)
c 434	126	6.1	80	2	A05324	collagen alpha 1(X)	c 507	120	5.8	1006	2	T42731	collagen alpha 1(I)
c 435	126	6.1	323	2	T27450	gamma-renin [EC 3.	c 508	120	5.9	1460	1	EDBEIF	immediate-early pr
c 436	126	6.2	779	1	CGBO1S	hypothetical prote	c 509	120	5.8	1464	2	S59856	collagen alpha 1(I)
c 437	126	6.1	1334	2	T50568	collagen alpha 1(I)	c 510	120	5.9	1759	2	T29351	collagen alpha 2(I)
c 438	126	6.2	1464	2	S59856	probable multi-dom	c 511	119.5	5.9	1958	2	B40505	hypothetical prote
c 439	126	6.1	3149	1	QBEB8	collagen alpha 1(I)	c 512	119.5	5.8	309	1	S09257	homeotic protein H
c 440	125.5	6.2	371	2	E88633	BPLF1 protein - hu	c 513	119.5	5.9	636	2	S41067	collagen alpha 1(I)
c 441	125	6.1	348	2	T29286	protein F56B3.1 [i	c 514	119	5.8	705	2	A35363	collagen I splice
c 442	125	6.1	426	2	JQ1696	hypothetical prote	c 515	119	5.8	227	2	C29149	proline-rich prote
c 443	125	6.1	558	2	JC2004	hypothetical prote	c 516	119	5.8	272	2	I50696	collagen alpha 1(I)
c 444	125	6.1	574	2	T38819	nuclear factor-kap	c 517	119	5.8	480	2	A40815	transcription fact
c 445	125	6.1	707	2	A46302	wiskott-aldrich sy	c 518	119	5.8	528	2	I47141	gastric mucin [clo
c 446	125	6.1	886	2	I50694	FTB-associated epl	c 519	119	5.8	680	1	CGHUID	collagen alpha 1(X)
c 447	125	6.1	1603	2	S23810	collagen alpha 1(I)	c 520	119	5.8	1763	2	S16366	collagen alpha 2(I)
c 448	125	6.1	1970	1	S21054	collagen alpha 1(X)	c 521	118.5	5.8	1775	2	A31893	collagen alpha 1(I)
c 449	125	6.1	1370	2	I38186	DNA-directed RNA p	c 522	118.5	5.7	526	2	A56573	nuclear pore compl
c 450	124.5	6.1	312	2	T25048	RNA polymerase II	c 523	118.5	5.7	586	2	T29695	hypothetical prote
c 451	124.5	6.0	402	2	E86185	hypothetical prote	c 524	118.5	5.7	742	2	F84643	hypothetical prote
c 452	124.5	6.1	418	2	T15142	hypothetical prote	c 525	118.5	5.8	920	2	B34493	collagen alpha 1(I)
										939	2	G75481	sensory box/GGDEF

C 526	118.5	5.8	1147	1	MWAXIB	myosin heavy chain	C 599	114.5	5.6	405	4	A61181	homeotic protein H
C 527	118.5	5.8	1366	1	CGH02S	collagen alpha 2(I	C 600	114.5	5.6	452	2	C41602	transcription fact
C 528	118.5	5.8	1736	2	T00391	hypothetical prote	C 601	114.5	5.6	469	2	A24450	collagen alpha 2(V
C 529	118.5	5.8	1758	2	T29350	hypothetical prote	602	114.5	5.5	797	1	VBEX1	gtpcoprotein x pre
C 530	118.5	5.8	2944	2	A54849	collagen alpha 1(V	603	114.5	5.5	846	2	S52418	GTP-binding regula
C 531	118.5	5.7	303	2	T19289	hypothetical prote	604	114.5	5.5	914	2	T25220	hypothetical prote
C 532	118.5	5.7	330	2	T26004	hypothetical prote	C 605	114.5	5.6	921	2	S40495	collagen alpha 1(I
C 533	118.5	5.8	373	2	A47234	homeobox protein H	C 606	114.5	5.5	961	2	A55380	factogenital dyspl
C 534	118.5	5.7	1285	2	T14171	ataxin-2 - mouse	C 607	114.5	5.6	1496	1	CGHU2V	collagen alpha 2(V
C 535	118.5	5.7	1453	2	S21626	collagen alpha 1(I	C 608	114.5	5.5	1670	1	CGHU3B	collagen alpha 3(I
C 536	118.5	5.7	1487	1	EDBEE1	immediate-early pr	C 609	114	5.6	204	2	JQ0321	hypothetical 19.8K
C 537	117.5	5.8	312	2	A61183	hypothetical prote	C 610	114	5.6	738	2	E87627	hypothetical prote
C 538	117.5	5.7	878	2	T21621	hypothetical prote	611	114	5.5	929	2	C96623	hypothetical prote
C 539	117.5	5.7	1388	2	A53317	collagen alpha 1(X	612	114	5.5	1323	2	S27224	N-methyl-D-asparta
C 540	117.5	5.7	1494	2	T14355	protein-tyrosine-p	613	114	5.5	1549	2	I48103	type VII collagen
C 541	117.5	5.7	1914	2	T42635	tenascin Y precurs	614	113.5	5.5	307	2	T16842	hypothetical prote
C 542	117.5	5.7	1959	1	AGRT	agrin - rat	615	113.5	5.5	319	2	T32250	hypothetical prote
C 543	117	5.7	279	2	S53363	mucin 5AC (clone J	616	113.5	5.5	383	2	T46707	proteophosphoglyca
C 544	117	5.7	290	2	A32249	collagen - sea urc	C 617	113.5	5.6	452	2	T30082	hypothetical prote
C 545	117	5.7	383	2	S32975	gene BCRF2 protein	618	113.5	5.5	456	2	T35474	50kD proline rich
C 546	117	5.7	393	2	PQ0479	pistil extensin-1I	619	113.5	5.5	593	2	S49525	glycoprotein G - s
C 547	117	5.7	471	2	T33997	hypothetical prote	620	113.5	5.5	647	2	T43952	hypothetical prote
C 548	117	5.7	487	2	A24442	nuclear protein B3	C 621	113.5	5.6	676	1	ED8E23	immediate-early pr
C 549	117	5.7	488	2	S27353	collagen alpha 1(I	622	113.5	5.5	729	2	E70803	hypothetical prote
C 550	117	5.7	525	2	A35596	nuclear pore glyco	623	113.5	5.5	818	2	A59433	KIAA0672 protein I
C 551	117	5.7	605	2	T33913	hypothetical prote	624	113.5	5.5	987	2	I48652	mouse developmenta
C 552	117	5.7	1299	2	T47182	hypothetical prote	625	113.5	5.5	987	2	I48953	eph-related recept
C 553	117	5.7	1532	2	A61262	collagen alpha 1(X	626	113.5	5.5	1001	2	T16419	hypothetical prote
C 554	117	5.7	1870	2	S37671	MHC class III hist	627	113.5	5.5	1032	2	T34433	hypothetical prote
C 555	117	5.7	1872	2	S36152	MHC class III hist	628	113.5	5.5	1165	2	T16420	hypothetical prote
C 556	117	5.7	3124	2	A40020	collagen alpha 1(X	C 629	113.5	5.6	1838	1	CGHU1V	collagen alpha 1(V
C 557	117	5.7	3511	2	A59295	unconventional myo	630	113.5	5.5	2187	2	T30826	nascent polypeptid
C 558	116.5	5.6	614	2	T33149	hypothetical prote	631	113.5	5.5	3938	2	T42761	Bassoon protein -
C 559	116.5	5.6	1146	2	A38587	collagen, cornea-s	C 632	113	5.6	381	2	S16506	hypothetical prote
C 560	116.5	5.6	1255	2	T31065	diaphanous protein	C 633	113	5.5	543	2	S35047	mucin JUL7 - human
C 561	116.5	5.7	1497	2	T149607	procollagen type V	C 634	113	5.6	618	2	S34436	collagen alpha 2(I
C 562	116	5.7	474	2	A41782	transcription fact	635	113	5.5	727	2	C84534	hypothetical prote
C 563	116	5.7	684	2	T36771	probable integral	636	113	5.5	730	2	A36226	collagen alpha 1 c
C 564	116	5.7	825	1	EDBEXD	immediate-early pr	637	113	5.5	753	2	JQ0532	Op protein - Kenne
C 565	116	5.7	862	2	T46289	hypothetical prote	638	113	5.5	786	2	T16509	hypothetical prote
C 566	116	5.6	865	2	A47282	calcium-binding pr	639	113	5.5	812	2	S31521	collagen COLF1 - f
C 567	116	5.7	964	1	CGCH2S	collagen alpha 2(I	640	113	5.5	1356	1	C45219	N-methyl-D-asparta
C 568	116	5.6	1367	1	S48478	glucan 1,4-alpha-g	C 641	113	5.5	1611	2	T38236	hypothetical prote
C 569	116	5.7	1549	2	I48103	type VII collagen	C 642	113	5.6	1712	1	CGHU2B	collagen alpha 2(I
C 570	115.5	5.7	300	2	T19929	hypothetical prote	643	113	5.5	1759	2	T29351	collagen alpha 2(I
C 571	115.5	5.6	303	2	T28999	hypothetical prote	644	113	5.5	3124	2	A40020	collagen alpha 1(X
C 572	115.5	5.6	304	2	T22602	hypothetical prote	645	112.5	5.4	317	2	T19143	hypothetical prote
C 573	115.5	5.7	422	1	KXH02	plasma protein 2 p	C 646	112.5	5.5	330	2	S46657	collagen alpha 1(X
C 574	115.5	5.7	676	1	EDBEE2	immediate-early pr	647	112.5	5.4	394	2	T33641	hypothetical prote
C 575	115.5	5.6	749	2	I38488	trophinin - human	C 648	112.5	5.5	401	2	A48423	engrailed homeodom
C 576	115.5	5.6	1132	2	T03844	telomerase catalyt	C 649	112.5	5.5	1039	2	T35878	hypothetical prote
C 577	115.5	5.6	1199	2	A40670	nuclear envelope p	C 650	112.5	5.5	1051	2	A35763	collagen alpha 2 c
C 578	115.5	5.6	1400	2	T31555	hypothetical prote	651	112.5	5.4	1400	2	T52359	hypothetical prote
C 579	115.5	5.6	1414	1	S23809	collagen alpha 2(I	C 652	112	5.5	305	2	T20906	hypothetical prote
C 580	115.5	5.7	1419	2	A41182	collagen alpha 1(I	C 653	112	5.5	319	2	F75420	hypothetical prote
C 581	115.5	5.7	1487	2	B41182	collagen alpha 1(I	654	112	5.4	492	2	S49147	ERF-2 protein - hu
C 582	115	5.6	285	1	A43556	homeotic protein H	655	112	5.4	591	2	T44868	probable membrane
C 583	115	5.6	461	2	T51044	related to spore c	656	112	5.4	600	2	D87232	conserved membrane
C 584	115	5.7	632	2	S42731	collagen alpha 1 c	C 657	112	5.5	730	2	A36226	collagen alpha 1 c
C 585	115	5.7	698	2	T17261	hypothetical prote	658	112	5.4	980	2	S54986	regulatory protein
C 586	115	5.7	775	1	EDBE11	immediate-early pr	C 659	112	5.5	1007	2	T01437	hypothetical prote
C 587	115	5.6	1142	2	JX0369	collagen alpha 1(X	660	112	5.4	1096	2	H86237	protein F14N23.29
C 588	115	5.6	1207	2	T00378	hypothetical glyci	661	112	5.4	1203	2	I55466	N-methyl-D-asparta
C 589	115	5.7	1381	2	E70806	adenomatous polyo	C 662	112	5.5	1215	2	T32734	myosin-IA - Acanth
C 590	115	5.7	2274	2	T30258	Bassoon protein -	663	112	5.4	1224	2	T40765	web1 protein homol
C 591	115	5.6	3942	2	T42730	elastase (EC 3.4.2	664	112	5.4	1251	2	A57293	latent transformin
C 592	114.5	5.5	85	2	S44461	hypothetical prote	665	111.5	5.4	302	2	A31921	collagen dpy-13 pr
C 593	114.5	5.5	290	2	T24586	collagen col-34 -	C 666	111.5	5.5	306	2	T21939	hypothetical prote
C 594	114.5	5.5	298	2	JC1448	collagen col-34 -	C 667	111.5	5.5	314	2	T34269	hypothetical prote
C 595	114.5	5.6	304	2	T23801	hypothetical prote	668	111.5	5.4	325	2	T32248	hypothetical prote
C 596	114.5	5.6	310	2	T29731	hypothetical prote	C 669	111.5	5.5	397	2	T35289	probable multifunc
C 597	114.5	5.5	319	2	A36600	growth factor-indu	C 670	111.5	5.5	405	2	T29167	hypothetical prote
C 598	114.5	5.5	377	2	A48018	mucin 7 precursor,	671	111.5	5.4	413	2	T12533	hypothetical prote

c 672	111.5	5.5	510	2	A42750	insulinoma-associat	745	109.5	5.3	4957	2	T03455	ALR protein - huma
c 673	111.5	5.5	627	1	JC5534	protein kinase 1 (746	109	5.3	317	2	S55316	mucin (clone PGM-2
c 674	111.5	5.4	907	2	E96636	hypothetical prote	c 747	109	5.4	587	2	T41653	probable transcrip
675	111.5	5.4	1132	2	A35098	MHC class III hist	748	109	5.3	615	2	A05289	collagen alpha 1(I
676	111.5	5.4	1323	2	I78557	N-methyl-D-asparta	749	109	5.3	760	2	R86387	probable Pto kinas
c 677	111.5	5.5	1670	1	CGHU3B	collagen alpha 3(I	c 750	109	5.4	780	2	T00366	hypothetical prote
c 678	111.5	5.5	3573	2	S23070	erythronolide synt	c 751	109	5.4	783	2	T35389	probable serine-th
679	111	5.4	317	2	A28996	proline-rich prote	752	109	5.3	815	2	R56708	extracellular sign
680	111	5.4	437	2	S05478	properdin - mouse	753	109	5.3	873	2	A47283	calphostin - fruit
681	111	5.4	439	2	A36385	surface antigen se	c 754	109	5.4	914	2	H70987	hypothetical glyci
682	111	5.4	533	2	T33912	hypothetical prote	c 755	109	5.4	920	2	A45748	collagen alpha 1(V
c 683	111	5.5	794	2	T10519	pre-pro-leguminin -	756	109	5.3	931	2	S13580	collagen alpha 1(I
c 684	111	5.5	888	2	A55318	serine/threonine p	757	109	5.3	1069	2	S27922	nuclear antigen EB
685	111	5.4	921	2	G02326	transcription fact	c 758	109	5.4	1170	2	A53612	laminin B1k chain
686	111	5.4	990	2	T14756	hypothetical prote	c 759	109	5.4	1752	2	A45407	collagen alpha 3(I
c 687	111	5.5	1184	2	S50832	atrophin-1 - human	760	109	5.3	3002	2	A47221	fibrillin 1 precur
c 688	111	5.5	1428	2	T13926	probable protein p	761	108.5	5.3	282	2	T16036	cuticle collagen c
689	111	5.4	1777	2	T34369	hypothetical prote	c 762	108.5	5.3	313	2	T22828	hypothetical prote
690	110.5	5.3	221	2	T02086	zinc inducible pro	c 763	108.5	5.3	316	2	S08169	collagen col-12 pr
691	110.5	5.3	240	2	A24264	proline-rich prote	c 764	108.5	5.3	316	2	S08170	collagen col-13 pr
692	110.5	5.3	256	2	A56593	trypsin-related pr	c 765	108.5	5.3	325	2	T32248	hypothetical prote
693	110.5	5.3	347	2	A43815	transforming prote	766	108.5	5.3	424	2	T33663	hypothetical prote
694	110.5	5.3	632	2	S42731	collagen alpha 1 c	767	108.5	5.3	522	2	S52216	viral proteinase -
695	110.5	5.3	642	1	S34416	transcription fact	768	108.5	5.3	571	2	T43456	hypothetical prote
696	110.5	5.3	920	2	B34493	collagen alpha 1(I	769	108.5	5.3	667	2	S74254	homeotic protein s
c 697	110.5	5.4	921	2	S42617	collagen alpha 1(I	770	108.5	5.3	796	2	JC7555	CI4orf4 protein -
698	110.5	5.3	1137	2	A86335	T20H2.9 protein -	771	108.5	5.3	886	2	I50694	collagen alpha 1(I
c 700	110.5	5.3	1497	2	I43607	procollagen type V	772	108.5	5.3	915	2	T09575	smoothelin - human
c 701	110.5	5.4	1690	1	CGHU4	collagen alpha 4(I	c 773	108.5	5.3	949	2	E75352	glycine cleavage s
702	110.5	5.3	1820	2	A55494	latent transformin	774	108.5	5.3	1496	1	CGHU2V	collagen alpha 2(V
703	110.5	5.3	2090	2	S26058	probable transform	c 775	108.5	5.3	1538	2	H70846	hypothetical glyci
704	110	5.3	3436	2	S56559	tegument protein 6	c 776	108.5	5.3	1572	2	T00027	brain-specific ang
705	110	5.3	302	2	T33211	hypothetical prote	777	108.5	5.3	1613	2	S39059	protein BRG1 - hum
c 706	110	5.4	311	2	T15268	hypothetical prote	778	108.5	5.3	1618	2	S21424	neatin - human
c 707	110	5.3	333	2	S11484	CABP1 protein - si	779	108.5	5.3	1647	2	S45252	SNF2beta protein -
708	110	5.3	401	2	E70563	hypothetical prote	c 780	108.5	5.3	1691	1	T22917	collagen alpha 5(I
709	110	5.3	455	2	A87913	protein B0205.10 I	781	108	5.2	316	2	T20497	hypothetical prote
c 710	110	5.3	534	2	S21961	proline-rich prote	782	108	5.2	333	2	T15257	hypothetical prote
c 711	110	5.3	589	2	C70767	probable pknJ - My	783	108	5.2	384	2	T29422	hypothetical prote
c 712	110	5.4	603	2	T45093	hypothetical glyci	784	108	5.2	677	2	S23296	collagen alpha 2(I
713	110	5.3	624	2	JC5471	regulatory protein	c 785	108	5.2	684	2	T36771	probable integral
714	110	5.3	628	2	S01955	hypothetical prote	786	108	5.3	744	2	S15435	collagen alpha 1(V
715	110	5.3	671	1	CGRT1S	collagen alpha 1(I	787	108	5.2	969	2	T15446	hypothetical prote
716	110	5.3	784	2	JQ0317	hypothetical 82K p	788	108	5.2	987	2	A75496	conserved hypotet
717	110	5.3	1135	2	T30561	Scythe protein - A	789	108	5.2	1054	2	T43226	translatin initia
718	110	5.3	1184	2	G01763	atrophin-1 - human	790	108	5.2	1184	2	S50832	atrophin-1 - human
719	110	5.3	1242	2	JS0670	insulin receptor s	791	108	5.2	1241	2	T18311	hypothetical prote
720	110	5.3	1589	2	T42233	submaxillary mucin	792	108	5.2	1360	2	T33922	hypothetical prote
721	110	5.3	1758	2	T29350	hypothetical prote	793	108	5.2	1546	1	CGHU2E	collagen alpha 2(I
c 722	110	5.4	1843	2	T18803	collagen alpha 1(V	c 795	108	5.3	1712	2	A38261	masking protein pr
723	110	5.3	2124	2	T28658	polyketide synthas	c 796	108	5.3	3149	1	QQBE8	BPLF1 protein - hu
724	109.5	5.3	61	2	PS0049	serine proteinase	c 797	108	5.3	3198	2	A43426	collagen alpha 2 f
725	109.5	5.3	142	2	B41132	collagen-related p	c 798	108	5.3	3530	2	A59266	unconventional myo
726	109.5	5.3	290	2	T24590	hypothetical prote	799	107.5	5.2	3942	2	T42730	Bassoon protein -
c 727	109.5	5.4	294	2	S13141	hypothetical prote	800	107.5	5.2	211	2	C87462	hypothetical prote
c 728	109.5	5.4	295	2	B48013	proline-rich prote	c 801	107.5	5.3	227	2	G70555	hypothetical prote
c 729	109.5	5.4	297	2	T18638	hypothetical prote	c 802	107.5	5.3	282	2	J50168	collagen col-8 - C
730	109.5	5.3	299	1	FRSMBG	streptogrisin B (E	c 803	107.5	5.3	282	2	T16036	cuticle collagen c
731	109.5	5.3	348	2	JQ0431	hypothetical 35.5K	c 804	107.5	5.2	300	2	T24482	hypothetical prote
c 732	109.5	5.4	374	1	A42046	surfactant protein	c 805	107.5	5.3	301	2	B31219	hypothetical prote
733	109.5	5.3	379	2	T05441	proline-rich prote	c 806	107.5	5.3	304	2	T22482	hypothetical prote
734	109.5	5.3	379	2	D85257	extensin-like prote	c 807	107.5	5.3	339	2	S20880	homeotic protein H
c 735	109.5	5.4	428	2	T24769	hypothetical prote	c 808	107.5	5.2	356	2	T22827	proline-rich prote
c 736	109.5	5.4	614	2	T33149	hypothetical prote	809	107.5	5.2	379	2	S31719	hypothetical prote
c 737	109.5	5.4	632	2	T00084	hypothetical prote	c 810	107.5	5.2	458	2	T11631	hypothetical prote
738	109.5	5.3	649	2	JQ0103	hypothetical 70K p	c 811	107.5	5.2	510	2	H84824	En/Spm-like transp
c 739	109.5	5.4	656	2	AC0573	outer membrane est	c 812	107.5	5.3	511	1	A48560	US54 protein - hum
740	109.5	5.3	1042	1	CGCH1S	collagen alpha 1(I	c 813	107.5	5.2	580	2	T43481	probable mucin Dkf
741	109.5	5.3	1126	2	T20801	hypothetical prote	c 814	107.5	5.3	725	2	T00492	hypothetical prote
c 742	109.5	5.4	1168	1	MWAXIC	myosin heavy chain	c 815	107.5	5.2	778	2	I38487	tastin - human
c 743	109.5	5.4	1660	1	A70869	hypothetical glyci	c 816	107.5	5.3	1747	2	A54121	collagen alpha-4 c
744	109.5	5.3	1707	2	A33526	collagen alpha 2(I	817	107	5.2	186	2	C41132	collagen-related p
								107	5.2	240	2	B24264	proline-rich prote

818	107	5.2	264	2	D34768	ORF4 protein - Orf	c 891	105.5	5.2	812	2	S31521	collagen COLP1 - f
c 819	107	5.3	304	2	T26185	hypothetical prote	892	105.5	5.1	873	2	F96615	probable Myb-famil
c 820	107	5.3	304	2	T26185	hypothetical prote	893	105.5	5.1	898	2	T14764	hypothetical prote
821	107	5.2	388	2	JC5437	spliceosome-associ	894	105.5	5.1	968	2	T00353	hypothetical prote
822	107	5.2	395	2	H75457	hypothetical prote	895	105.5	5.1	1063	2	T03743	bifocal protein -
823	107	5.2	432	2	A25483	env polyprotein, r	896	105.5	5.1	1106	1	TVHUGL	transforming prote
824	107	5.2	539	2	T28770	hypothetical prote	c 897	105.5	5.2	1122	2	T14180	exit protein - Myc
c 825	107	5.3	573	2	JQ0135	hypothetical prote	c 898	105.5	5.2	1198	2	T28678	polyketide synthas
c 826	107	5.3	576	2	T36729	probable serine/th	c 899	105.5	5.1	1603	2	S23810	collagen alpha 1(X
c 827	107	5.2	592	2	D70863	hypothetical prote	c 900	105.5	5.2	1691	1	CGHU6B	collagen alpha 6(I
c 828	107	5.3	615	2	A05269	collagen alpha 1(I	901	105.5	5.1	2774	2	A43359	microtubule-associ
c 829	107	5.2	616	2	JQ1441	hypothetical 67K p	902	105.5	5.1	2776	2	T17428	FK506 polyketide s
c 830	107	5.2	635	2	F96660	protein F2K11.10	903	105	5.1	297	2	T27525	hypothetical prote
c 831	107	5.3	675	2	S20819	collagen alpha 3(I	904	105	5.1	304	2	T22482	hypothetical prote
c 832	107	5.2	738	2	S40992	hypothetical prote	905	105	5.1	380	2	T28888	cuticle collagen d
c 833	107	5.3	744	1	A34246	collagen alpha 1(V	c 906	105	5.1	439	1	A48099	transcription fact
c 834	107	5.3	744	1	S23298	collagen alpha 1(V	c 907	105	5.2	440	2	S71795	actin-depolymerizi
835	107	5.2	801	2	T29018	hypothetical prote	c 908	105	5.1	505	2	S72273	3C3.18c protein -
836	107	5.2	847	1	A53800	mixed-lineage prot	c 909	105	5.2	517	2	T10927	hypothetical prote
837	107	5.2	967	2	S66852	hypothetical prote	c 910	105	5.2	518	2	T23745	hypothetical prote
838	107	5.2	1040	2	T29092	TSC-22 protein hom	c 911	105	5.2	532	2	T07903	tubulin delta chai
c 839	107	5.3	1306	2	A70934	hypothetical glyci	c 912	105	5.2	542	2	T29707	hypothetical prote
c 840	107	5.3	1323	2	T78557	N-methyl-D-asparta	c 913	105	5.2	589	2	T29299	hypothetical prote
841	107	5.2	1464	1	CGHUI8	collagen alpha 1(I	914	105	5.1	628	2	S19150	hypothetical prote
842	107	5.2	1466	1	CGHUI7L	collagen alpha 1(I	915	105	5.1	636	2	D84823	hypothetical prote
843	107	5.2	1574	2	T13954	MEGF6 protein - ra	916	105	5.1	660	2	JW0067	chitinase (EC 3.2.
844	107	5.2	1669	1	CGHU4B	collagen alpha 1(I	917	105	5.1	674	2	S13301	collagen alpha 1(X
845	107	5.2	1752	2	A45407	collagen alpha 3(I	c 918	105	5.2	680	2	S21323	probable endogluca
846	107	5.2	2649	2	T51023	hypothetical prote	c 919	105	5.2	969	2	AB3388	soluble lytic mure
847	107	5.2	3534	2	T42567	tegument protein 2	c 920	105	5.2	1151	2	T18535	high molecular mas
c 848	106.5	5.2	302	2	T15936	hypothetical prote	921	105	5.1	1231	2	S30185	insulin receptor s
c 849	106.5	5.2	316	2	T20497	hypothetical prote	c 922	105	5.2	1282	2	T14320	calcineurin inhibi
850	106.5	5.2	355	2	T29932	hypothetical prote	c 923	105	5.2	3176	2	CGHU3A	collagen alpha 3(V
851	106.5	5.2	514	2	H70699	probable ppp prote	c 924	105	5.2	3707	2	S18252	heparan sulfate pr
c 852	106.5	5.2	529	2	T45134	hypothetical prote	925	104.5	5.1	164	2	I53641	mucin SAC - human
853	106.5	5.2	635	2	A57131	collagen alpha 2(V	926	104.5	5.1	266	2	T22706	hypothetical prote
854	106.5	5.2	684	2	T25603	hypothetical prote	c 927	104.5	5.1	267	1	UJCH	major prion protei
855	106.5	5.2	823	2	T02812	probable membrane	928	104.5	5.1	287	2	T15779	hypothetical prote
856	106.5	5.2	876	2	T49801	hypothetical prote	929	104.5	5.1	300	2	T19929	hypothetical prote
857	106.5	5.2	915	2	S36327	clathrin assembly	930	104.5	5.1	306	2	T09067	extensin-like prot
858	106.5	5.2	1298	1	EDBE75	immediate-early pr	931	104.5	5.1	313	2	T22828	hypothetical prote
859	106.5	5.2	1373	1	A43291	collagen alpha 2(I	932	104.5	5.1	341	2	S09913	hypothetical prote
860	106.5	5.2	1892	2	T18314	hypothetical prote	933	104.5	5.1	356	2	T22827	hypothetical prote
861	106.5	5.2	13288	2	T03099	mucin, submaxillar	c 934	104.5	5.1	379	2	S49999	collagen 1 - marin
862	106	5.1	149	2	A41132	collagen-related p	c 935	104.5	5.1	380	2	A48295	inulinoma-associa
c 863	106	5.2	297	2	T27525	hypothetical prote	936	104.5	5.1	510	2	A42750	hypothetical prote
864	106	5.1	304	2	T26185	hypothetical prote	937	104.5	5.1	589	2	T29299	hypothetical prote
c 865	106	5.1	304	2	T26184	hypothetical prote	c 938	104.5	5.1	636	2	S41067	collagen alpha 1(I
c 866	106	5.2	314	2	T32985	hypothetical prote	c 939	104.5	5.1	641	1	QJBE31	nuclear antigen EB
867	106	5.1	509	2	D86911	conserved hypotet	c 940	104.5	5.1	674	2	S13301	collagen alpha 1(X
868	106	5.1	509	2	T10013	probable phosphopr	941	104.5	5.1	684	2	A56154	Abl substrate ena
c 869	106	5.2	704	2	A48097	rabphilin-3A - bov	942	104.5	5.1	708	2	D96711	hypothetical prote
c 870	106	5.1	814	2	T49207	receptor kinase-li	943	104.5	5.1	924	2	S27923	gene LR3 protein -
c 871	106	5.2	832	2	B87673	ABC transporter, H	944	104.5	5.1	1048	1	XPBEA9	large structural p
872	106	5.1	873	2	B75514	penicillin-binding	945	104.5	5.1	1402	2	I46707	translation initia
c 873	106	5.1	1079	2	B70807	hypothetical glyci	c 946	104.5	5.1	1638	2	A42091	transcription acti
874	106	5.1	1176	2	T49482	hypothetical prote	947	104.5	5.1	2240	2	T37057	probable multi-dom
c 875	106	5.2	1237	2	T45070	protein kinase hom	c 948	104.5	5.1	3002	2	A47221	fibrillin 1 precur
c 876	106	5.1	1843	2	S18803	collagen alpha 1(V	949	104	5.0	49	2	B24696	tissue kallikrein
c 877	106	5.2	2715	2	T13049	collagen alpha 1(X	950	104	5.0	270	2	H83619	hypothetical prote
c 878	105.5	5.2	177	2	S37749	eyelid - fruit fly	951	104	5.0	272	2	H87075	probable conserved
c 879	105.5	5.2	273	2	A46280	prion protein - ch	952	104	5.0	283	2	E88597	protein Y47D38.6 l
880	105.5	5.1	291	2	T26576	hypothetical prote	953	104	5.0	287	2	S65765	chitinase (EC 3.2.
881	105.5	5.1	294	2	T22639	hypothetical prote	954	104	5.0	290	2	A32249	collagen - sea urc
c 882	105.5	5.1	307	2	B72677	hypothetical prote	955	104	5.0	310	1	PIHUSD	salivary proline-r
c 883	105.5	5.2	309	2	T28708	hypothetical prote	956	104	5.0	314	2	T32985	hypothetical prote
884	105.5	5.1	310	2	T22641	hypothetical prote	c 957	104	5.1	314	2	T32247	hypothetical prote
885	105.5	5.1	366	2	T70907	hypothetical prote	c 958	104	5.1	316	2	G84187	hypothetical prote
c 886	105.5	5.1	504	2	T34995	probable integral	c 959	104	5.1	358	1	WMBE38	infected cell prot
c 887	105.5	5.2	584	2	G70804	hypothetical glyci	960	104	5.0	365	2	T24955	hypothetical prote
888	105.5	5.1	626	2	B70754	probable serine/th	961	104	5.0	421	2	T30709	core protein homol
889	105.5	5.1	715	1	TNBE77	77K alpha trans-in	962	104	5.0	441	2	T23461	hypothetical prote
c 890	105.5	5.2	754	2	A55267	collagen alpha 5(I	c 963	104	5.1	469	1	S29126	properdin precurs

964	104	5.0	563	2	C70987	hypothetical prote	1037	102.5	5.0	390	4	S03158	hypothetical BCR/A
c 965	104	5.1	577	2	A40220	cleavage stimulat	c1038	102.5	5.0	438	2	S138946	melanoma ubiquitou
966	104	5.0	586	2	H86914	conserved hypothet	1039	102.5	5.0	439	2	S51939	chitinase (EC 3.2.
c 967	104	5.1	597	2	JQ0107	hypothetical 66K p	c1040	102.5	5.0	525	2	JN0059	hypothetical 57.4K
968	104	5.0	574	2	S23297	collagen alpha 1(X	c1041	102.5	5.0	528	2	B75310	conserved hypothet
c 969	104	5.1	784	2	JQ0317	hypothetical 82K p	1042	102.5	5.0	530	2	A45690	transactivator EBN
970	104	5.0	1029	2	T30351	mucin-like protein	1043	102.5	5.0	540	2	S21825	vicilin-like stora
971	104	5.0	1039	2	T35878	hypothetical prote	1044	102.5	5.0	542	2	A44358	zyxin - chicken
972	104	5.0	1257	2	S28764	neurocan precursor	1045	102.5	5.0	548	2	E70546	hypothetical prote
973	104	5.0	1428	2	T08852	lustrin A - Calif	1046	102.5	5.0	559	2	T02825	probable membrane
974	104	5.0	2205	1	MWVRN	nonstructural poly	1047	102.5	5.0	576	2	T36729	probable serine/th
975	103.5	5.0	64	2	A30981	prostatic arginine	1048	102.5	5.0	627	2	A70888	hypothetical prote
976	103.5	5.0	386	2	T36169	hypothetical prote	1049	102.5	5.0	631	2	S52257	epitaxin - mouse
977	103.5	5.0	410	2	T15142	hypothetical prote	1050	102.5	5.0	693	1	TVHUA2	bcr (breakpoint cl
978	103.5	5.0	448	2	JC7807	Wiskott-Aldrich sy	1051	102.5	5.0	698	2	T32594	hypothetical prote
979	103.5	5.0	461	2	T10741	extensin-like prot	c1052	102.5	5.0	767	2	S55618	hypothetical prote
980	103.5	5.0	469	1	S23126	properdin precursor	1053	102.5	5.0	867	2	S57795	probable deoxyribo
c 981	103.5	5.1	496	2	S28402	homeotic protein H	1054	102.5	5.0	900	2	B70694	probable infB - My
982	103.5	5.0	538	2	S65764	chitinase (EC 3.2.	1055	102.5	5.0	940	2	A38149	RNA-directed RNA p
983	103.5	5.0	688	2	A53330	collagen alpha 2(I	1056	102.5	5.0	992	1	GNWVR3	structural polypro
c 984	103.5	5.1	729	2	E70803	hypothetical prote	1057	102.5	5.0	1089	2	T30843	serine-repeat anti
985	103.5	5.0	772	2	T13078	KIAA0992 protein -	1058	102.5	5.0	1122	2	T47424	hypothetical prote
986	103.5	5.0	825	2	T23634	hypothetical prote	1059	102.5	5.0	1142	2	T00022	B120 protein - hum
987	103.5	5.0	866	2	T45462	membrane glycoprot	1060	102.5	5.0	1271	1	TVHUEP	bcr (breakpoint cl
988	103.5	5.0	867	2	T45463	hypothetical 119.5	c1061	102.5	5.0	1334	2	S50568	probable multi-dom
989	103.5	5.0	1106	2	JQ0405	hypothetical prote	c1062	102.5	5.0	1571	2	T00062	hypothetical prote
990	103.5	5.0	1110	2	T19673	mucin, tracheobron	1063	102.5	5.0	1747	2	A45974	collagen alpha 1(X
991	103.5	5.0	1118	2	A48292	probable iron-sulf	1064	102.5	5.0	1791	2	T02345	hypothetical prote
992	103.5	5.0	1132	2	C75259	collagen, cornea-s	c1065	102	5.0	237	2	A88640	protein C34H4.4 li
c 993	103.5	5.1	1146	2	A38587	hypothetical prote	1066	102	4.9	255	2	JQ0320	hypothetical 24.7K
c 994	103.5	5.1	1216	2	T34101	hypothetical prote	c1067	102	5.0	267	2	S27953	Mx protein - pig (
c 995	103.5	5.1	1298	1	EDBE75	immediate-early pr	1068	102	4.9	286	2	S34665	collagen, cuticula
996	103.5	5.0	1460	1	EDBEIF	immediate-early pr	1069	102	4.9	315	2	T06806	proline rich prote
997	103.5	5.0	1487	1	CGHU6C	collagen alpha 1(I	1070	102	4.9	316	2	T19288	hypothetical prote
998	103.5	5.0	1621	2	T15264	hypothetical prote	1071	102	4.9	323	2	T19142	hypothetical prote
c 999	103.5	5.1	1855	2	T32633	hypothetical prote	c1072	102	5.0	416	2	T32458	hypothetical prote
1000	103.5	5.0	1838	1	CGHU1V	collagen alpha 1(V	1073	102	4.9	495	1	S31223	transcription fact
1001	103.5	5.0	1857	2	S31212	collagen alpha 1(X	1074	102	4.9	551	2	S57447	HPBRII-7 protein - hu
1002	103.5	5.0	1888	2	S78476	collagen alpha 1(X	c1075	102	5.0	575	2	JG0181	XIIIL2 protein - hu
1003	103.5	5.0	1964	2	T09059	notch4 - mouse	1076	102	4.9	665	1	VCVWEM	env polypeptin -
1004	103.5	5.0	2555	2	A40043	notch protein homo	1077	102	4.9	667	2	A41311	transcription fact
1005	103	5.0	214	2	T10737	extensin-like cell	c1078	102	5.0	680	1	CGHUID	collagen alpha 1(X
1006	103	5.0	214	2	T09854	proline-rich cell	1079	102	4.9	760	2	T16726	hypothetical prote
1007	103	5.0	269	2	T26957	hypothetical prote	1080	102	4.9	1001	2	T13807	potassium channel
c1008	103	5.1	303	2	T19289	hypothetical prote	1081	102	4.9	1008	2	T04462	hypothetical prote
c1009	103	5.1	363	2	T16831	hypothetical prote	1082	102	4.9	1069	2	D85383	hypothetical prote
c1010	103	5.1	401	1	OZQOAC	circumsporozoite p	c1083	102	5.0	1098	2	T08599	probable transcrip
1011	103	5.0	422	2	T51199	hypothetical prote	1084	102	4.9	1235	1	S16948	insulin receptor s
1012	103	5.0	464	2	JC7143	endoglucanase I -	1085	102	4.9	2274	2	T30258	adenomatous polypo
1013	103	5.0	530	2	T32812	hypothetical prote	c1086	102	5.0	2414	2	A54277	transcription adap
c1014	103	5.1	566	2	T34842	probable transfera	c1087	102	5.0	13288	2	T03099	mucin, submaxillar
1015	103	5.0	600	2	S07638	spore coat protein	1088	101.5	4.9	210	2	B44984	collagen - nematod
c1016	103	5.1	623	2	A45137	collagen alpha 4(I	c1089	101.5	5.0	283	2	T39837	hypothetical prote
1017	103	5.0	646	2	T35002	probable respirato	c1090	101.5	5.0	294	2	T29839	hypothetical prote
c1018	103	5.1	679	2	T36426	probable oxidoredu	1091	101.5	4.9	312	2	A31846	hypothetical prote
1019	103	5.0	680	2	S31216	collagen alpha 1(X	1092	101.5	4.9	324	2	S13497	130K paracrystalli
1020	103	5.0	711	2	S43464	ecdysteroid-induce	1093	101.5	4.9	324	2	T34203	cAMP-binding prote
c1021	103	5.1	718	2	A36068	major ampuillate fi	1094	101.5	4.9	327	2	T34203	hypothetical prote
c1022	103	5.1	801	2	T29018	hypothetical prote	1095	101.5	4.9	371	2	F70555	hypothetical prote
1023	103	5.0	920	2	A45748	collagen alpha 1(V	c1096	101.5	5.0	379	2	S31719	proline-rich prote
1024	103	5.0	938	1	Q0BE24	nuclear antigen BB	1097	101.5	4.9	439	2	S75561	transcription fact
1025	103	5.0	1076	2	C96620	protein T30E16.23	1098	101.5	4.9	449	2	A44993	cellulase (EC 3.2.
c1026	103	5.1	1446	1	A45344	immediate-early pr	1099	101.5	4.9	583	1	S22544	transcription fact
1027	103	5.0	1454	2	T13709	diacylglycerol kin	1100	101.5	4.9	592	2	T42078	serine/threonine p
c1028	103	5.0	1589	2	T13606	hypothetical prote	c1101	101.5	5.0	635	2	F75477	hypothetical prote
c1029	103	5.1	1655	2	T13998	gene mastermind pr	c1102	101.5	5.0	638	2	AF3463	flagellar protein
1030	103	5.0	2321	2	S78549	notch3 protein - h	1103	101.5	4.9	725	2	A41258	a-agglutinin core
1031	102.5	5.0	221	2	C34768	ORF2 protein - Orf	c1104	101.5	5.0	749	2	A70812	hypothetical glyci
1032	102.5	5.0	282	2	JS0168	collagen col-8 - C	1105	101.5	4.9	880	2	S89756	protein T23E7.2b l
1033	102.5	5.0	283	2	T29837	hypothetical prote	1106	101.5	4.9	896	2	S36326	clathrin assembly
1034	102.5	5.0	289	2	T26812	hypothetical prote	c1107	101.5	5.0	918	2	S23377	collagen alpha 2(V
1035	102.5	5.0	294	2	T29839	hypothetical prote	1108	101.5	4.9	932	2	T21338	hypothetical prote
1036	102.5	5.0	357	2	T21152	hypothetical prote	1109	101.5	4.9	997	2	T28872	hypothetical prote

c1110	101.5	5.0	1022	2	S04111	collagen alpha 2(V	c1183	100.5	4.9	1264	2	S41603	type V adenylyl cy
c1111	101.5	4.9	1339	1	S61918	protein kinase C (c1184	100.5	4.9	1486	1	B40333	collagen alpha 1(I
c1112	101.5	5.0	1329	2	S70917	hypothetical glyci	c1185	100.5	4.9	1560	2	T42727	proliferation pote
c1113	101.5	5.0	1356	1	C45219	N-methyl-D-asparta	c1186	100.5	4.9	1690	1	CGHUI8	collagen alpha 4(I
c1114	101.5	4.9	1797	2	T21889	hypothetical prote	c1187	100.5	4.9	1737	2	T00209	MEGF8 protein - hu
c1115	101.5	4.9	1805	2	T21888	hypothetical prote	c1188	100.5	4.9	1747	2	A45974	collagen alpha 1(X
c1116	101.5	5.0	1870	2	S37671	MHC class III hist	c1189	100.5	4.9	2526	2	T20531	hypothetical prote
c1117	101.5	5.0	1872	2	S36152	MHC class III hist	c1190	100.5	4.9	2722	2	T20532	hypothetical prote
c1118	101.5	5.0	2468	2	A03412	hypothetical prote	c1191	100.5	4.9	2738	2	E88320	protein F07A11.6 l
c1119	101.5	4.9	5262	2	T03454	ALR protein - huma	c1192	100	4.8	188	2	D29149	proline-rich prote
c1120	101.5	5.0	7576	2	T17428	FK506 polyketide s	c1193	100	4.8	263	2	A87149	conserved hypothet
c1121	101	4.9	232	2	A60095	larval glue protei	c1194	100	4.8	307	2	T27609	hypothetical prote
c1122	101	4.9	257	2	T10586	small nuclear ribo	c1195	100	4.8	346	2	T46916	hypothetical prote
c1123	101	5.0	279	2	T26125	hypothetical prote	c1196	100	4.8	394	2	C84905	probable extensin
c1124	101	4.9	284	2	G75447	hypothetical prote	c1197	100	4.8	469	2	A24450	collagen alpha 2(V
c1125	101	4.9	299	2	T24833	hypothetical prote	c1198	100	4.9	591	2	I48141	acroganin I - guine
c1126	101	4.9	300	2	T24482	hypothetical prote	c1199	100	4.8	691	2	A25704	synapsin I - kat
c1127	101	4.9	302	2	T15936	hypothetical prote	c1200	100	4.8	731	2	T04455	hypothetical prote
c1128	101	4.9	326	2	T29810	hypothetical prote	c1201	100	4.8	977	2	I52657	seizure-related pr
c1129	101	4.9	326	2	JS0169	collagen col-14 -	c1202	100	4.9	1263	2	T13805	spalt-related prot
c1130	101	4.9	330	2	S46657	collagen alpha 1(X	c1203	100	4.8	1418	2	T45467	collagen alpha 1(I
c1131	101	4.9	387	2	T21370	hypothetical prote	c1204	100	4.8	1419	2	A41182	collagen alpha 1(I
c1132	101	5.0	414	2	T49916	hypothetical prote	c1205	100	4.8	1487	2	B41182	collagen alpha 1(I
c1133	101	5.0	474	2	I38246	transcription fact	c1206	100	4.9	1669	1	CGMS4B	collagen alpha 1(I
c1134	101	5.0	476	2	A38478	surface glycoprote	c1207	100	4.8	1691	1	CGHUEB	collagen alpha 6(I
c1135	101	5.0	491	2	T70916	hypothetical glyci	c1208	100	4.9	2142	2	B35098	MHC class III hist
c1136	101	5.0	532	2	F70580	hypothetical glyci	c1209	100	4.9	2639	2	T13128	fibroin - Chinese
c1137	101	4.9	656	2	E75468	hypothetical prote	c1210	99.5	4.8	208	2	T36390	hypothetical prote
c1138	101	4.9	706	2	E30411	synapsin Ia - bovi	c1211	99.5	4.8	237	2	S46964	microfilarial shea
c1139	101	5.0	720	1	A55160	Trg protein - frui	c1212	99.5	4.9	255	1	S04899	myb-related protei
c1140	101	4.9	798	2	T21369	hypothetical prote	c1213	99.5	4.9	270	2	A60830	keratin, 70k type
c1141	101	4.9	850	2	S26015	gastric mucin MU05	c1214	99.5	4.8	271	2	D84199	hypothetical prote
c1142	101	5.0	808	2	JC5399	dual leucine zippe	c1215	99.5	4.9	290	2	T24586	hypothetical prote
c1143	101	4.9	966	2	T00039	hypothetical prote	c1216	99.5	4.8	296	2	T21070	hypothetical prote
c1144	101	4.9	948	2	A57640	retinoblastoma bin	c1217	99.5	4.9	307	2	B72677	hypothetical prote
c1145	101	5.0	1006	2	T42731	atrophin-1 related	c1218	99.5	4.8	307	2	T37287	collagen 36 - Caen
c1146	101	4.9	1317	2	T03748	apoptosis associat	c1219	99.5	4.9	318	2	JC4963	metalloproteinase
c1147	101	4.9	1446	1	A45344	immediate-early pr	c1220	99.5	4.8	325	2	A55558	albumin D-box bind
c1148	101	4.9	1459	2	T32271	hypothetical prote	c1221	99.5	4.9	340	2	T20807	hypothetical glyci
c1149	101	4.9	1541	2	T02831	AAA protein L4171	c1222	99.5	4.8	340	2	T34423	hypothetical prote
c1150	101	5.0	3137	2	A37797	collagen alpha 3(V	c1223	99.5	4.8	343	2	H70517	probable lppd prot
c1151	100.5	4.9	242	2	S60143	cellulase (EC 3.2.	c1224	99.5	4.8	360	2	T37285	collagen dpy-2 - C
c1152	100.5	4.9	245	1	W4WZ5	E4 protein - human	c1225	99.5	4.8	363	2	T16831	hypothetical prote
c1153	100.5	4.9	267	2	A37372	prion protein homo	c1226	99.5	4.8	365	2	A34894	hepatic transcript
c1154	100.5	4.9	283	2	T29980	hypothetical prote	c1227	99.5	4.8	389	2	S27200	proline-rich prote
c1155	100.5	4.9	290	2	T24590	hypothetical prote	c1228	99.5	4.8	457	2	A53669	streptogristin C (E
c1156	100.5	4.9	299	2	T25407	hypothetical prote	c1229	99.5	4.8	474	2	S65763	chitinase (EC 3.2.
c1157	100.5	4.9	301	2	B31219	collagen 2 - Caeno	c1230	99.5	4.9	486	1	A57601	transcription fact
c1158	100.5	4.9	305	2	I57039	genomic screen hom	c1231	99.5	4.8	535	2	S65762	chitinase (EC 3.2.
c1159	100.5	4.9	316	2	S08169	collagen col-12 pr	c1232	99.5	4.9	562	2	B70953	hypothetical glyci
c1160	100.5	4.9	316	2	S08170	collagen col-13 pr	c1233	99.5	4.9	674	2	S23297	collagen alpha 1(X
c1161	100.5	4.9	317	2	T19143	hypothetical prote	c1234	99.5	4.9	705	2	A35363	synapsin I splice
c1162	100.5	4.9	333	2	T20436	hypothetical prote	c1235	99.5	4.8	770	1	S30293	transcription fact
c1163	100.5	4.9	339	2	T22607	hypothetical prote	c1236	99.5	4.9	888	2	S28791	collagen alpha 1(X
c1164	100.5	4.9	402	1	CG8028	collagen alpha 2(I	c1237	99.5	4.8	921	2	S40495	collagen alpha 1(I
c1165	100.5	4.9	416	2	T34279	hypothetical prote	c1238	99.5	4.8	1101	2	T16840	hypothetical prote
c1166	100.5	4.9	440	2	I61183	transcription fact	c1239	99.5	4.9	1167	2	T42704	hypothetical prote
c1167	100.5	4.9	476	1	SGMSV	vitronectin precur	c1240	99.5	4.8	1258	2	JC5765	inositol polyphosp
c1168	100.5	4.9	486	2	T35445	probable integral	c1241	99.5	4.8	1275	2	T33369	hypothetical prote
c1169	100.5	4.9	516	2	C44479	collagen alpha 1(X	c1242	99.5	4.9	1323	2	S27224	N-methyl-D-asparta
c1170	100.5	4.9	538	2	T49849	related to DRPLA p	c1243	99.5	4.8	1329	2	T29074	hypothetical prote
c1171	100.5	4.9	538	2	S57459	hook-containing pr	c1244	99.5	4.8	1332	2	T15670	hypothetical prote
c1172	100.5	4.9	542	2	I39540	chitinase (EC 3.2.	c1245	99.5	4.8	1344	1	A35175	mucin 1 precursor,
c1173	100.5	4.9	552	2	T42671	ABC transporter, A	c1246	99.5	4.9	1532	2	A61262	collagen alpha 1(X
c1174	100.5	4.9	613	2	F73511	hypothetical prote	c1247	99.5	4.8	1655	2	T32633	hypothetical prote
c1175	100.5	4.9	745	2	S13586	triacylglycerol li	c1248	99.5	4.8	1669	1	CGMS4B	collagen alpha 1(I
c1176	100.5	4.9	883	2	S57653	brevican precursor	c1249	99.5	4.9	2297	2	T34918	polyketide synthas
c1177	100.5	4.9	888	2	S28791	collagen alpha 1(X	c1250	99.5	4.8	2440	2	S39162	transcription coac
c1178	100.5	4.9	896	2	T51891	hypothetical prote	c1251	99.5	4.8	3198	2	A43426	collagen alpha 2 f
c1179	100.5	4.9	963	2	T19140	hypothetical prote	c1252	99.5	4.9	5069	2	T17464	rifamycin polyketi
c1180	100.5	4.9	1038	2	JT0663	ras GTPase-activat	c1253	99	4.8	217	2	S29309	hypothetical prote
c1181	100.5	4.9	1045	2	A35199	endoglucanase B (E	c1254	99	4.8	283	2	T29980	hypothetical prote
c1182	100.5	4.9	1182	2	I48378	hairless protein -	c1255	99	4.9	296	2	T21070	hypothetical prote

c1256	99	4.9	298	2	T27644	hypothetical prote	1329	98.5	4.8	987	2	A54092	protein-tyrosine k
1257	99	4.9	309	2	GB3013	polyhydroxyalkanoa	c1330	98.5	4.8	1101	2	G70951	probable ATP-depen
c1258	99	4.9	310	1	PIHUSD	salivary proline-r	1331	98.5	4.8	1213	2	A41724	limb deformity (ld
1259	99	4.8	312	2	T25048	hypothetical prote	1332	98.5	4.8	1282	2	JB0120	glycoprotein A - m
1260	99	4.8	328	2	C42756	hypothetical prote	c1333	98.5	4.8	1489	2	D70807	hypothetical glyci
1261	99	4.8	344	2	T40167	hypothetical prote	c1334	98.5	4.8	1857	2	S31212	collagen alpha 1(X
1262	99	4.8	346	2	S76923	hypothetical prote	1335	98.5	4.8	1859	1	A34092	DNA-directed RNA p
c1263	99	4.9	347	2	H75253	hypothetical prote	1336	98.5	4.8	1862	2	T29959	collagen alpha 1(X
c1264	99	4.9	367	2	J06087	helix-loop-helix t	c1337	98.5	4.8	1888	2	S78476	collagen polyketid
1265	99	4.8	371	2	E88633	protein P56B3.1 li	c1338	98.5	4.8	2103	2	G86925	CRGB-binding prote
c1266	99	4.9	391	2	D83021	hypothetical prote	c1339	98.5	4.8	3190	2	T13828	tenascin-X bovin
c1267	99	4.9	392	2	B48423	homeotic protein e	c1340	98.5	4.8	4135	2	T42629	collagen-related p
c1268	99	4.9	404	2	T44590	tylosin biosynthes	1341	98	4.7	172	2	D41132	hypothetical prote
c1269	99	4.9	413	2	E70661	probable PE protei	1342	98	4.7	202	2	AB2378	hypothetical 24.7K
c1270	99	4.9	443	1	S29334	transcription fact	c1343	98	4.8	255	2	JQ0320	infected cell prot
1271	99	4.8	470	2	A30136	developmental cont	c1344	98	4.8	261	1	WMBEXE	hypothetical prote
1272	99	4.8	487	2	T29424	hypothetical prote	1345	98	4.7	291	2	T20083	glycine-rich prote
c1273	99	4.9	512	1	WMBEY4	UL54 protein - hum	c1346	98	4.8	299	2	T00837	hypothetical prote
c1274	99	4.9	517	2	T37225	hypothetical prote	1347	98	4.7	310	2	T29731	hypothetical prote
1275	99	4.8	548	2	S59133	ETS2 repressor fac	1348	98	4.7	317	2	T29960	hypothetical prote
1276	99	4.8	617	2	S52797	mufi protein - hum	1349	98	4.7	329	2	T32783	hypothetical prote
1277	99	4.8	628	2	JQ0110	hypothetical 69K p	1350	98	4.7	356	2	A96826	T8K14.10 [importe
1278	99	4.8	653	2	T08984	auxin response fac	1351	98	4.7	362	2	A44083	meq protein - Mare
1279	99	4.8	683	2	A82704	1,4-beta-cellobios	1352	98	4.7	384	2	H70580	hypothetical prote
1280	99	4.8	707	2	A46302	PTB-associated spl	1353	98	4.7	403	2	S52796	prpL2 protein - hu
c1281	99	4.9	710	2	A31641	daughterless (da)	1354	98	4.7	416	2	G71965	glycine hydroxymet
c1282	99	4.9	718	1	VCPVIM	coat protein VP1 -	1355	98	4.7	429	2	JC4965	elk1 protein - mou
c1283	99	4.9	733	2	JC7679	dendritic cell-der	1356	98	4.7	449	2	S16748	proline-rich prote
c1284	99	4.9	784	2	A26601	elastin precursor	1357	98	4.7	463	2	A48375	cellulase (EC 3.2.
c1285	99	4.9	841	2	C87331	ISCC2, transposase	1358	98	4.7	473	2	S50755	hypothetical prote
c1286	99	4.9	1028	1	CGHUIA	collagen alpha 1(V	1359	98	4.7	502	2	A48679	probable transcrip
1287	99	4.8	1032	2	D83637	serine/threonine p	1360	98	4.7	587	2	T41653	hypothetical prote
c1288	99	4.9	1056	2	AS3767	mucin MUC5B, trach	1361	98	4.8	589	2	G87485	hypothetical prote
c1289	99	4.9	1062	2	T30255	inversin - mouse	c1362	98	4.7	602	2	T45760	hypothetical prote
1290	99	4.8	1290	2	T00018	period protein hom	1363	98	4.7	625	2	S71930	neuron-derived rec
1291	99	4.8	1366	1	CGHUS2	collagen alpha 2(I	c1364	98	4.8	625	2	A34615	proflilaggrin - rat
c1292	99	4.9	1574	2	T13954	MEGF6 protein - ra	1365	98	4.7	634	2	T00359	hypothetical prote
c1293	99	4.9	1618	2	S21424	nestin - human	1366	98	4.7	710	2	D96728	hypothetical prote
c1294	99	4.9	1659	1	CGHU4B	collagen alpha 1(I	1367	98	4.7	712	2	T18195	gag protein - silk
1295	99	4.8	2027	2	S60123	hypothetical prote	1368	98	4.7	748	2	T49633	glucan 1,4-alpha-g
1296	99	4.8	2056	2	G88564	protein R10E11.1 l	1369	98	4.7	771	2	B38252	granulocyte colony
1297	99	4.8	2395	1	S50820	surface protein ty	c1370	98	4.7	811	2	S08579	hypothetical prote
c1298	99	4.9	3229	2	S27852	probable cell-surf	c1371	98	4.8	853	2	A70896	hypothetical glyci
c1299	98.5	4.8	152	2	T34649	hypothetical prote	c1372	98	4.8	859	2	T35785	probable beta-gluc
1300	98.5	4.8	213	2	E72548	hypothetical prote	c1373	98	4.8	864	2	A48266	protein-tyrosine k
1301	98.5	4.8	217	2	T09556	hypothetical prote	c1374	98	4.8	901	2	A44825	phosphoprotein, sy
1302	98.5	4.8	234	1	Q0BE43	membrane antigen 9	1375	98	4.7	903	2	T00705	N-chimerin homolog
1303	98.5	4.8	298	2	T27644	hypothetical prote	1376	98	4.7	1127	2	A25018	circadian rhythm p
1304	98.5	4.8	302	2	T32872	hypothetical prote	1377	98	4.7	1130	1	TVHUA	protein-tyrosine k
1305	98.5	4.8	313	2	T26465	hypothetical prote	1378	98	4.7	1218	2	A26588	period clock prote
c1306	98.5	4.8	357	2	D84395	1-allo-threonine a	1379	98	4.7	1218	2	A26427	period clock prote
1307	98.5	4.8	363	2	D75423	hypothetical prote	1380	98	4.8	1323	2	T30253	spalt protein - mo
c1308	98.5	4.8	381	2	T27806	hypothetical prote	c1381	98	4.8	1329	2	T29074	hypothetical prote
c1309	98.5	4.8	404	2	S54729	RNA-binding protei	c1382	98	4.8	1575	2	S68448	synaptotagmin, 170K
1310	98.5	4.8	423	2	A41207	hypothetical prote	c1383	98	4.7	1655	2	T13998	gene mastermind pr
1311	98.5	4.8	430	2	D70599	collagen 13, nonfi	1384	98	4.7	1736	2	T00391	hypothetical prote
1312	98.5	4.8	439	2	S66671	neuron-derived rec	1385	98	4.7	1736	2	T30283	polyketide synthas
1313	98.5	4.8	499	2	S09880	hypothetical prote	c1386	98	4.8	6420	2	T30283	microfilarial shea
c1314	98.5	4.8	516	2	C44479	collagen alpha 1(X	1387	97.5	4.7	228	2	S46965	hypothetical prote
c1315	98.5	4.8	532	2	JC5412	epidermal growth f	1388	97.5	4.7	273	2	A84332	hypothetical prote
c1316	98.5	4.8	537	2	B33485	spore coat protein	c1389	97.5	4.8	305	2	T30165	hypothetical prote
1317	98.5	4.8	589	2	JG0196	protein kinase DYR	1390	97.5	4.7	306	2	T52340	cell wall-plasma m
c1318	98.5	4.8	591	2	B70523	hypothetical glyci	1391	97.5	4.7	316	2	T19291	hypothetical prote
1319	98.5	4.8	598	2	A37251	probable nuclear h	c1392	97.5	4.8	348	2	A34705	collagen - Caenorh
1320	98.5	4.8	628	2	JC2493	neuron derived orp	1393	97.5	4.7	349	2	T43457	hypothetical prote
1321	98.5	4.8	629	2	JG0195	protein kinase DYR	1394	97.5	4.7	354	2	S39406	homeotic protein o
c1322	98.5	4.8	691	2	A40024	regulatory protein	1395	97.5	4.7	364	2	I48186	gene NKX6.1 protei
1323	98.5	4.8	698	2	T17261	hypothetical prote	1396	97.5	4.7	366	2	T26449	hypothetical prote
c1324	98.5	4.8	775	2	A61228	collagen alpha 2(I	1397	97.5	4.7	396	2	T35659	probable transmemb
1325	98.5	4.8	886	2	S29605	glycoprotein 350/2	1398	97.5	4.7	428	1	TVHUEK	transforming prote
1326	98.5	4.8	907	1	Q0BE21	membrane antigen 9	c1399	97.5	4.8	430	2	T28143	tapasin 1 homolog,
1327	98.5	4.8	913	2	S20590	exo-alpha-sialidas	1400	97.5	4.7	431	2	S09824	hypothetical prote
c1328	98.5	4.8	947	2	T02979	pyruvate, phosphat	1401	97.5	4.7	471	2	S33679	ribonucleoprotein

transcription fact
hypothetical prote
hypothetical 57.4K
hypothetical prote
zyxin - human
hypothetical prote
gag-like protein -
hypothetical 67K p
collagen alpha 1(X
transcription fact
class A helix-loop
hypothetical glyci
probable tkt prote
1-phosphatidylinos
collagen alpha 1(V
probable ABC trans
hypothetical prote
mixed-lineage prot
hypothetical prote
hypothetical prote
hypothetical prote
collagen alpha 2 c
nucleoporin Nup133
C-terminal domain-
hypothetical prote
collagen alpha 1(X
fibroin - Chinese
TonB protein, prob
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
alkaline serine pr
type 1 angiotensin
hypothetical glyci
CD30 antigen precu
hypothetical prote
collagen alpha 3(I
immediate-early pr
rabphilin-3A - mou
hypothetical glyci
probable serine-th
glycogen debranchi
elastin precursor
hypothetical prote
collagen alpha 3(V
fibrinogen alpha c
hypothetical prote
basal transcriptio
mannose receptor,
ATP dependent DNA
collagen type IV a
low voltage-activa
CREB-binding prote
fatty-acid synthas
otogelin - mouse
rifamycin polyketi
tenascin-X precurs
Bassoon protein -
zein, 27K - maize
hypothetical prote
hypothetical prote
glutelin 2 precurs
B4 protein - human
hypothetical prote
salivary proline-r
gene MAC25 protein
hypothetical prote

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4.7 245 2 T31187
4.7 251 1 PIHUPF
4.7 277 2 I52825
4.7 289 2 T34241

hypothetical prote
hypothetical prote
homeotic protein o
collagen col-6 - C
cysteine proteinas
proline-rich prote
otxin protein - mou
homeodomain protei
hypothetical prote
collagen dpy-2 - C
hypothetical prote
hypothetical prote
cutical collagen 6
homeotic protein H
probable oxidoredu
hypothetical prote
zinc finger DNA-bi
enigma - human
ribonucleoprotein
DNA-directed RNA p
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serine-rich protei
transcription fact
X-linked PEEST-cont
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proline-rich prote

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4.7 403 2 A53662
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ALIGNMENTS

RESULT 1

I56559

C:Species: Mus musculus (house mouse)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C:Accession: I56559

J. Neurosci. 15, 5088-5097, 1995

A>Title: Expression and activity-dependent changes of a novel limbic-serine protease gene

A:Reference number: I56559; MUID:95348817; PMID:7623137

A:Accession: I56559

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-260 <RES>

A:Cross-references: UNIPROT:061955; GB:D30785; NID:gi648847; PIDN:BAA06451.1; PID:gi102005

C:Superfamily: trypsin; trypsin homology

F:33-252/Domain: trypsin homology <TRY>

Alignment Scores:

Pred. No.:	1.25e-33	Length:	260
Score:	622.50	Matches:	121
Percent Similarity:	60.32%	Conservative:	28
Best Local Similarity:	48.9%	Mismatches:	93
Query Match:	30.13%	Indels:	5
DB:	2	Gaps:	3

US-10-015-385A-193 (1-1091) x I56559 (1-260)

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QY	184	ATTTTCAATGGCACGTAGTGTGGCGTAACTCACAGCGTGCAGTGGGTGTTTGTAG	243
DB	33	IleLeuGluGlyArgGlyCysIleProHisSerGlnProTrpGlnAlaLeuPheGln	52
QY	244	GGCACCAGCTCGGTGGGGGTCTCTCTATTATGACCACAGGTGGGTCTCTACAGCGCT	303
DB	53	GlyGluArgLeuLeuCysGlyGlyValLeuValGlyAspArgTrpValLeuThrAla	72
QY	304	CACTGACGGCAGCAGGTACTGGGTGGCGCTTGGGGGAACACAGCTCAGCAGCTCGAC	363
DB	73	HisCysLysLysGlnLysTyrSerValArgLeuGlyAspHisSerLeuGlnSerArgAsp	92


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Db      |||||
QY 424 TCG---ACAGACGACAGACAGACCTCCGGCTGTGCGGCTGCGCTGCCCTCCGCGTA 480
Db      |||||
QY 113 AsnProGluAspHisSerHisAspIleMetLeuIleArgLeuGlnAsnSerAlaAsnLeu 132
Db      |||||
QY 481 ACCAGCAGGTTCAACCCCTGCCCTGCCATGCTGCAACCCGCTGGCACCAGATGC 540
Db      |||||
QY 133 GlyAspLysValLysProValGlnLeuAlaAsnLeuCysProLysValGlnLysCys 152
Db      |||||
QY 541 CACGCTCAGGCTGGGGCATCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 600
Db      |||||
QY 153 IleIleSerGlyTyrGlyThrValThrSerProGlnGluAsnPheProAsnThrLeuAsn 172
Db      |||||
QY 601 TGCCTCAACCTCTCCATCTCTCCCATGCCACCTGCGATGCTGATCCCGGAGATC 660
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QY 232 ProCysGlyLysProGluLysProGlyValTyrThrLysIleCysArgTyrThrThrTrp 251
Db      |||||
QY 841 ATCCGGATGATCATGAGGAAC 861
Db      |||||
QY 252 IleLysLysThrMetAspAsn 258
Db      |||||

RESULT 2
S55066
trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken
N:Alternate names: trypsinogen II
C:Species: Gallus gallus (chicken)
C>Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C:Accession: S55066; S72347
R:Wang, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479, 1995
A:Title: Isolation and characterization of the chicken trypsinogen gene family.
A:Reference number: S55065; MUID:95251611; PMID:7733885
A:Accession: S55066
A:Molecule type: mRNA
A:Residues: 1-248 <WAN2>
A:Cross-references: UNIPROT:Q90629; EMBL:U15157; NID:g603906; PIDN:AAA79914.1; PID:g6039
A:Experimental source: clone 2-P29
A:Accession: S72347
A:Molecule type: DNA
A:Residues: 1-248 <WAN2>
A:Cross-references: EMBL:U15157; NID:g603906; PIDN:AAA79914.1; PID:g603907
A:Experimental source: clone 2-P29
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-25/Domain: activation peptide #status predicted <APT>
F:26-248/Product: trypsin II #status predicted <NAT>
F:26-241/Domain: trypsin homology <TRY>
F:165,109,202/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.: 3,98e-30 Length: 248
Score: 569.50 Matches: 116
Percent Similarity: 63.52% Conservative: 39
Best Local Similarity: 47.54% Mismatches: 78
Query Match: 27.57% Indels: 11
DB: 2 Gaps: 6
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US-10-015-385a-193 (1-1091) x S55066 (1-248)
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Db      |||||
QY 4  LeuPheLeuIleLeuSerCysLeuGlyAlaValAlaPheProGlyGlyAlaAspAsp 23
Db      |||||
QY 178 CCGAAGATTTTCAATGGCAGCTAGTGTGGGGTAACTCACAGCCGCTGGCAGGTGGGGCTG 237
Db      |||||
QY 24  AspLysIleValGlyGlyTyrThrCysProGluHisSerValProTyrGlnValSerLeu 43
Db      |||||
QY 238 TTTGAGGACACAGCCTCGCTGCGGGGTCTTTATTGATGACACAGTGGTGGTCTCTACA 297
Db      |||||
QY 44  AsnSerGlyTyrHisPhe---CysGlyGlySerLeuIleAsnSerGlnTrpValLeuSer 62
Db      |||||
QY 298 GGGGCTCACTCAGCGGACAGAGTACTGGGTGGCGCTGGGGGAAACACAGCCTCAGCCAG 357
Db      |||||
QY 63  AlaAlaHisCysTyrLysSerArgIleGlnValArgLeuGlyLysLeuAlaVal 82
Db      |||||
QY 358 CTCGACTGGACCGAGATCGGCACAGCGGCTCTCTGTGACCCATCCCGGCTACCTG 417
Db      |||||
QY 83  GlnGluAspSerGluValValArgSerSerValIleIleArgHisProLysTyr--- 101
Db      |||||
QY 418 GGAGCCTCGACGACGACGACGACGACCTCCGGCTGCTGCGGCTGCGGCTGCGGCTCGGC 477
Db      |||||
QY 102 ---SerSerIleThrLeuAsnAsnAspIleMetLeuIleLysLeuAlaSerAlaValGlu 120
Db      |||||
QY 478 GTAACACGACGAGTTCACCCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCACCCGAG 537
Db      |||||
QY 121 TyrSerAlaAspIleGlnProIleAlaLeuProSerSerCysAlaLysAlaGlyThrGlu 140
Db      |||||
QY 538 TGCCACGCTCAGGCTGGGGGATCACCAACCAACCAACCAACCAACCAACCAACCAACCA 597
Db      |||||
QY 141 CysLeuIleSerGlyTyrGlyAsnThrLeuSerAsnGlyTyrAsnTyrProGluLeuLeu 160
Db      |||||
QY 598 CAGTGCCTCAACCTCTCCATGCTCCCATGCCATGCCATGCCATGCCATGCCATGCCATG 657
Db      |||||
QY 161 GlnCysLeuAsnAlaProIleLeuSerAspGlnGluCysGlnGluAlaTyrProGlyAsp 180
Db      |||||
QY 658 ATCAGACGACACATGCTGTGTGACGCGCGCTCCCG---GGCAGGATGCCTGCCAGGGT 714
Db      |||||
QY 181 IleThrSerAsnMetIleCysValGlyPheLeuGluGlyGlyLysAspSerCysGlnGly 200
Db      |||||
QY 715 GATTCTGGGGGCCCCCTGCTGTGTGGGGAGTCTTCAAGTCTGCTGCTGCTGCTGCTGCTG 774
Db      |||||
QY 201 AspSerGlyGlyProValValCysAsnGlyGluLeuGlnGlyIleValSerTrpGly--- 219
Db      |||||
QY 775 GTGGGGCCCTGTGGACAGATGGCATCCCTGGAGTCTACACCTATATTGCAAGTATGTC 834
Db      |||||
QY 220 IleGly---CysAlaLeuLysGlyTyrProGlyValTyrThrLysValCysAsnTyrVal 238
Db      |||||
QY 835 GACTGGATCCGG 846
Db      |||||
QY 239 AspTrpIleGln 242
Db      |||||

RESULT 3
S55067
trypsin (EC 3.4.21.4) I precursor, pancreatic - chicken
N:Alternate names: trypsinogen I
C:Species: Gallus gallus (chicken)
C>Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C:Accession: S55067; S72345; S55065; S72346; S71155
R:Wang, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479, 1995
A:Title: Isolation and characterization of the chicken trypsinogen gene family.
A:Reference number: S55065; MUID:95251611; PMID:7733885
A:Accession: S55067
A:Molecule type: mRNA
A:Residues: 1-248 <WAN1>
A:Cross-references: UNIPROT:Q90627; UNIPROT:Q90628; EMBL:U15156; NID:g603904
A:Experimental source: clone 1-P38
A:Accession: S72345
A:Molecule type: DNA
```


A;Residues: 1-248 <WAN2>
A;Experimental source: Clone 1-P38
A;Accession: S55065
A;Molecule type: mRNA
A;Residues: 1-9,'V',11-12,'T',14-102,'A',104-214,'I',216-248 <WAN3>
A;Cross-references: EMBL:U15155; NID:g603902; PIDN:AAA79912.1; PID:g603903
A;Experimental source: Clone P1
A;Accession: S72346
A;Molecule type: DNA
A;Residues: 1-9,'V',11-12,'T',14-102,'A',104-214,'I',216-248 <WAN4>
A;Cross-references: GB:U15155; NID:g603902; PIDN:AAA79912.1; PID:g603903
A;Experimental source: Clone P1
R;Wang, K.
submitted to the EMBL Data Library, September 1994
A;Reference number: S71155
A;Accession: S71155
A;Molecule type: mRNA
A;Residues: 1-102,'A',104-248 <WAN5>
A;Cross-references: EMBL:U15156; NID:g603904; PIDN:AAA79913.1; PID:g603905
A;Experimental source: Clone 1-P38
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-25/Domain: activation peptide #status predicted <APT>
F;26-248/Product: trypsin I #status predicted <MAT>
F;26-241/Domain: trypsin homology <TRY>
F;65,109,202/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.: 5,82e-30 Length: 248
Score: 567.00 Matches: 115
Percent Similarity: 60.47% Conservative: 38
Best Local Similarity: 45.45% Mismatches: 88
Query Match: 27.44% Indels: 12
DB: 2 Gaps: 6

US-10-015-385A-193 (1-1091) x S55067 (1-248)

QY 127 CTCAGCATCTTTTGTCTCTCTGTGTCTTGGG-----CTCAGCCAG 168
Db 1 MetLysPheLeuValLeuValAlaPheLeuGlyValAlaValAlaPheProIleSerAsp 20

QY 169 GCAGCCACACCGAAGATTTTCAATGCACCTAGTGTGGCGGTAACTCAGCCGTCGAG 228
Db 21 GluAspAspAspLysIleValGlyGlyTyrSerCysAlaArgSerAlaAlaProTyrGln 40

QY 229 GTGGGCTGTTTGGAGGCACACCGTCCGCTGGCGGGGGTCTCTATTGACACAGGTGG 288
Db 41 ValSerLeuAsnSerGlyTyrHisPhe---CysGlyGlySerLeuIleSerSerGlnTrp 59

QY 289 GTCTCTACAGCGGCTCACTGCAGCGCAGCAGGTACTGTGGTGGCTCTGGGGGAACACAGC 348
Db 60 ValLeuSerAlaAlaHisCysTyrLysSerSerIleGlnValLysLeuGlyGlyLysAsn 79

QY 349 CTCAGCAGCTCGACTGGACCGAGCAGATCCGGCAGACGGGCTTCTCTGTGACCCATCCC 408
Db 80 LeuAlaAlaGlnAspGlySerGluGlnThrIleSerSerSerLysValIleArgHisSer 99

QY 409 GGTACTCTGGAGCCTCGAGGACCGACAGCAGCAGCTCGGCTGGTGTGGTGGCGCCCTG 468
Db 100 GlyTyr-----AsnSerAsnThrLeuAsnAsnAspIleMetLeuIleLysLeuSerLys 117

QY 469 CCGTCCGGGTAAACAGCAGCGTTCAACCCCTGCCCTGCCAATGACTGTGCAACCGCT 528
Db 118 AlaAlaThrLeuAsnSerTyrValAsnThrValProLeuProThrSerCysValThrAla 137

QY 529 GGCACCGAGTGGCAGCTCTCAGGCTGGGGCATCACCACCGAACCCATTCCTCCG 588
Db 138 GlyThrThrCysLeuIleSerGlyTyrGlyAsnThrLeuSerSerGlySerLeuTyrPro 157

QY 589 GATCTGCTCAGTGCTCAACCTCTCCATGCTCTCCATGCTCCGATGCCACCTGCTGTAT 648
Db 158 AspValLeuGlnCysLeuAsnAlaProValLeuSerSerSerGlnCysSerSerAlaTyr 177

QY 649 CCGGGAGAAATCACGAGCAATCGTGTGTGTGAGCGGCGTC---CCGGGCGAGATGCC 705
Db 178 ProGlyArgIleThrSerAsnMetIleCysIleGlyTyrLeuAsnGlyGlyLysAspSer 197

QY 706 TGCACGGGTGATCTCTGGGGCCCCCTGGTGTGTGTGGGGAGTCTTCAAGTCTGTGTGCC 765
Db 198 CysGlnGlyAspSerGlyGlyProValValCysAsnGlyGlnLeuGlnGlyPheValSer 217

QY 766 TGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTGCC 825
Db 218 TrpGly---IleGly---CysAlaGlnLysGlyTyrProGlyValTyrThrLysValCys 235

QY 826 AAGTATGTGATCGGATCCGGATGATCATCGAGGACAAC 864
Db 236 AsnTyrValSerTrpIleLysThrThrMetSerSerAsn 248

RESULT 4
TRPGTR
trypsin (BC 3.4.21.4) precursor - pig (tentative sequence)
N;Contains: trypsinogen
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A90641; A90368; A00947
R;Charles, M.; Rovey, M.; Guidoni, A.; Desmuelle, P.
Biochim. Biophys. Acta 69, 115-129, 1963
A;Title: Su le trypsinogene et la trypsine de porc.
A;Reference number: A90641
A;Accession: A90641
A;Molecule type: protein
A;Residues: 1-10 <CHA>
A;Cross-references: UNIPROT:P00761
R;Hermanson, M.A.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.
Biochemistry 12, 3146-3153, 1973
A;Title: Determination of the amino acid sequence of porcine trypsin by sequenator analysis
A;Reference number: A90368; MUID:73258692; PMID:4738933
A;Accession: A90368
A;Molecule type: protein
A;Residues: 9-231 <HER>
A;Note: at position 20, Ile and Val occur alternatively
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; polymorphism; protein digestion; serine proteinase; zymogen
F;1-231/Product: trypsinogen #status experimental <ZYM>
F;1-8/Domain: activation peptide #status experimental <APT>
F;9-231/Product: trypsin #status experimental <MAT>
F;9-224/Domain: trypsin homology <TRY>
F;15-145,33-49,117-218,124-191,156-170,181-205/Disulfide bonds: #status predicted
F;48,92,185/Active site: His, Asp, Ser #status predicted
F;60,62,65,70/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Alignment Scores:
Pred. No.: 1,46e-29 Length: 231
Score: 561.00 Matches: 107
Percent Similarity: 63.76% Conservative: 39
Best Local Similarity: 46.72% Mismatches: 77
Query Match: 27.15% Indels: 6
DB: 1 Gaps: 4

US-10-015-385A-193 (1-1091) x TRPGTR (1-231)

QY 181 AAGATTTTCAATGGCACTGAGTGTGGCGTAACCTACAGCCGTGGCAGGTGGGCTGTTT 240
Db 8 LysIleValGlyGlyTyrThrCysAlaAlaAsnSerIleProTyrGlnValSerLeuAsn 27

QY 241 GAGGGCAGCAGCTGGCTGGCGGGGTGCTTTATTGACACAGTGGGTCTTCACAGCG 300
Db 28 SerGlySerHisPhe---CysGlyGlySerLeuIleAsnSerGlnTrpValValSerAla 46

QY 301 GCTCACTGCGAGCGGAGCAGGTACTGGTGGCGCTGGGGGAAACACAGCTCAGCCAGCTC 360
Db 47 AlaHisCysTyrLysSerArgIleGlnValAlaGlyLeuGlyGlyHisAlaSerValLeu 66

QY 361 GACTGGACCGAGCAGATCCGGCAGCAGCGGCTTCTGTGTGACCATCCCGGCTACCTGGGA 420


```

Score: 555.00 Matches: 115
Percent Similarity: 58.91% Conservative: 37
Best Local Similarity: 44.57% Mismatches: 90
Query Match: 26.86% Indels: 16
DB: 2 Gaps: 6

US-10-015-385A-193 (1-1091) x AS3968 (1-253)

QY 121 ATGGGGCTCAGCATCTTTTGTCTCTGTGTGTCTTGGGCTCAGC----- 165
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20

QY 166 -----CAGGAGCACCACCGAAGATTTTCATGGCACTGAGTGTGGGGTAACTCA 216
   ::::: ::::: ::::: ::::: ::::: :::::
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40

QY 217 CAGCCGTGGCAGGTGGGGCTGTTTGAGGSCACACAGCTGCGCTGGGGGGTGCCTTATT 276
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 600

QY 277 GACCACAGGTGGCTCTCACAGCGGCTCACTCAGCGGCGAGGAGTACTGGCTGGCGCTG 336
   ::: |||::: |||::: |||::: |||::: |||:::
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTyThrValHisLeu 80

QY 337 GGGGAACACAGCTCAGCCAGCTCGCACTGGACCGAGCAGATCCGGCAGACGGCTTCT 396
   ::::: ::::: |||::: |||::: |||::: |||:::
Db 81 GlySerAspThrLeuGly-----AspArgAArgAlaGlnArgIleLysAlaSerLysSer 98

QY 397 GTGACCATCCGGGTACTGGGAGCCTCGACGACGCCAGCAGCACTCCGGCTGGCTG 456
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 99 PheArgHisProGlyTyr-----SerThrGlnThrHisValAsnAspLeuMetLeuVal 116

QY 457 CGGCTCGCCTGCCCGTCCGGTAACACAGCAGCGTTCAACCCCTGCCCTGCCCAATGAC 516
   ::::: |||::: |||::: |||::: |||::: |||:::
Db 117 LysLeuAsnSerGlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArg 136

QY 517 TGTGAACCGGTGGCAGCGAGTCCACGCTCAGCTGGGGCATCACCAACACCCACGG 576
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 137 CysGluProProGlyThrThrCysThrValSerGlyTyrGlyThrThrThrSerProAsp 156

QY 577 AACCCATTCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGTCTCCATGCCACCTGC 636
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 157 ValThrPheProSerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCys 176

QY 637 CATGCTGTGTATCCCGGAGAAATCAGACCAATGTTGTGTGACGGCGGCTCCGGGG 696
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 177 ThrLysValTyrLysAspLeuLeuGlnAsnSerMetLeuCysAla--GlyIleProAsp 195

QY 697 -----CAGATGCTGCCAGGTGATCTGGGGGCCCCCTGCTGTGTGGGGAGTCTT 750
   ::::: ::::: |||::: |||::: |||::: |||::: |||:::
Db 196 SerLysLysAsnAlaCysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeu 215

QY 751 CAAGTCTGTGTCTCTGGGGTCTGTGGGGCCCTGTGGACAGATGGCATCCTGGAGTGC 810
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 216 GlnGlyLeuValSerTrpGlyThrPhe---ProCysGlyGlnProAsnAspProGlyVal 234

QY 811 TACACCTATATTTCGAAGTATGTGGACTGGATCCGGATGATCATCAGGAGAACAC 864
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 235 TyrThrGlnValCysLysPheThrLysTrpIleAsnAspThrMetCysLysHis 252

RESULT 7
B25528
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: B25528
R:Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
Nucleic Acids Res. 14, 8307-8330, 1986
A:Title: Sequence organisation and transcriptional regulation of the mouse elase
A:Reference number: A93646; MUID:87066713; PMID:3641189
A:Accession: B25528
A:Molecule type: mRNA
A:Residues: 1-246 <STE>

```

A;Cross-references: UNIPROT:P07146; GB:X04574; NID:G54918; PIDN:CRA28243.1; PID:G5491919
C:Superfamily: trypsin; trypsin homology
C:Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F1-23/Domain: signal sequence #status predicted <SIG>
F:24-246/Product: trypsin #status predicted <WAT>
F:24-239/Domain: trypsin homology <TRY>
F:30-160, 48-64, 133-233, 139-206, 171-185/Disulfide bonds: #status predicted
F:63, 107, 200/Active site: His, Asp, Ser #status predicted
F:75, 77, 80, 85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Alignment Scores:			
Pred. No.:	4,9e-29	Length:	246
Score:	553.00	Matches:	113
Percent Similarity:	62.45%	Conservative:	45
Best Local Similarity:	44.66%	Mismatches:	81
Query Match:	26.77%	Indels:	14
DB:	2	Gaps:	7

US-10-015-385A-193 (1-1091) x B25528 (1-246)			
QY	127	CTCAGCATCTTTTGTCTCTGCTGTGTTCTTGGGCTCAGCCAGGCA-----GCC	174
Db	1	MetSerAlaLeuLeuIleLeuAlaValAlaPheProValAsp	20
QY	175	ACACCGAAGATTTTCAATGGCACTGAGTGTGGGGTAACTCACAGCCGTGGCAGGTGGGG	234
Db	21	AspAspIysIleValGlyGlyThrCysArgGluSerSerValProTyGlnValSer	40
QY	235	CTGTTTGAAGGACACAGCTCGCTGGGGGGGTCTTTATTGACCACAGGTGGGTCTCTC	294
Db	41	LeuAsnAlaGlyTyRHisphe--CysGlyGlySerLeuIleAsnAspGlnTrpValVal	59
QY	295	ACAGCGCTCACTCAGCGGCGAGCAGTACTGGTGGCGCTGGGGGAACACAGCCTCAGC	354
Db	60	SerAlaAlaHisCysTyRysTyRArgIleGlnValArgLeuGlyGluHisAsnIleAsn	79
QY	355	CAGCTCGACTGGACCGGACGACAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTAC	414
Db	80	ValLeuGluGlyAsnGluGlnPheValAspSerAlaIysIleIleArgHisProAsnTyR	99
QY	415	CTGGGAGCTCGACGAGCCACGACGACGACCTCCGGCTGTGGCGCTGGCGCTGCCGCTC	474
Db	100	-----AsnSerTrpThrLeuAspAsnAspIleMetLeuIleLysLeuAlaSerProVal	117
QY	475	CGCGTAACACGACGCGTCAACCCCTGCCTCGCCCAATGACTGTGCAACCGCTGGCACC	534
Db	118	ThrLeuAsnAlaArgValAlaSerValProLeuProSerSerCysAlaProAlaGlyThr	137
QY	535	GAGTGCACGCTCTCAGGTGGGGC-----ATCACCAACCAACCCACGGAACCCATTCCCG	588
Db	138	GlnCysLeuIleSerGlyTrpGlyAsnThrLeuSerAsnGlyValAsnAsn-----Pro	155
QY	589	GATCTGCTCAGTGCTCAACCTCTCCATGCTCTCCCATGGCCACTGGCATGGTGTGTAT	648
Db	156	AspLeuLeuGlnCysValAspAlaProValLeuProGlnAlaAspCysGluAlaSerTyR	175
QY	649	CCGGGAGAAATCACAGCAACATCGTGTGTGTCAGCGCGCTCCCG--GGCAGGATGCC	705
Db	176	ProGlyAspIleThrAsnAsnMetCileCysValGlyPheLeuGluGlyGlyLysAspSer	195
QY	706	TGCCAGGGTGATTCTGGGGGGCCCTCGTGTGTGGGGAGTCTTTCAAGGTCTGTGTGCC	765
Db	196	CysGlnGlyAspSerGlyGlyProValValCysAsnGlyGluLeuGlnGlyIleValSer	215
QY	766	TGGGGGTCTGTGGGGCCCTGTGGCAAGATGGCATCCCTGGAGTCTACACCTATATTTCG	825
Db	216	TrpGlyTyR-----GlyCysAlaGlnProAspAlaProGlyValTyRThrLysValCys	233
QY	826	AAGTATGTGACGTGATCCGGATCATATGAGGAACAAC	864
Db	234	AsnTyRValAspTrpIleGlnAsnThrIleAlaAspAsn	246

RESULT 8

RESULT 8

Alignment Scores:	
Pred. No.:	5,738-29
Score:	552.00
Percent Similarity:	63.76%
Best Local Similarity:	46.29%
Query Match:	26.72%
DR:	1
Length:	229
Matches:	106
Conservative:	40
Mismatches:	77
Indels:	6
Gaps:	4

181 AAGA TTTTCA ATGGCA CTGAGTGTGGCGTA A CTCA CAGCGTGGCAGGTGGCGCTGTTT 240

25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1

100

[illegible]

D6 26 SerGlyTyrHisPhe---CysGlyGlySerLeuIleAsnSerGlnTrpValValSerAla 44

Qy 301 GCTCACTGCAGCGGCAGCAGTACTGGGTGCGCCTGGGGAAACACAGCCTCAGCCAGTC 360

Db 45 AlaHisCysTyrLysSerGlyIleGlnValArgLeuGlyGluAspAsnIleAsnValVal 64

QY 361 GACTGGACCGAGCAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGA 420

Db 65 GluGlyAsnGluGlnPheIleSerAlaSerLysSerIleValHisProSerTyr----- 82

C... 401 CCTCTCCGCGTGGCCTCGGTGA 480

[illegible]

1. Introduction

A;Accession: S15013
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-247 <HUE>
A;Cross-references: UNIPROT:Q29463; EMBL:X54703; NID:g829; PIDN:CAA38513.1; PID:
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase
F;24-239/Domain: trypsin homology <TRY>
F;63.107.200/Active site: His, Asp, Ser #status predicted

Alignment Scores:

Filed: NO.:
 7.740-25
 Matches: 113
 Score: 550.00

Percent Similarity:	61.94%	Conservative:	40
Post Local Similarity:	45.75%	Mismatches:	84

Query Match:	26.62%	Indels:	10
			5

US-10-013-383A-133 (1-1021) X DISCLOS (1 217)

QY 139 TTGCTCCGTGTGTCTTGGGCTCAGCCAGGCA-----GCCACACCGAAGATTT 188
|||...||| ...||| ...||| |||||
QY 139 TTGCTCCGTGTGTCTTGGGCTCAGCCAGGCA-----GCCACACCGAAGATTT 188
|||...||| ...||| ...||| |||||

D_b 5 LeuIleLeuAlaPheValGlyAlaAlaValAlaPheProSerAspAspAspLysIle 24

Qy 187 TTCAATGGCACTGAGTGTGGCGTAACTCACAGCCGTGGCAGGTGGGCTGTTTGAGGGC 246

Db 25 valGlyGlyTyrThrCysAlaGluAsnSerValProTyrGlnValSerLeuAsnAlaGly 44

247 ACCAGCCTGCGCTGCGGGGGTGTCTCTTA TTGACCA CAGGTGGTCTTCACAGCGGCTCAC 306

45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065

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DB 64 CUSTYGNINYNBVTREGNVAATAGDREUGTUNU KASNNTEKRVATECNCIANTY CS

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QY 367 ACCGAGCAGATCCGGCAGACAGCGGCTTCTCTGTGACCCATCCGGCTACTCGGAGCGCTCG 426
Db      |||||
84 GlyGluGlnPheIleAspAlaSerIlylleArgHisProLysTyr-----SerSer 101
QY 427 ACGAGCCAGCAGCAGCAGCTCCGGCTGTCGGCTCGCGCTCCGCTCCGCTACACCGC 486
Db      |||||
102 TrpThrLeuAspAsnAspIleLeuLeuLeuLeuLeuSerThrProAlaValIleAsnAla 121
QY 487 ACGGTTCAACCCCTGCTCCCAATGACTGTGCAACCGCTGGCAGCAGTGCACGCTC 546
Db      |||||
122 ArgValSerThrLeuLeuLeuProSerAlaCysAlaSerAlaGlyThrGluCysLeuIle 141
QY 547 TCAGCTGGGGCATCACCAACACCGAGAACCCATTCCTCCGAGATCTGTCAGTGCCTC 606
Db      |||||
142 SerGlyTyrPglYasnThrLeuSerSerGlyValAsnTyrProAspLeuLeuGlnCysLeu 161
QY 607 AACCTCTCCATCGTCTCCATCCGCTCCGCTGCTGATGCTGATGCTGATGCTGATGCTG 666
Db      |||||
162 ValAlaProLeuLeuSerHisAlaAspCysGluAlaSerTyrProGlyGlnIleThrAsn 181
QY 667 AACATGGTGTGTCAGCGCGCTCCG---GGCAGGATGCTGCGCAGGCTGATCTGGG 723
Db      |||||
182 AsnMetIleCysAlaGlyPheLeuGluGlyGlyLysAspSerCysGlnGlyAspSerGly 201
QY 724 GCGCCCTGCTGTGGGGAGTCTCTCAAGTCTGTGCTGCTGCGGGTCTGTGGGGCCC 783
Db      |||||
202 GlyProValAlaCysAsnGlyGlnLeuGlnGlyIleValSerTrpGlyTyr-----Gly 219
QY 784 TGTGACACAGATGCGATCCCTGAGTCTACACTATATTTGCAAGTATGTCAGTGGATC 843
Db      |||||
220 CysAlaGlnLysGlyLysProGlyValTyrThrLysValCysAsnTyrValAspTrpIle 239
QY 844 CGGATGATCATCAGGAACAAC 864
Db      |||||
240 GlnGluThrIleAlaAlaAsn 246

RESULT 10
TRDGC
trypsin (EC 3.4.21.4) precursor, anionic - dog
N:Alternate names: cationic trypsinogen
C:Species: Canis lupus familiaris (dog)
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: A26273
R:Pinsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 2669-2676, 1985
A:Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA sequen
A:Reference number: A26273; MUID:86284628; PMID:3841794
A:Accession: A26273
A:Molecule type: mRNA
A:Residues: 1-247 <PIN>
A:Cross-references: UNIPROT:P06872; GB:M11589; NID:g164094; PIDN:AAA30899.1; PID:g164095
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-23/Domain: activation peptide #status predicted <APT>
F:24-247/Product: trypsin, anionic #status predicted <ENZ>
F:24-239/Domain: trypsin homology <TRY>
F:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F:63,107,200/Active site: His, Asp, Ser #status predicted
F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Alignment Scores:
Pred. No.: 1,42e-28 Length: 247
Score: 546.00 Matches: 113
Percent Similarity: 60.8% Conservative: 38
Best Local Similarity: 45.56% Mismatches: 85
Query Match: 26.43% Indels: 12
DB: 1 Gaps: 6

US-10-015-385A-193 (1-1091) x TRDG (1-247)
QY 139 TTGCTCTGTGTGTTCTTGGGCTCAGCCAGGACGACACCG-----AAG 183
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Db      |||||
5 LeuIleLeuAlaPheLeuGly---AlaAlaValAlaThrProThrAspAspAspAspLys 23
QY 184 ATTTTCAATGGCACTAGTGTGGCGTAACTCACAGCCGTGGCAGGTGGGTGTTTGAG 243
Db      |||||
24 IleValGlyGlyTyrThrCysGluGluAsnSerValProTyrGlnValSerLeuAsnAla 43
QY 244 GGCACAGCCTCGCTGGGGGTGCTTATTGACACAGTGGGTCTCTCAGCGGCT 303
Db      |||||
44 GlyTyrHisPhe--CysGlySerLeuIleSerAspGlnTrpValValSerAlaAla 62
QY 304 CACTCAGCGGACAGGTACTGGGTGGCGCTGGGGGACACAGCCTCAGCCAGCTCGAC 363
Db      |||||
63 HisCysTyrLysSerArgIleGlnValArgLeuGlyGlyTyrAsnIleAspValLeuGlu 82
QY 364 TGGACCGAGCAGATCCGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCC 423
Db      |||||
83 GlyAsnGluGlnPheIleAsnSerAlaLysValIleArgHisProAsnTyr-----Asn 100
QY 424 TCGACAGCCAGCAGCAGCAGCTCCGGTGTGCTGGCTGGCTGGCTGGCTGGCTGGCTG 483
Db      |||||
101 SerTrpIleLeuAspAsnAspIleMetLeuIleLysLeuSerSerProAlaValLeuAsn 120
QY 484 AGCAGCGTTCACCCCTGCCCTGCCATGACTGTGCAACCGCTGGCAGCCGAGTCCAC 543
Db      |||||
121 AlaArgValAlaThrIleSerLeuProArgAlaCysAlaAlaProGlyThrGlnCysLeu 140
QY 544 GTCTCAGGCTGGGGCATCACCAACACCCACCGAACCCATTCCTCCGATCTGTCTCAGTGC 603
Db      |||||
141 IleSerGlyTyrPglYasnThrLeuSerSerGlyThrAsnTyrProGluLeuLeuGlnCys 160
QY 604 CTCACCTCTCCATCGTCTCCATCCACCTCCATGCTGTGTATCCCGGAGAAATCAG 663
Db      |||||
161 LeuAspAlaProIleLeuThrGlnAlaGlnCysGluAlaSerTyrProGlyGlnIleThr 180
QY 664 AGCAACATGCTGTGTGGCGGCTCCG---GGCAGGATGCTGCTGGGGTCTGTGGGG 720
Db      |||||
181 GluAsnMetIleCysAlaGlyPheLeuGluGlyLysAspSerCysGlnGlyAspSer 200
QY 721 GGGGGCCCTCGTGTGGGGAGTCTCTCAAGTCTGCTGCTGCTGGGGTCTGTGGGG 780
Db      |||||
201 GlyGlyProValValCysAsnGlyGluLeuGlnGlyIleValSerTrpGlyTyr----- 218
QY 781 CCCTGTGGACAGATGGATCCCTGGAGTCTACACTATATTTGCAAGTATGTGGACTGG 840
Db      |||||
219 GlyCysAlaGlnLysAsnLysProGlyValTyrThrLysValCysAsnPheValAspTrp 238
QY 841 ATCCGGATGATCATGAGGAACAAC 864
Db      |||||
239 IleGlnSerThrIleAlaAlaAsn 246

RESULT 11
TRDGC
trypsin (EC 3.4.21.4) precursor, cationic - dog
N:Alternate names: cationic trypsinogen
C:Species: Canis lupus familiaris (dog)
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: B26273
R:Pinsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 2669-2676, 1985
A:Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA sequen
A:Reference number: A26273; MUID:86284628; PMID:3841794
A:Accession: B26273
A:Molecule type: mRNA
A:Residues: 1-246 <PIN>
A:Cross-references: UNIPROT:P06871; GB:M11590; NID:g164096; PIDN:AAA30900.1; PID:g164097
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-23/Domain: activation peptide #status predicted <APT>
F:24-246/Product: trypsin, cationic #status predicted <ENZ>
F:24-239/Domain: trypsin homology <TRY>
F:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
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Db 236 TyrValAsnTrpIleGlnThrValAlaAAsn 247

RESULT 13

TRRT1

trypsin (EC 3.4.21.4) I precursor - rat

N:Alternate names: trypsinogen I

C:Species: Rattus norvegicus (Norway rat)

C>Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 09-Jul-2004

C:Accession: B22657; A00948

R:Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.

J. Biol. Chem. 259, 14255-14264, 1984

A:Title: Structure of two related rat pancreatic trypsin genes.

A:Reference number: A22657; MUID:85054880; PMID:6094547

A:Accession: B22657

A:Molecule type: DNA

A:Residues: 1-246 <CRA>

A:CROSS-references: UNIPROT:P00762; GB:J00778; NID:G206507; PIDN:AAA98518.1; PID:G206508

A:Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 17

R:MacDonald, R.J.; Stary, S.J.; Swift, G.H.

J. Biol. Chem. 257, 9724-9732, 1982

A:Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of

A:Reference number: A00948; MUID:82265624; PMID:6896710

A:Accession: A00948

A:Molecule type: mRNA

A:Residues: 1-246 <MAC>

A:CROSS-references: GB:J00778; NID:G206507; PIDN:AAA98518.1; PID:G206508

C:Genetics:

A:Introns: 14/1; 67/2; 152/1; 197/3

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen

F:1-15/Domain: signal sequence #status predicted <SIG>

F:16-23/Domain: activation peptide #status predicted <APT>

F:24-246/Product: trypsin I #status predicted <ENZ>

F:24-239/Domain: trypsin homology <TRY>

F:30-160, 48-64, 132-233, 139-206, 171-185/Disulfide bonds: #status predicted

F:63, 107, 200/Active site: His, Asp, Ser #status predicted

F:75, 77, 80, 85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Alignment Scores:

Pred. No.: 2,256-28 Length: 246

Score: 543.00 Matches: 110

Percent Similarity: 63.56% Conservative: 47

Best Local Similarity: 44.53% Mismatches: 76

Query Match: 26.28% Indels: 14

DB: 1 Gaps: 7

US-10-015-385A-193 (1-1091) x TRRT1 (1-246)

QY 127 CTCAGCATCTTTGCTCTCTGTGTCTTGGCTCAGCCAGGCA-----GCC 174

Db 1 MetSerAlaLeuIleLeuAlaValGlyAlaAlaValAlaPheProLeuGluAsp 20

QY 175 ACACCGAGATTTCAGTGCAGTGTGGCGTAACTACAGCGTGGCAGGTGGGG 234

Db 21 AspAspLysIleValGlyGlyThrCysProGluHisSerValProGlnValSer 40

QY 235 CTGTTTGAGGCGACCCAGCTCGCGTGGCGGGGTGCTCTTATTGACACAGTGGGTCCTC 294

Db 41 LeuAsnSerGlyThrHisPhe---CysGlyGlySerLeuIleAsnAspGlnTrpValVal 59

QY 295 ACAGCGGCTACTGACGGCGAGCAGGTACTGGTGGCGCTGGCGGGAACACAGCTCAGC 354

Db 60 SerAlaAlaHisCysTyrLysSerArgIleGlnValArgLeuGlyGluHisAsnIleAsn 79

QY 355 CAGCTCGAGTGGACCGAGATCCGGCACAGCGGCTCTCTGTGACCCATCCCGGCTAC 414

Db 80 ValLeuGluGlyAspGlnGlnPheIleAsnAlaAlaLysIleIleLysHisProAntyr 99

QY 415 CTGGGAGCCTCGACGAGCGACGACGACCTCCGCGCTGCTGGCTGGCGCTGGCGGTC 474

Db 100 -----SerSerTrpThrLeuAsnAsnAspIleMetLeuIleLysLeuSerSerProVal 117

QY 475 CCGGTAAACAGCAGCGGTTCACCCCTGCGCCCTGCGCCCAATGACTGTGTGCAACCGCTGGCACC 534

Db 118 LysLeuAsnAlaArgValAlaProValAlaLeuProSerAlaCysAlaProAlaGlyThr 137

QY 535 GAGTCCACAGTCTCAGGCTGGGG-----ATCACCAACCCACCGGAAACCATTCCTCCG 588

Db 138 GlnCysLeuIleSerGlyTrpGlyAsnThrLeuSerAsnGlyValAsnAen-----Pro 155

QY 589 GATCTGCTCCAGTGCCTCAACCTCTCCATCGTCTCCATGCCACCTGCCATCGTGTGTAT 648

Db 156 AspLeuLeuGlnCysValAspAlaProValLeuSerGlnAlaAspCysGluAlaLafyr 175

QY 649 CCGGAGAGATCACCAGCAACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 705

Db 176 ProGlyGluIleThrSerSerWetIleCysValGlyPheLeuGluGlyGlyLysAspSer 195

QY 706 TGCCAGGTGATTTCTGGGGGCCCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 765

Db 196 CysGlnGlyAspSerGlyGlyProValValCysAsnGlyGlnLeuGlnGlyIleValSer 215

QY 766 TGGGGGTCTGTGGGGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 825

Db 216 TrpGlyTyr-----GlyCysAlaLeuProAspAsnProGlyValTrpThrLysValCys 233

QY 826 AAGTATGTGACTGATCGATCGCG 846

Db 234 AsnPheValGlyTrpIleGln 240

RESULT 14

S31779

trypsin (EC 3.4.21.4) III precursor - Atlantic salmon (fragment)

C:Species: Salmo salar (Atlantic salmon)

C>Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C:Accession: S66657; S31779

R:Male, R.; Lorens, J.B.; Smalas, A.O.; Torriassen, K.R.

Eur. J. Biochem. 232, 677-685, 1995

A:Title: Molecular cloning and characterization of anionic and cationic variants of trypsin

A:Reference number: S66657; MUID:96035908; PMID:7556223

A:Accession: S66657

A:Molecule type: mRNA

A:Residues: 1-238 <MAL>

A:CROSS-references: UNIPROT:P35033; EMBL:X70074; NID:G64387; PIDN:CAA49679.1; PID:G64388

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; serine proteinase

F:1-7/Domain: signal sequence (fragment) #status predicted <SIG>

F:8-15/Domain: activation peptide #status predicted <APT>

F:16-238/Product: trypsin III #status predicted <MAT>

F:16-231/Domain: trypsin homology <TRY>

F:22-152, 40-56, 124-225, 131-198, 163-177, 188-212/Disulfide bonds: #status predicted

F:55, 99, 192/Active site: His, Asp, Ser #status predicted

Alignment Scores:

Pred. No.: 3,556-28 Length: 238

Score: 540.00 Matches: 108

Percent Similarity: 63.3% Conservative: 37

Best Local Similarity: 47.16% Mismatches: 78

Query Match: 26.14% Indels: 6

DB: 2 Gaps: 4

US-10-015-385A-193 (1-1091) x S31779 (1-238)

QY 181 AGATTTCATATGGCACTGAGTGTGGCGTAACACAGCCGTGGCAGGTGGGCTGTGTT 240

Db 15 LysIleValGlyGlyTyrGluCysArgLysAsnSerAlaSerTrpGlnAlaSerLeuGln 34

QY 241 GAGGCGACCGCTCGGCTGGCGGGGTGTCCTTATTGACACAGGTGGGTCTCTCACAGCG 300

Db 35 SerGlyTyrHisPhe---CysGlyGlySerLeuIleSerSerThrTrpValSerAla 53

QY 301 GCTCACTGCGCGGCGAGGAGTACTGGGTGGCGCTCTGGGGGAACACAGCTCAGCCAGCTC 360

Db 54 AlaHisCysTyrLysSerArgIleGlnValArgLeuGlyGluHisAsnIleAlaValAsn 73

QY 361 GACTGGACCGAGCAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGA 420

```
Db 74 GluGlyThrGluGlnPheIleAspSerValIleMetHisProSerTyr----- 91
QY 421 GCCTCGACGAGCCACGACGACACCTCCGGCTGCTCGCGCTCGCGCTCGCGCTA 480
Db 92 AsnSerArgAsnLeuAsnAspIleMetLeuIleLysLeuSerLysProAlaSerLeu 111
QY 481 ACCAGCAGCGTTCAACCCCTGCGCCCTGCGCAATGACTGTGCAACCGCTGGCAGGTGC 540
Db 112 AsnSerTyrValSerThrValAlaLeuProSerSerCysAlaSerSerGlyThrArgCys 131
QY 541 CACGCTCAGGTGGGCGCATCCAAACACCCACCGAACCATTCCCGATCTGCTCCAG 600
Db 132 LeuValSerGlyTrpGlyAsnLeuSerGlySerSerSerAsnTyrProAspThrLeuArg 151
QY 601 TGCCTCAACCTTCATCTCTCCATGCCATGCCATGGTGTGTATCCCGGAGATC 660
Db 152 CysLeuAspLeuProIleLeuSerSerSerSerCysAsnSerAlaTyrProGlyGlnIle 171
QY 661 ACAGCAACATGTTGTGTGACGCGCGCTCCG---GGCAGCATGCCCTGCCAGGTGAT 717
Db 172 ThrSerAsnMetPheCysAlaGlyPheMetGluGlyGlyAspSerCysGlnGlyAsp 191
QY 718 TGTGGGCGCCCTGCTGTGTGGGAGTCTTCAAGTCTGCTGCTGCTGGGCTGTG 777
Db 192 SerGlyGlyProValValCysAsnGlyGlnLeuGlnGlyValValSerTrpGlyTyr--- 210
QY 778 GGGCCCTGGGCAAGATCGCATCCCTGAGCTACACCTATATTTGCAAGTATGTGGAC 837
Db 211 ---GlyCysAlaGlnArgAsnLysProGlyValTyrThrLysValCysAsnTyrArgSer 229
QY 838 TGGATCCGGATCATCATGAGGAACAAC 864
Db 230 TrpIleSerSerThrMetSerSerAsn 238
```

RESULT 15

```
S05494
trypsin (EC 3.4.21.4) IV precursor - rat
N/Alternate names: 23K protein; trypsinogen IV precursor
C/Species: Rattus norvegicus (Norway rat)
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C/Accession: S05494
R/Buttcke, H.; Rausch, U.; Vasiloudes, P.; Scheele, G.A.; Kern, H.F.
Nucleic Acids Res. 17, 6736, 1989
A/Title: A fourth trypsinogen (P23) in the rat pancreas induced by CCK.
A/Reference number: S05494; MUID:89386010; PMID:2780302
A/Accession: S05494
A/Molecule type: mRNA
A/Residues: 1-247 <LUE>
A/Cross-references: UNIPROT:P12788; EMBL:X15679; NID:g56813; PID:g56814
C/Superfamily: trypsin; trypsin homology
C/Keywords: calcium binding; hydrolase; protein digestion; serine proteinase; zymogen
F/1-15/Domain: signal sequence #status predicted <SIG>
F/16-23/Domain: activation peptide #status predicted <APT>
F/24-247/Product: trypsin IV #status predicted <MAT>
F/24-240/Domain: trypsin homology <TRY>
F/30-161, 49-65, 133-234, 140-207, 172-186/Disulfide bonds: #status predicted
F/64, 108, 201/Active site: His, Asp, Ser #status predicted
F/76, 78, 81, 86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
```

Alignment Scores:

Pred. No.:	9.54e-28	Length:	247
Score:	533.50	Matches:	109
Percent Similarity:	59.76%	Conservative:	41
Best Local Similarity:	43.43%	Mismatches:	94
Query Match:	25.82%	Indels:	7
DB:	2	Gaps:	4

US-10-015-385A-193 (1-1091) x S05494 (1-247)

```
QY 121 ATGGGGCTCAGCATCTTT-----TTGCTCTGTGTGTCTTGGGCTCAGCGAGGCC 174
Db 1 MetLysIleSerIlePhePheAlaPheLeuGlyAlaAlaValAlaLeuProValAsnAsp 20
```

```
QY 175 ACACCGAAGATTTTCAATGGCGCACTGAGTGTGGCGTAACCTCACAGCCGTGGCAGGTGGG 234
Db 21 AspAspLysIleValGlyGlyTyrThrCysProLysHisLeuValProTyrGlnValSer 40
QY 235 CTGTTTGAAGGACACGACCTGCTGCGGGGTGCTTATTATGACACAGGTGGGTCTCTC 294
Db 41 LeuHisAspGlyIleSerHisGlnCysGlyGlySerLeuIleSerAspGlnTrpValLeu 60
QY 295 ACAGCGGCTCACTGCGCGGACGAGGTACTGGGTGGCGCTGGGGGAACACAGCTCAGC 354
Db 61 SerAlaAlaHisCysTyrLysArgLysLeuGlnValArgLeuGlyGluHisAsnIleHis 80
QY 355 CAGCTCGACTGACCGACGACGATCCGCGACAGCGCTTCTCTGTACACCTCCCGGTAC 414
Db 81 ValLeuGluGlyGlyGluGlnPheIleAspAlaGluLysIleIleArgHisProGluTyr 100
QY 415 CTGGGAGGCTCGACGAGCCACGACGACCTCCGGCTGCTGGCGCTGGCGCTGCCCTGC 474
Db 101 -----AsnLysAspThrLeuAspAsnAspIleMetLeuIleLysLeuLysSerProAla 118
QY 475 CGCGTAACACGACGAGGTTCACACCTCCCTGCGCCCAATGACTGTGCAACCGCTGCAC 534
Db 119 ValLeuAsnSerGlnValSerThrValSerLeuProArgSerCysAlaSerThrAspAla 138
QY 535 GAGTCCACGCTCTCAGGCTGGGGCATCACCAACACCCACCGAACCATTCCCGGATCTG 594
Db 139 GlnCysLeuValSerGlyTrpGlyAsnThrValSerIleGlyGlyLysTyrProAlaLeu 158
QY 595 TTCAGTGCTCAACCTCTCCATGCTCTCCATGCCACCTGCCATGGTGTGTATCCCGGG 654
Db 159 LeuGlnCysLeuGluAlaProValLeuSerAlaSerSerCysLysLysSerTyrProGly 178
QY 655 AGAATCAGCAGCAACATGTTGTGTGACGCGCGCTCCCG---GGCAGGATGCCGCCAG 711
Db 179 GlnIleThrSerAsnMetPheCysLeuGlyPheLeuGluGlyGlyLysAspSerCysAsp 198
QY 712 GGTGATTTCTGGGGCCCCCTGTTGTGTGGGGAGTCTTCAAGGTCTGTTGCTCTGGGGG 771
Db 199 GlyAspSerGlyGlyProValValCysAsnGlyGluIleGlnGlyIleValSerTrpGly 218
QY 772 TCTGTGGGGCCCTGTGGGCAAGATGGCATCCCTGGAGTCTACACCTATATTGCAAGTAT 831
Db 219 SerVal-----CysAlaMetArgGlyLysProGlyValTyrThrLysValCysAsnTyr 236
QY 832 GTGGACTGATCCGCGATCATGATGAGGAACAAC 864
Db 237 LeuSerTrpIleGlnGluThrMetAlaAsnAsn 247
```

Search completed: March 5, 2005, 23:10:05

Job time : 60 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 5, 2005, 23:00:39 ; Search time 221 Seconds

(without alignments)
5055.913 Million cell updates/sec

Title: US-10-015-385A-193

Perfect score: 2066

Sequence: 1 caagcaggtcatccctctgg.....aggggcaaaaaaaaaa 1091

Scoring table:

BLASUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cn2.1/USPTO spool_p/US10015385/runat_05032005_173554_17304/app_query.fasta_1.1287
-DB=Uniprot_03 -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10015385 @CN 1.1.244 @runat_05032005_173554_17304 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Uniprot 03:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1374	66.5	248	1	KLXC HUMAN
2	952.5	46.1	234	2	Q9CV76
3	632.5	30.6	260	1	KLX8 HUMAN
4	629.5	30.5	260	2	Q8IW69
5	625.5	30.3	260	1	NRPN RAT
6	622.5	30.1	260	1	NRPN MOUSE
7	618.5	29.9	250	1	KLX8 HUMAN
8	611	29.6	255	2	Q7JIG6
9	610	29.5	250	2	Q632F2
10	608	29.4	254	2	Q8CGR4
11	601	29.1	275	2	Q8IXD7
12	599	29.0	255	2	Q6IS10
13	599	29.0	256	1	KLXF HUMAN
14	597.5	28.9	249	2	Q9QTN4
15	597.5	28.9	276	2	Q9QTN3
16	595	28.8	255	2	Q96RQ0
					Q9ukr0 homo sapien
					Q9cv76 mus musculus
					Q8IW69 homo sapien
					Q81w69 homo sapien
					Q81w69 mus musculus
					Q61955 mus musculus
					Q9ubx7 homo sapien
					Q7jig6 saginus oe
					Q632f2 rattus norv
					Q8cgr4 mus musculus
					Q8ixd7 homo sapien
					Q6is10 homo sapien
					Q9id25 homo sapien
					Q9qyn4 mus musculus
					Q9qyn3 m hippostas
					Q96rq0 homo sapien

17	588.5	28.5	293	2	Q9D140	Q9d140 mus musculus
18	588	28.5	276	2	Q8CGR6	Q8cgr6 mus musculus
19	586	28.4	250	2	Q8CGR5	Q8cgr5 mus musculus
20	578	28.0	242	2	Q80VS4	Q80vs4 mus musculus
21	576	27.9	246	2	Q6P3Z0	Q6p3z0 mus musculus
22	569.5	27.6	248	1	TRY3_CHICK	Q90c29 gallus gall
23	569.5	27.6	251	1	KLX8_HUMAN	Q9p9g3 homo sapien
24	569.5	27.6	251	2	Q6B089	Q6b089 homo sapien
25	568.5	27.5	250	1	KLK9_HUMAN	Q9ukg9 homo sapien
26	567	27.4	277	1	KLKD_HUMAN	Q9ukr3 homo sapien
27	566	27.4	248	1	TRY2_CHICK	Q90c28 gallus gall
28	565	27.3	248	1	TRY1_CHICK	Q90c27 gallus gall
29	564.5	27.3	293	1	KLX5_HUMAN	Q9y337 homo sapien
30	564	27.3	248	2	Q7SZT1	Q7sztl1 xenopus lae
31	564	27.3	276	1	KLXA_HUMAN	Q43240 homo sapien
32	563	27.3	244	1	TRY2_XENLA	P70059 xenopus lae
33	563	27.3	255	2	Q6GNU2	Q6gnu2 xenopus lae
34	561	27.2	231	1	TRYP_PIG	P00761 sus scrofa
35	561	27.2	243	1	TRY1_BOVIN	P00760 bos taurus
36	561	27.2	244	1	KLK6_HUMAN	Q92876 homo sapien
37	557	27.0	237	2	Q6GYJ5	Q6gyj5 struthio ca
38	555	26.9	111	2	Q9UKR2	Q9ukr2 homo sapien
39	555	26.9	243	1	TRY1_XENLA	P19799 xenopus lae
40	555	26.9	243	2	Q7SZ06	P78206 xenopus lae
41	555	26.9	253	1	KLK7_HUMAN	P49862 homo sapien
42	555	26.9	253	2	Q91Y82	Q91y82 mus musculus
43	553.5	26.8	246	2	O88301	O88301 mus musculus
44	553	26.8	246	1	TRY2_MOUSE	P07146 mus musculus
45	551	26.7	251	2	O54854	O54854 rattus norv
46	550.5	26.6	247	2	Q9D7Y7	Q9d7y7 mus musculus
47	550	26.6	247	1	TRY2_BOVIN	Q29463 bos taurus
48	549.5	26.6	247	2	Q9CPN9	Q9cpn9 m mus muscu
49	548	26.4	246	2	Q6IE66	P61666 rattus norv
50	546	26.4	247	1	TRY1_CANFA	P06872 canis fami
51	545	26.4	246	1	TRY3_CANFA	P06871 canis fami
52	544.5	26.4	247	1	TRY3_RAT	P08426 rattus norv
53	544	26.3	253	2	Q8NSN9	Q8nsn9 homo sapien
54	543	26.3	246	1	TRY1_RAT	P00762 rattus norv
55	543	26.3	246	2	Q792Z1	Q792z1 mus musculus
56	541.5	26.2	247	2	Q9CPN7	Q9cpn7 mus musculus
57	540	26.1	238	1	TRY3_SALSA	P35033 salmo salar
58	540	26.1	246	2	Q792Y8	Q792y8 mus musculus
59	538.5	26.1	249	2	Q91VE3	Q91ve3 m thymopsin
60	536	25.9	246	2	Q7TT42	Q7tt42 mus musculus
61	536	25.9	246	2	Q9R0T7	Q9r0t7 m pancreati
62	535.5	25.9	245	2	Q6R670	Q6r670 oreochromis
63	535.5	25.9	261	2	Q6H320	Q6h320 bos taurus
64	534.5	25.9	245	2	Q6R671	Q6r671 oreochromis
65	533.5	25.8	245	2	Q792Y9	Q792y9 mus musculus
66	533.5	25.8	247	1	TRY4_RAT	P12788 rattus norv
67	533	25.8	246	1	TRY2_RAT	P00763 rattus norv
68	533	25.8	246	2	Q9Z1R9	Q9z1r9 mus musculus
69	532	25.8	246	2	Q9QUK9	Q9quk9 mus musculus
70	528	25.6	246	2	Q792Z0	Q792z0 mus musculus
71	528	25.6	263	2	Q6H319	Q6h319 sus scrofa
72	527.5	25.5	261	1	KLX7_RAT	P36373 rattus norv
73	525	25.4	240	2	Q98TH0	Q98th0 engraulis j
74	523.5	25.3	246	2	Q7M754	Q7m754 mus musculus
75	522	25.3	244	2	Q8QGW3	Q8qgw3 anguilla ja
76	521.5	25.2	246	1	KLK_PIG	P00752 sus scrofa
77	521.5	25.2	261	1	KLK6_MOUSE	P15947 mus musculus
78	520.5	25.2	258	2	Q632F4	Q632f4 rattus norv
79	519	25.1	246	1	TRYA_RAT	P32821 rattus norv
80	518	25.1	246	1	TRYB_RAT	P32822 rattus norv
81	518	25.1	261	1	KLX8_RAT	P36374 rattus norv
82	514.5	24.9	242	2	Q7TIR8	Q7tir8 pangasius h
83	514	24.9	239	2	Q63275	P36375 rattus norv
84	513.5	24.9	231	1	TRY2_SALSA	P35032 salmo salar
85	513.5	24.9	239	1	KLK2_CAVPO	P12323 cavia porce
86	513.5	24.9	243	2	Q8AV83	Q8av83 brachydanio
87	513.5	24.9	261	2	Q9NIQ1	Q9niq1 saginus oe
88	513.5	24.9	278	2	Q99M20	Q99m20 mus musculus
89	512	24.8	279	2	Q6IE55	Q6ie55 rattus norv

90	511.5	24.8	261	2	Q29474	Q29474	canis famil	163	476.5	23.1	675	2	Q9W6J8	Q9W6J8	dissoestichu
91	510.5	24.7	238	2	Q9W706	Q9W706	paralichthy	164	475.5	23.0	219	2	Q91036	Q91036	gadus morhu
92	510.5	24.7	261	1	KLK3_MOUSE	Q9W756	mus musculu	165	472.5	22.9	235	2	Q66PG8	Q66PG8	fugu rubrip
93	509.5	24.7	222	2	Q9AV11	P08V11	oncorhynch	166	471	22.8	249	2	Q6DIW2	Q6DIW2	xenopus tro
94	509.5	24.7	235	2	KLK3_MOUSE	Q63274	rattus norv	167	470.5	22.8	257	2	Q6LDS3	Q6LDS3	homo sapien
95	508	24.6	242	1	TRX1_SALSA	P35031	salmo salar	168	470.5	22.8	261	1	KLK3_MOUSE	KLK3_MOUSE	homo sapien
96	508	24.6	242	2	Q9W707	Q9W707	paralichthy	169	470	22.7	258	2	Q71QI1	Q71QI1	trimeresuru
97	507	24.5	244	2	Q9W707	O42159	petromyzon	170	469.5	22.7	261	1	KLK8_MOUSE	KLK8_MOUSE	mus musculu
98	507	24.5	259	2	Q632F5	Q632F5	rattus norv	171	469.5	22.7	261	2	Q8C232	Q8C232	mus musculu
99	506	24.5	245	2	Q42160	O42160	petromyzon	172	468	22.7	261	2	KLK2_MOUSE	KLK2_MOUSE	rattus norv
100	505	24.4	242	2	Q7SX90	Q7SX90	brachydanio	173	467.5	22.6	261	1	KLKQ_MOUSE	KLKQ_MOUSE	mus musculu
101	505	24.4	242	2	Q92046	Q92046	dissoestichu	174	467	22.6	258	2	Q71QH6	Q71QH6	trimeresuru
102	505	24.4	260	1	ESTA_CANFA	P09582	canis famil	175	464	22.5	258	2	Q8AY80	Q8AY80	trimeresuru
103	505	24.4	282	2	Q76BA5	Q76BA5	blarina bre	176	462.5	22.4	261	2	Q8K0C6	Q8K0C6	mus musculu
104	504.5	24.4	269	2	Q8IU55	Q8IU55	homo sapien	177	461.5	22.3	259	1	KLK9_MOUSE	KLK9_MOUSE	rattus norv
105	503	24.3	241	2	Q98TG9	Q98TG9	engraulis j	178	458.5	22.2	250	1	TRYP_PLRPL	TRYP_PLRPL	pleuronecte
106	503	24.3	263	1	KLK3_MOUSE	P32824	praomys nat	179	458.5	22.2	261	2	KLK2_MOUSE	KLK2_MOUSE	homo sapien
107	502	24.3	249	1	Q9W6K0	Q9W6K0	notothenia	180	452	21.9	260	2	Q71QJ4	Q71QJ4	trimeresuru
108	502	24.3	259	1	KLK3_MOUSE	P36376	rattus norv	181	451	21.8	260	2	Q7T229	Q7T229	bothrops ja
109	501.5	24.3	237	2	Q91515	Q91515	fugu rubrip	182	450	21.8	258	1	VSP1_TRIST	VSP1_TRIST	trimeresuru
110	501	24.2	242	2	Q93266	Q93266	pseudopleur	183	450	21.8	260	2	Q8UVX1	Q8UVX1	agkistrodon
111	501	24.2	247	1	TRX2_HUMAN	P07478	homo sapien	184	448	21.7	258	2	Q8AY78	Q8AY78	trimeresuru
112	501	24.2	247	1	Q9W705	Q9W705	paralichthy	185	447.5	21.7	258	1	VSP2_AKAC	VSP2_AKAC	agkistrodon
113	499.5	24.2	241	1	TRX1_GADMO	Q91041	gadus morhu	186	446.5	21.6	257	2	VSP3_MOUSE	VSP3_MOUSE	trimeresuru
114	499	24.2	239	2	Q8N1C9	Q8N1C9	homo sapien	187	446.5	21.6	257	2	Q71QI5	Q71QI5	trimeresuru
115	498	24.1	249	2	Q788V0	Q788V0	dissoestichu	188	446	21.6	258	1	VSP3_MOUSE	VSP3_MOUSE	bothrops ja
116	498	24.1	254	1	KLK4_MOUSE	Q9Y5K2	homo sapien	189	444.5	21.5	249	2	Q8JF07	Q8JF07	gadus morhu
117	497	24.1	257	2	Q61E61	Q61E61	rattus norv	190	441	21.3	257	1	VSP4_MOUSE	VSP4_MOUSE	trimeresuru
118	497	24.1	258	1	KLK1_PAPHA	Q28773	papio hamad	191	439.5	21.3	257	2	VSP7_MOUSE	VSP7_MOUSE	trimeresuru
119	497	24.1	261	1	Q725F4	Q725F4	homo sapien	192	439	21.2	279	2	Q9YQJ8	Q9YQJ8	agkistrodon
120	496.5	24.0	261	1	KLK5_MOUSE	P15945	mus musculu	193	438.5	21.2	257	1	VSP2_MOUSE	VSP2_MOUSE	trimeresuru
121	496	24.0	242	2	Q92059	Q92059	paranotothe	194	438	21.2	259	1	VSP1_MOUSE	VSP1_MOUSE	vipera lebe
122	496	24.0	247	2	Q42158	O42158	petromyzon	195	437.5	21.1	233	2	Q9PT51	Q9PT51	agkistrodon
123	496	24.0	262	2	Q82608	Q82608	petromyzon	196	436.5	21.1	250	2	Q93955	Q93955	praomys nat
124	496	24.0	262	2	Q82608	Q82608	petromyzon	197	436.5	21.1	257	2	VSP5_MOUSE	VSP5_MOUSE	trimeresuru
125	495.5	24.0	257	1	KLK1_MACFA	Q07276	macaca fasc	198	436.5	21.1	257	2	Q71QI7	Q71QI7	trimeresuru
126	495.5	24.0	261	1	KLK8_MOUSE	P15946	mus musculu	199	435.5	21.1	257	2	VSP2_MOUSE	VSP2_MOUSE	trimeresuru
127	495	24.0	261	2	Q725F3	Q725F3	homo sapien	200	435	21.0	258	1	VSP2_MOUSE	VSP2_MOUSE	trimeresuru
128	495	24.0	261	2	Q6H322	Q6H322	equus cabal	201	434	21.0	258	1	VSP3_MOUSE	VSP3_MOUSE	trimeresuru
129	494.5	23.9	247	1	TRX1_HUMAN	P07477	homo sapien	202	434	21.0	260	2	VSPB_MOUSE	VSPB_MOUSE	trimeresuru
130	493.5	23.9	248	2	Q66L05	Q66L05	homo sapien	203	434	21.0	260	2	Q71QI9	Q71QI9	trimeresuru
131	493	23.9	262	1	KLK1_HUMAN	P06870	homo sapien	204	433.5	21.0	260	2	Q71QJ0	Q71QJ0	trimeresuru
132	492	23.8	262	2	Q66U59	Q66U59	homo sapien	205	433	21.0	260	2	VSP1_MOUSE	VSP1_MOUSE	agkistrodon
133	491.5	23.8	241	1	TRX1_GADMO	P16049	gadus morhu	206	432	20.9	236	1	VSPA_MOUSE	VSPA_MOUSE	daboia rube
134	491	23.8	256	1	KLK4_MOUSE	P00757	mus musculu	207	432	20.9	257	2	Q9PTL3	Q9PTL3	agkistrodon
135	490.5	23.7	229	1	TRXP_MOUSE	P00764	squalus aca	208	432	20.9	260	2	VSP2_MOUSE	VSP2_MOUSE	agkistrodon
136	490.5	23.7	261	1	KLK2_MOUSE	P36368	mus musculu	209	432	20.9	260	2	Q738D0	Q738D0	agkistrodon
137	489.5	23.7	261	1	KLK1_MOUSE	Q61759	mus musculu	210	431.5	20.9	205	2	Q96JEO	Q96JEO	homo sapien
138	489	23.7	244	1	KLK3_MOUSE	P36375	rattus norv	211	431.5	20.9	257	2	Q71QJ1	Q71QJ1	trimeresuru
139	488	23.6	247	2	Q8NHM4	Q8NHM4	homo sapien	212	431.5	20.9	261	1	KLK2_MOUSE	KLK2_MOUSE	equus cabal
140	488	23.6	265	2	Q9B8Q8	Q9B8Q8	mus musculu	213	431.5	20.9	261	1	KLK3_MOUSE	KLK3_MOUSE	mus musculu
141	487.5	23.6	251	2	Q9B8Q8	Q9B8Q8	mus musculu	214	431	20.9	260	2	VSPA_MOUSE	VSPA_MOUSE	trimeresuru
142	486	23.5	242	2	Q6R179	Q6R179	tautogolabr	215	431	20.9	262	1	VSP1_MOUSE	VSP1_MOUSE	agkistrodon
143	485.5	23.5	234	2	Q88309	Q88309	mus musculu	216	429.5	20.8	205	2	Q96JEO	Q96JEO	homo sapien
144	485.5	23.5	261	2	TRX3_HUMAN	P35030	homo sapien	217	429.5	20.8	205	2	Q96JEO	Q96JEO	homo sapien
145	485	23.5	304	1	Q8N2U3	Q8N2U3	homo sapien	218	429	20.8	176	2	Q8K5D7	Q8K5D7	mus musculu
146	484.5	23.5	251	2	KLK3_MOUSE	Q8N2U3	homo sapien	219	429	20.8	258	1	VSP3_MOUSE	VSP3_MOUSE	trimeresuru
147	484.5	23.4	259	1	KLK3_MOUSE	P15948	mus musculu	220	429	20.8	260	2	Q8QHK3	Q8QHK3	crotalus at
148	484	23.4	255	2	Q920M1	Q920M1	mus musculu	221	428.5	20.7	262	2	Q8QHK3	Q8QHK3	crotalus at
149	483.5	23.4	261	1	KLK1_MOUSE	P00758	rattus norv	222	427	20.7	234	2	Q9YGS1	Q9YGS1	agkistrodon
150	482	23.3	255	2	Q9JIS2	Q9JIS2	mus musculu	223	427	20.7	260	2	Q93502	Q93502	agkistrodon
151	481.5	23.3	261	1	KLK9_MOUSE	P15949	mus musculu	224	426.5	20.6	257	1	VSPC_MOUSE	VSPC_MOUSE	trimeresuru
152	481.5	23.3	254	2	Q9XSN6	Q9XSN6	sus scrofa	225	425	20.6	260	1	VSP1_MOUSE	VSP1_MOUSE	agkistrodon
153	480.5	23.3	263	1	KLK3_MOUSE	Q9Jm71	mus musculu	226	424.5	20.5	257	2	Q71QJ3	Q71QJ3	trimeresuru
154	479	23.2	261	2	Q6DT45	P33619	macaca mula	227	423	20.5	204	2	Q96JEO	Q96JEO	homo sapien
155	479	23.2	261	2	Q6DT45	P33619	macaca mula	228	423	20.5	238	1	VSP1_MOUSE	VSP1_MOUSE	agkistrodon
156	478.5	23.2	248	2	Q6GFX7	Q6GFX7	xenopus lae	229	422.5	20.5	259	2	Q8UUK2	Q8UUK2	crotalus ad
157	478.5	23.2	250	2	Q93265	Q93265	pseudopleur	230	422	20.4	256	2	Q7SYF1	Q7SYF1	cerastes ce
158	477.5	23.1	256	2	Q61E12	Q61E12	rattus norv	231	421.5	20.4	163	2	Q66H01	Q66H01	xenopus lae
159	477.5	23.1	261	1	KLK1_MOUSE	P00755	mus musculu	232	420.5	20.4	257	2	Q71QI8	Q71QI8	trimeresuru
160	477.5	23.1	263	1	KLK3_MOUSE	P00755	mus musculu	233	420	20.3	258	2	Q8QHK2	Q8QHK2	crotalus at
161	477	23.1	247	2	Q66PG9	Q61754	mus musculu	234	419.5	20.3	234	2	Q8UUK1	Q8UUK1	agkistrodon
162	476.5	23.1	344	2	Q9W6J9	Q9W6J9	dissoestichu	235	418.5	20.3	257	2	Q71QI6	Q71QI6	trimeresuru

Q9W6J8 dissoestichu
Q91036 gadus morhu
Q66PG8 fugu rubrip
Q6DIW2 xenopus tro
Q6LDS3 homo sapien
P07288 homo sapien
Q71QI1 trimeresuru
P07628 mus musculu
Q8C232 mus musculu
P00759 rattus norv
P36369 mus musculu
Q71QI6 trimeresuru
Q8AY80 trimeresuru
Q8K0C6 mus musculu
P07647 rattus norv
P35034 pleuronecte
P20151 homo sapien
Q71QJ4 trimeresuru
Q7T229 bothrops ja
Q91516 trimeresuru
Q8UVX1 agkistrodon
Q8AY78 trimeresuru
Q8I8X1 agkistrodon
Q8I509 trimeresuru
Q71QI5 trimeresuru
Q8JF07 bothrops ja
Q8I510 trimeresuru
Q8G84 trimeresuru
Q9YJ8 agkistrodon
Q91508 trimeresuru
Q9PT41 vipera lebe
Q91507 trimeresuru
Q9PT51 agkistrodon
Q03955 praomys nat
Q91511 trimeresuru
Q91517 trimeresuru
Q9DF67 trimeresuru
Q9DF66 trimeresuru
Q13061 trimeresuru
Q71QI9 trimeresuru
Q71QJ0 trimeresuru
Q9YJ2 agkistrodon
P18964 daboia rube
Q9PT13 agkistrodon
Q9YJ6 agkistrodon
Q73800 agkistrodon
Q961E0 homo sapien
Q71QJ1 trimeresuru
Q6H321 equus cabal
P04071 mus musculu
Q13060 trimeresuru
Q8AY81 trimeresuru
Q91053 agkistrodon
Q96JEO homo sapien
Q8K5D7 mus musculu
Q13063 trimeresuru
Q71QI0 trimeresuru
Q8QHK3 crotalus at
Q9YGS1 agkistrodon
Q93502 agkistrodon
Q13062 trimeresuru
Q918X2 agkistrodon
Q71QJ3 trimeresuru
Q96JEO homo sapien
P81176 agkistrodon
Q8UUK2 crotalus ad
Q7SYF1 cerastes ce
Q66H01 xenopus lae
Q71QI8 trimeresuru
Q8QHK2 crotalus at
Q8UUK1 agkistrodon
Q71QI6 trimeresuru

236	418	20.2	260	2	Q8AV82	Q8AV82 trimeresuru	309	372.5	18.0	270	2	Q8I9P2	Q8I9P2 aplysina fi
237	417	20.2	236	1	VSPG_DABRU	P18965 dabia rus	310	371.5	18.0	855	2	Q7Z410	Q7Z410 homo sapien
238	415.5	20.1	178	2	O93594	O93594 dicentrarch	311	371.5	18.0	1059	2	Q7Z411	Q7Z411 homo sapien
239	415.5	20.1	237	2	Q7I0H8	Q7I0H8 trimeresuru	312	371	18.0	234	1	VSP1_AGKRH	P26324 agkistrodon
240	414	20.0	257	2	Q8UUJ2	Q8UUJ2 agkistrodon	313	371	18.0	259	1	CFAD_PIG	P51779 sus scrofa
241	414	20.0	258	1	VSP1_TRIGA	O13059 trimeresuru	314	371	18.0	263	1	CTR2_CANFA	P04813 canis famli
242	414	20.0	260	1	VSP1_TRIFL	P05620 trimeresuru	315	371	18.0	271	1	EL2_RAT	P00774 rattus norv
243	413	20.0	258	2	Q7SZE1	Q7szel gloydus sa	316	370.5	17.9	204	2	Q86VI7	Q86vi7 homo sapien
244	413	20.0	260	1	VSP2_VIPLE	Q9740 vipera lebe	317	370.5	17.9	638	1	KAT_HUMAN	P03952 homo sapien
245	412	19.9	258	2	Q7I0H7	Q7I0H7 trimeresuru	318	368	17.8	418	1	HATT_HUMAN	O60235 homo sapien
246	411.5	19.9	228	1	VSPA_LACMU	P33589 lachesis sh	319	367	17.8	267	2	Q640E1	Q640e1 xenopus lae
247	411	19.9	239	2	Q6T5L0	Q6t5l0 gloydus mu	320	366	17.7	258	1	VSP2_AGKRH	P47797 agkistrodon
248	411	19.9	260	2	Q7SZC3	Q7azc3 gallus gall	321	366	17.7	260	2	Q9W7Q3	Q9W7q3 paralichthy
249	408.5	19.8	257	2	Q8JH62	Q8Jh62 vipera lebe	322	366	17.7	307	2	Q6ZND6	Q6znd6 homo sapien
250	408	19.7	235	1	VSP2_AGKBI	Q9psn3 agkistrodon	323	365.5	17.7	245	2	Q9X160	Q9xy60 ctenocephal
251	408	19.7	232	2	Q8AY79	Q8AY79 trimeresuru	324	365	17.7	263	2	Q7SX97	Q7sx97 brachydania
252	407.5	19.7	258	1	VSP1_BOTJA	P81824 bothrops ja	325	364.5	17.6	265	2	Q6P326	Q6p326 xenopus tro
253	407	19.7	232	2	O93421	O93421 agkistrodon	326	364.5	17.6	387	2	Q9XY57	Q9xy57 ctenocephal
254	407	19.7	237	2	VSP2_AGKCA	O43207 agkistrodon	327	363.5	17.6	314	1	TEST_HUMAN	Q9Y6m0 homo sapien
255	407	19.7	260	1	VSP2_TRIFL	O13057 trimeresuru	328	363.5	17.6	339	2	Q9JL44	Q9Jl44 mus musculus
256	406.5	19.7	231	1	VSP1_AGKCO	P09872 agkistrodon	329	363	17.6	340	2	Q8BJV6	Q8bjv6 mus musculus
257	406.5	19.7	257	2	Q7I0H5	Q7I0H5 trimeresuru	330	363	17.6	342	1	PS8_MOUSE	Q9esd1 mus musculus
258	405.5	19.6	257	2	Q7I0I3	Q7I0i3 trimeresuru	331	362.5	17.5	246	1	MCT1_MERUN	P50340 meriones un
259	405	19.6	234	2	Q7SZB2	Q7aze2 agkistrodon	332	361.5	17.5	267	2	Q7SZ51	Q7sz51 brachydania
260	405	19.6	260	1	VSP1_FRIJE	Q9df68 trimeresuru	333	361.5	17.5	344	2	Q640F8	Q640f8 xenopus lae
261	403.5	19.5	233	2	Q6IWF1	Q6Iwf1 bothrops al	334	361	17.4	255	2	Q6WGR1	Q6Wgr1 ictalurus p
262	402.5	19.5	257	2	Q9YJG9	Q9Yjg9 agkistrodon	335	360	17.4	331	2	Q8RI16	Q8ria6 mus musculus
263	402	19.5	255	1	VSPA_BOTAT	P04971 bothrops at	336	360	17.4	331	2	Q8OX17	Q8ox17 mus musculus
264	402	19.5	260	1	VSP6_TRIMU	Q9dg83 trimeresuru	337	359.5	17.4	259	2	Q6AZC2	Q6azc2 brachydania
265	401.5	19.4	257	2	Q8OG86	Q8OG86 bothrops in	338	359.5	17.4	269	2	Q6ISU5	Q6isau5 homo sapien
266	401	19.4	234	1	VSP2_AGKCO	P82981 agkistrodon	339	359.5	17.4	277	1	TRY2_ANOGA	P35036 anopheles g
267	401	19.4	235	2	Q9OZ47	Q9oz47 agkistrodon	340	359.5	17.4	1019	1	LFC_TACTR	F28175 tachypleus
268	400	19.4	258	2	Q8O2F0	Q8O2f0 agkistrodon	341	359.5	17.4	1019	2	Q8T9S1	Q8t9s1 tachypleus
269	399	19.3	260	2	Q7I0J2	Q7I0j2 trimeresuru	342	359	17.4	311	2	Q8OX23	Q8ox23 rattus norv
270	397.5	19.2	257	1	VSP2_BOTJA	O13069 bothrops ja	343	359	17.4	321	2	Q6GNK3	Q6gnk3 xenopus lae
271	397	19.2	260	1	Q7I0I4	Q7I0i4 trimeresuru	344	359	17.4	430	2	Q804X0	Q804x0 fugu rubrip
272	396.5	19.2	260	1	VSP4_AGKAC	Q918w9 agkistrodon	345	358.5	17.4	245	1	MCT1_SHEEP	P08931 ovis aries
273	395.5	19.1	260	2	Q9ER05	Q9er05 mus musculus	346	358.5	17.4	263	1	CTRB_HUMAN	P17538 homo sapien
274	395	19.1	260	2	Q7I0H9	Q7I0h9 trimeresuru	347	358.5	17.4	444	1	FA7_RABIT	P98139 oryctolagus
275	393.5	19.0	264	2	Q9D7P8	Q9d7p8 mus musculus	348	358	17.3	277	2	Q7T0T6	Q7t0t6 xenopus lae
276	392	19.0	258	2	Q7I0I2	Q7I0i2 trimeresuru	349	358	17.3	318	2	Q7RTY9	Q7rtty9 homo sapien
277	391.5	18.9	257	1	VSP3_TRIFL	O13058 trimeresuru	350	358	17.3	812	1	PLMN_BOVIN	P06968 bos taurus
278	391.5	18.9	264	2	Q9EQZ8	Q9eqz8 rattus norv	351	357.5	17.3	232	2	Q9XY45	Q9xy45 ctenocephal
279	391	18.9	253	2	Q8WZB4	Q8wzb4 homo sapien	352	357.5	17.3	321	1	TRYG_HUMAN	Q9nr12 homo sapien
280	391	18.9	258	2	Q98TT5	Q98tt5 agkistrodon	353	357.5	17.3	321	2	Q96RZ8	Q96r28 homo sapien
281	390	18.9	258	2	Q8JH85	Q8Jh85 vipera lebe	354	357.5	17.3	371	2	Q8MS52	Q8ms52 drosophila
282	390	18.9	258	2	Q9I961	Q9I961 agkistrodon	355	357.5	17.3	643	2	Q97506	Q97506 sus scrofa
283	389	18.8	253	1	CFAD_HUMAN	P00746 homo sapien	356	357	17.3	262	1	GRAA_HUMAN	P12544 homo sapien
284	388	18.8	232	1	VSPA_BOTJA	P81661 bothrops ja	357	357	17.3	271	1	CTR1_PENVA	Q00871 penaeus van
285	388	18.8	257	1	VSP3_AGKAC	Q918x0 agkistrodon	358	357	17.3	806	1	PLMN_MACEU	O18783 macropus eu
286	388	18.8	269	1	EL2_PIG	P08419 sus scrofa	359	356.5	17.3	260	2	Q9V7G4	Q9v7g4 drosophila
287	387	18.7	181	2	Q8NFV7	Q8nf77 homo sapien	360	356.5	17.3	261	2	Q9W7Q4	Q9W7q4 paralichthy
288	387	18.7	243	2	Q8SVJ5	Q8svj5 homo sapien	361	355.5	17.2	276	1	MCT6_MOUSE	P21845 mus musculus
289	386.5	18.7	1524	2	Q91674	Q91674 xenopus lae	362	355	17.2	311	2	Q8WZM5	Q8wzm5 trichoderna
290	386	18.7	258	2	Q9W7S1	Q9w7s1 agkistrodon	363	355	17.2	342	1	PS8_RAT	Q9es87 rattus norv
291	386	18.7	260	2	Q6T6S7	Q6t6s7 bitis gabon	364	354.5	17.2	249	2	Q6QX59	Q6qx59 lepeopathe
292	385.5	18.7	188	1	KLX3_RAT	P15950 rattus norv	365	354.5	17.2	263	1	CTRA_GADMO	P47796 gadus morhu
293	385.5	18.7	264	1	CTRL_HUMAN	P40313 homo sapien	366	354	17.1	260	1	GRAA_MOUSE	P11032 mus musculus
294	385.5	18.7	264	2	Q9D960	Q9d960 mus musculus	367	354	17.1	260	2	Q9W7P9	Q9W7p9 paralichthy
295	385.5	18.7	269	2	Q8IUW0	Q8Iuw0 mus musculus	368	354	17.1	271	1	EL2_MOUSE	P05208 mus musculus
296	385	18.6	263	1	CFAD_RAT	P32038 rattus norv	369	354	17.1	558	2	Q6L711	Q6l711 rattus norv
297	384.5	18.6	195	2	Q7D277	Q7D277 homo sapien	370	353.5	17.1	263	2	Q6PGS4	Q6pgs4 xenopus lae
298	381	18.4	256	1	TRP3_PSEAM	O93267 pseudopleur	371	353.5	17.1	270	1	TRYT_MERUN	P50342 meriones un
299	380.5	18.4	235	2	Q8N4E0	Q8n4e0 homo sapien	372	353.5	17.1	311	1	TRYG_MOUSE	Q9qu17 mus musculus
300	380	18.4	157	2	Q6B338	Q6b338 symphysodon	373	353.5	17.1	333	2	Q7Q5Z6	Q7q5z6 anopheles g
301	380	18.4	455	2	Q7SY86	Q7sy86 xenopus lae	374	353	17.1	505	2	Q966V4	Q966v4 halocynthia
302	379	18.3	220	2	Q8NCW4	Q8ncw4 homo sapien	375	353	17.1	274	1	MCT6_RAT	P50343 rattus norv
303	378	18.3	261	2	Q6DHD9	Q6dh9 brachydania	376	353	17.1	278	2	Q7PNF6	Q7pnf6 anopheles g
304	376	18.2	343	1	PS8_HUMAN	Q16651 homo sapien	377	353	17.1	456	1	PRTC_CANFA	Q28278 canis famli
305	374.5	18.1	259	1	CFAD_MOUSE	P03953 mus musculus	378	353	17.1	459	1	PRTC_PIG	Q9glp2 sus scrofa
306	374	18.1	261	2	Q8CJF4	Q8cjf4 rattus norv	379	352	17.0	304	1	DISP_RAT	P83748 rattus norv
307	373.5	18.1	330	2	Q6NVR7	Q6nvr7 xenopus tro	380	352	17.0	1130	2	Q7QIM7	Q7qim7 anopheles g
308	372.5	18.0	228	2	Q6FWH3	Q6fhw3 homo sapien	381	351.5	17.0	317	2	Q9DGR3	Q9dgr3 xenopus lae

382	351.5	17.0	460	1	PTRC_MOUSE	P33587	mus musculus	455	342.5	16.6	437	1	ACRO_RAT	P23293	rattus norv
383	351.5	17.0	719	2	Q6DJ90	Q6DJ90	xenopus tro	456	342.5	16.6	624	1	FAIL_MOUSE	Q91y47	mus musculus
384	351.5	17.0	1019	1	LFC_CARRO	Q26422	carcinoscor	457	342.5	16.6	810	1	PLMN_HUMAN	P00747	homo sapien
385	351.5	17.0	1083	2	Q6423	Q26423	carcinoscor	458	342.5	16.6	811	1	TMS6_HUMAN	Q81u80	homo sapien
386	351	17.0	310	1	DISP_MOUSE	Q9GY29	mus musculus	459	342	16.6	275	1	TRB1_HUMAN	Q15661	homo sapien
387	351	17.0	328	2	Q80Z40	Q80Z40	rattus norv	460	342	16.6	335	2	Q8VIF2	Q8vif2	mus musculus
388	351	17.0	456	1	PTRC_BOVIN	P00745	bos taurus	461	342	16.6	355	2	Q7PQR9	Q7PQR9	anopheles g
389	350.5	17.0	265	2	Q804G1	Q804G1	brachydanio	462	342	16.6	812	1	PLMN_MOUSE	P20918	mus musculus
390	350.5	17.0	274	2	Q16133	Q16133	anopheles s	463	341.5	16.5	258	1	GRAK_RAT	Q49864	rattus norv
391	350.5	17.0	274	2	Q17086	Q17086	anopheles s	464	341.5	16.5	455	1	TMS5_MOUSE	Q9er04	mus musculus
392	350.5	17.0	434	2	Q7T3B6	Q7c3b6	brachydanio	465	341.5	16.5	573	2	Q9V516	Q9v516	drosophila
393	350.5	17.0	503	2	Q8AYE4	Q8aye4	brachydanio	466	341	16.5	251	2	Q9GLN2	Q9gln2	bos taurus
394	350	16.9	263	2	Q6EPI1	Q6epi1	homo sapien	467	341	16.5	263	1	GRAK_MOUSE	Q3s205	mus musculus
395	350	16.9	268	2	Q6QES9	Q6qes9	xenopus lae	468	341	16.5	271	2	Q803Z4	Q803z4	brachydanio
396	350	16.9	268	2	Q642S8	Q642s8	xenopus tro	469	341	16.5	572	2	Q7RTY8	Q7rty8	homo sapien
397	350	16.9	271	2	Q18487	Q18487	penaeus van	470	341	16.5	704	1	CRAR_MOUSE	P90064	mus musculus
398	350	16.9	1134	2	Q7RTY7	Q7rty7	homo sapien	471	340.5	16.5	246	1	MCT4_MOUSE	P21812	mus musculus
399	349.5	16.9	261	2	Q68HW9	Q6t8w9	brachydanio	472	340.5	16.5	274	1	TRY1_ANOGA	P35035	anopheles g
400	349.5	16.9	269	1	EL2A_HUMAN	P08217	homo sapien	473	340.5	16.5	329	2	Q42272	Q42272	xenopus lae
401	349.5	16.9	269	2	Q61CV2	Q61cv2	homo sapien	474	340.5	16.5	418	2	Q7PGU3	Q7pgu3	anopheles g
402	349.5	16.9	277	2	Q96899	Q96899	scolopendra	475	340.5	16.5	432	2	Q6UX37	Q6ux37	homo sapien
403	349.5	16.9	371	2	Q8CJ16	Q8cj16	rattus norv	476	340.5	16.5	437	1	TMS4_HUMAN	Q9nrs4	homo sapien
404	349.5	16.9	445	2	Q8CJ17	Q8cj17	rattus norv	477	340.5	16.5	446	1	FA7_RAT	Q8k3u6	rattus norv
405	349	16.9	467	2	Q96TX8	Q96tx8	panulirus a	478	340.5	16.5	624	2	Q9DRT3	Q9dat3	mus musculus
406	348.5	16.9	429	2	Q8AVB0	Q8avb0	brachydanio	479	340	16.5	273	2	Q9KSM1	Q9xsm1	ovis aries
407	348.5	16.9	799	2	Q6PF94	Q6pf94	mus musculus	480	340	16.5	360	2	Q17489	Q17489	anopheles g
408	348.5	16.9	811	1	TMS6_MOUSE	Q9dbi0	mus musculus	481	340	16.5	458	1	PTRC_RABIT	Q28661	oryctolagus
409	348.5	16.9	818	2	Q6PBA6	Q6pba6	brachydanio	482	339.5	16.4	247	2	Q08732	Q08732	mesocricetu
410	348	16.8	267	1	TRY7_ANOGA	P35041	anopheles g	483	339.5	16.4	253	1	TRYB_DROER	P54625	drosophila
411	348	16.8	269	2	Q61SN8	Q61sn8	homo sapien	484	339.5	16.4	258	1	GRAM_RAT	Q03238	rattus norv
412	347	16.8	275	2	Q6FHB8	Q6fhb8	homo sapien	485	339.5	16.4	263	2	Q9D8X6	Q9d8x8	mus musculus
413	347	16.8	284	2	Q8NFF8	Q8nff8	homo sapien	486	339.5	16.4	333	1	PLMN_CANFA	P80009	canis fami
414	347	16.8	414	1	TMS5_HUMAN	Q9h3s3	homo sapien	487	339	16.4	321	2	Q61E60	Q61e60	rattus norv
415	347	16.8	461	1	PTRC_HUMAN	P04070	homo sapien	488	339	16.4	461	1	FA9_HUMAN	P00740	homo sapien
416	346.5	16.8	263	2	Q63ZK0	Q63zk0	xenopus lae	489	339	16.4	461	1	FA9_PANTR	Q95nd7	pan troglod
417	346.5	16.8	267	2	Q9BK47	Q9bk47	luidia foli	490	339	16.4	556	2	Q903D5	Q903d5	brachydanio
418	346.5	16.8	269	1	EL2_BOVIN	Q29461	bos taurus	491	339	16.4	625	1	FAIL_HUMAN	P03951	homo sapien
419	346.5	16.8	334	2	Q46507	Q46507	papio hamad	492	339	16.4	812	1	PLMN_RAT	Q01177	rattus norv
420	346.5	16.8	351	2	Q816K0	Q816k0	holotrichia	493	338.5	16.4	256	2	Q18599	Q18599	drosophila
421	346.5	16.8	435	1	TMS4_MOUSE	Q8vca5	mus musculus	494	338.5	16.4	258	1	EL1_HUMAN	Q9unil	homo sapien
422	346.5	16.8	435	2	Q9NFF2	Q9nff2	anopheles g	495	338.5	16.4	258	2	Q867B0	Q867b0	canis fami
423	346.5	16.8	446	1	FA7_MOUSE	P70375	mus musculus	496	338.5	16.4	260	2	Q8P2V9	Q8p2v9	xenopus tro
424	346.5	16.8	456	2	Q7QC30	Q7qc30	anopheles g	497	338.5	16.4	263	2	Q9CR35	Q9crl35	m mus muscu
425	346.5	16.8	461	1	PTRC_RAT	P731394	rattus norv	498	338.5	16.4	263	2	Q9DC86	Q9dc86	mus musculus
426	346.5	16.8	612	2	Q68FY8	Q68fy8	rattus norv	499	338.5	16.4	264	2	Q02569	Q02569	culex quinq
427	346.5	16.8	612	2	Q804W7	Q804w7	fugu rubrip	500	338.5	16.4	402	2	Q7QB73	Q7qb73	anopheles g
428	346	16.7	282	2	Q6NZY1	Q6nzy1	homo sapien	501	338.5	16.4	455	2	Q8CDR0	Q8cdr0	mus musculus
429	346	16.7	322	2	Q920S2	Q920s2	mus musculus	502	338.5	16.4	562	2	Q7PN85	Q7pn85	anopheles g
430	346	16.7	389	2	Q9PVX7	Q9pvx7	xenopus lae	503	338.5	16.4	802	2	Q6UXD8	Q6uxd8	homo sapien
431	345.5	16.7	454	2	Q46506	Q46506	papio hamad	504	338	16.4	210	2	Q63Z11	Q63z11	xenopus lae
432	345	16.7	253	1	TRYD_DROER	P54626	drosophila	505	338	16.4	365	2	Q97366	Q97366	holotrichia
433	345	16.7	328	2	Q61RA4	Q61ra4	xenopus lae	506	338	16.4	388	2	Q44330	Q44330	manduca sex
434	344.5	16.7	117	2	Q9PUF3	Q9puf3	bothrops ja	507	338	16.4	625	1	THRB_BOVIN	P00735	bos taurus
435	344.5	16.7	187	2	Q6EKF3	Q6pk75	homo sapien	508	338	16.4	701	2	Q9JUS9	Q9jjs9	rattus norv
436	344.5	16.7	275	2	Q6B0S1	Q6b0s1	homo sapien	509	338	16.4	703	2	Q8CHN8	Q8chn8	rattus norv
437	344	16.7	257	2	Q8BZ04	Q8bz04	mus musculus	510	337.5	16.3	238	1	TRY5_ABDAB	P29787	aedes aegypt
438	344	16.7	265	1	Q8QXG1	Q6qx61	lepeophthei	511	337.5	16.3	261	2	Q6QX60	Q6qx60	lepeophthei
439	344	16.7	275	2	Q8QXG1	P20231	homo sapien	512	337.5	16.3	264	1	GRAK_HUMAN	P49863	homo sapien
440	344	16.7	280	2	Q8N171	Q8n171	homo sapien	513	337.5	16.3	282	2	Q9D4I3	Q9d4i3	mus musculus
441	344	16.7	297	2	Q88781	Q88781	rattus ratt	514	337.5	16.3	432	2	Q6GNA2	Q6gna2	xenopus lae
442	344	16.7	417	2	Q8BZ10	Q8bz10	mus musculus	515	337.5	16.3	471	2	Q8CFE0	Q8cfe0	mus musculus
443	343.5	16.6	266	2	Q46644	Q46644	macaca fasc	516	337	16.3	247	2	Q17039	Q17039	anopheles g
444	343.5	16.6	271	2	Q8HYJ2	Q8hyj2	bos taurus	517	337	16.3	256	2	Q9R0K0	Q9r0k0	mus musculus
445	343.5	16.6	273	1	MCT7_MOUSE	Q02844	mus musculus	518	337	16.3	275	2	Q96RZ6	Q96r26	homo sapien
446	343.5	16.6	273	2	Q921N4	Q921n4	mus musculus	519	337	16.3	434	1	UR0K_CHICK	P15120	gallus gall
447	343.5	16.6	517	2	Q8K0D2	Q8k0d2	mus musculus	520	336.5	16.3	247	1	MCT1_PAPHA	P52195	papio hamad
448	343	16.6	275	1	TRYT_CANFA	P15944	canis fami	521	336.5	16.3	251	1	MCT3_SHEEP	P52195	papio hamad
449	342.5	16.6	248	2	Q16126	Q16126	boltenia vi	522	336.5	16.3	318	2	Q8MNY6	Q8mny6	niilaparvaca
450	342.5	16.6	248	2	Q9XY52	Q9xy52	ctenoccephal	523	336.5	16.3	428	2	Q8WPM7	Q8wpm7	oikopleura
451	342.5	16.6	273	1	MCT7_RAT	P27435	rattus norv	524	336.5	16.3	581	2	Q8BYE2	Q8bye2	homo sapien
452	342.5	16.6	273	2	Q6P6W8	Q6p6w8	rattus norv	525	336.5	16.3	638	1	KAL_MOUSE	P26262	mus musculus
453	342.5	16.6	433	2	Q80JH0	Q8jhd0	brachydanio	526	336	16.3	227	2	Q8IX14	Q8ix14	homo sapien
454	342.5	16.6	433	2	Q90YK1	Q90yk1	brachydanio	527	336	16.3	273	1	TRIT_SHEEP	Q9xsm2	ovis aries

528	336	16.3	280	2	Q64ID5	Q64id5 anthonomus	601	329.5	15.9	253	1	TRYD_DROME	P42276 drosophila
529	336	16.3	416	1	FA9_BOVIN	P00741 bos taurus	602	329.5	15.9	262	2	Q7ZID6	Q8w16 lepeophthei
530	336	16.3	485	1	Q7PRK0	P07k0 anopheles g	603	329.5	15.9	266	2	Q8WR10	Q8w10 paralithode
531	336	16.3	654	2	Q6GNF4	Q6gnf4 canis famli	604	329.5	15.9	269	1	EL2B_HUMAN	P08218 homo sapien
532	336	16.3	790	1	PLMN_PIG	P06967 sus scrofa	605	329.5	15.9	270	2	Q64ID1	Q64id1 anthonomus
533	336	16.3	1303	2	Q6GS84	Q6gs84 oikopleura	606	329.5	15.9	283	2	Q6UWY2	Q6uwY2 homo sapien
534	335.5	16.2	258	2	Q6ISM6	Q6ism6 homo sapien	607	329.5	15.9	320	2	Q7PEV6	Q7peV6 anopheles g
535	335.5	16.2	266	1	ELJ_BOVIN	Q28153 bos taurus	608	329.5	15.9	324	1	TEST_MOUSE	Q9jfy7 mus musculus
536	335.5	16.2	275	1	TRYT_PIG	Q9n2d1 sus scrofa	609	329.5	15.9	336	2	Q6QYD8	Q80yD8 mus musculus
537	335.5	16.2	558	2	Q86YM4	Q86ym4 homo sapien	610	329.5	15.9	578	2	Q6QO17	Q6qo17 bos taurus
538	335	16.2	216	2	Q9UD19	Q9ud19 homo sapien	611	329.5	15.9	1420	1	AP0A_WACMU	P14417 macaca mula
539	335	16.2	433	2	Q804X5	Q804x5 gallus gall	612	329	15.9	216	1	VSPP_LACMU	P84036 lacheisia mu
540	334.5	16.2	247	2	Q70500	Q70500 rattus norv	613	329	15.9	264	2	O08643	O08643 mus musculus
541	334.5	16.2	275	2	Q7Y862	Q7y862 equus cabal	614	329	15.9	279	2	Q99MS4	Q99mS4 mus musculus
542	334.5	16.2	537	2	Q9BYE1	Q9bye1 homo sapien	615	329	15.9	306	1	BSS4_MOUSE	Q9er10 mus musculus
543	334	16.2	234	2	Q15096	Q15096 homo sapien	616	329	15.9	572	2	Q8BIK6	Q8bik6 mus musculus
544	334	16.2	245	1	CTRA_BOVIN	P07666 bos taurus	617	329	15.9	575	2	Q7Q9W3	Q7q9W3 anopheles g
545	334	16.2	264	2	Q8QGF6	Q8qgf6 xenopus lae	618	329	15.9	681	2	Q7ZT70	Q7zT70 lampetra ja
546	334	16.2	320	2	Q7T0X2	Q7t0x2 xenopus lae	619	329	15.9	722	2	Q6NUF5	Q6nuF5 xenopus lae
547	333.5	16.1	253	2	Q8MKZ1	Q8mkz1 drosophila	620	328.5	15.9	239	2	Q8T4P3	Q8t4P3 lepeophthei
548	333.5	16.1	253	2	Q8SXZ4	Q8sxz4 drosophila	621	328.5	15.9	245	1	CTRB_GADMO	P80646 gadus morhu
549	333.5	16.1	263	1	CTRB_RAT	P07338 rattus norv	622	328.5	15.9	253	1	TRYG_DROME	P42277 drosophila
550	333.5	16.1	275	2	Q7PNE7	Q7pnf7 anopheles g	623	328.5	15.9	260	1	MCT1_RAT	P09650 rattus norv
551	333.5	16.1	290	1	PRZ7_HUMAN	Q9bqr3 homo sapien	624	328.5	15.9	261	2	Q8T4P1	Q8t4P1 lepeophthei
552	333.5	16.1	824	2	Q6ICC2	Q6icc2 homo sapien	625	328.5	15.9	275	2	Q86TMB	Q86cm8 homo sapien
553	333	16.1	285	1	FA9_CAYPO	P16295 cavia porce	626	328.5	15.9	276	2	Q86UA5	Q86ua5 homo sapien
554	333	16.1	355	2	Q7PEW0	Q7pew0 anopheles g	627	328.5	15.9	338	1	PLMN_HORSE	P80010 equus cabal
555	333	16.1	360	2	Q7PEV7	Q7peV7 anopheles g	628	328.5	15.9	432	2	Q7QK14	Q7qk14 anopheles g
556	333	16.1	391	2	Q9V3Z2	Q9v3z2 drosophila	629	328.5	15.9	524	2	Q7SKH8	Q7sxh8 brachydanio
557	333	16.1	910	1	PLMN_ERIEU	Q29485 erinaceus e	630	328.5	15.9	615	2	Q6GNK4	Q6gnK4 xenopus lae
558	332.5	16.1	247	2	Q35342	Q35342 mesocricetu	631	328.5	15.9	683	2	Q8MRH5	Q8mrh5 drosophila
559	332.5	16.1	254	2	Q8T637	Q8t637 aedes aegyp	632	328.5	15.9	786	1	STUB_DROME	Q05319 drosophila
560	332.5	16.1	260	2	Q8T4P6	Q8t4P6 lepeophthei	633	328.5	15.9	787	2	Q9VEY6	Q9vey6 drosophila
561	332.5	16.1	262	2	Q8T4P7	Q8t4P7 lepeophthei	634	328	15.9	226	1	COGS_UCAPU	P00771 uca pugilat
562	332.5	16.1	263	2	Q7Z1D5	Q7z1d5 lepeophthei	635	328	15.9	270	2	Q27824	Q27824 uca pugilat
563	332.5	16.1	264	2	Q7Y8S9	Q7y8s9 lepeophthei	636	328	15.9	328	2	Q6BEA2	Q6bea2 rattus norv
564	332.5	16.1	307	2	Q7TMD0	Q7tmd0 mus musculus	637	328	15.9	452	1	FAS_CANFA	F19540 canis famli
565	332.5	16.1	490	1	TMS2_MOUSE	Q9jfiq8 mus musculus	638	328	15.9	699	1	CRAR_HUMAN	P48740 h complemen
566	332.5	16.1	638	1	KAL_RAT	P14272 rattus norv	639	328	15.9	767	2	Q9DGR2	Q9dgr2 xenopus lae
567	332.5	16.1	810	1	PLMN_WACMU	P12545 macaca mula	640	327.5	15.9	247	1	MCT1_MACFA	P56435 macaca fasc
568	332	16.1	247	2	Q70T74	Q70t74 equus cabal	641	327.5	15.9	263	2	Q9TV16	Q9tv16 penaeus van
569	332	16.1	251	2	Q7Q9W2	Q7q9W2 anopheles g	642	327.5	15.9	266	2	Q27761	Q27761 penaeus van
570	332	16.1	258	2	Q97399	Q97399 phaeton coc	643	327.5	15.9	269	2	Q96QV5	Q96qv5 homo sapien
571	332	16.1	266	2	Q92077	Q92077 gadus morhu	644	327.5	15.9	269	2	Q6ISM5	Q6ism5 homo sapien
572	332	16.1	277	2	Q8SQ44	Q8sq44 sus scrofa	645	327.5	15.9	269	2	Q6GN82	Q6gn82 xenopus lae
573	332	16.1	355	2	Q9NFM1	Q9nfu1 anopheles g	646	327.5	15.9	277	2	Q80WM7	Q80wm7 mus musculus
574	332	16.1	364	2	Q917V4	Q9i7v4 drosophila	647	327	15.8	259	1	DEF3_DERFA	P49275 dermatophag
575	331.5	16.0	250	2	Q8T4P4	Q8t4P4 lepeophthei	648	327	15.8	263	2	Q7SY84	Q7sy84 xenopus lae
576	331.5	16.0	254	2	Q8MMK9	Q8mmk9 aedes aegyp	649	327	15.8	466	2	Q6SA95	Q6sa95 felis silve
577	331.5	16.0	256	1	TRYA_DROME	P04814 drosophila	650	327	15.8	600	2	Q7ZTR2	Q7ztr2 xenopus lae
578	331.5	16.0	260	2	Q8T4P5	Q8t4P5 lepeophthei	651	326.5	15.8	248	1	GRAC_MOUSE	P08882 mus musculus
579	331.5	16.0	263	2	Q9PWQ6	Q9pwq6 gadus morhu	652	326.5	15.8	263	2	Q6GNF7	Q6gnf7 xenopus lae
580	331.5	16.0	264	2	Q6GPY5	Q6gpy5 xenopus lae	653	326.5	15.8	266	1	EL1_PIG	EL1 pig
581	331.5	16.0	275	1	TRY3_ANOGA	P35037 anopheles g	654	326.5	15.8	266	2	Q91X79	Q91x79 mus musculus
582	331.5	16.0	679	2	Q96PQ8	Q96pq8 homo sapien	655	326.5	15.8	369	2	Q7QKL1	Q7qkl1 anopheles g
583	331	16.0	622	1	THRB_HUMAN	P00734 homo sapien	656	326.5	15.8	490	2	Q7TNO4	Q7tn04 mus musculus
584	331	16.0	722	2	Q8AW90	Q8aw90 lampetra ja	657	326	15.8	248	1	GR21_RAT	GR21 rat
585	331	16.0	722	2	Q9PSZ5	Q9psz5 lampetra ja	658	326	15.8	268	2	O46151	O46151 pacifastacu
586	331	16.0	722	2	Q9PSZ5	Q9psz5 lampetra ja	659	326	15.8	271	1	CTR2_PENVA	P36178 penaeus van
587	330.5	16.0	237	2	Q29464	Q29464 bos taurus	660	326	15.8	329	2	Q7PEV8	Q7peV8 anopheles g
588	330.5	16.0	247	1	MCT1_HUMAN	P23946 homo sapien	661	325.5	15.8	259	2	Q8IRE0	Q8ire0 drosophila
589	330.5	16.0	256	1	TRYA_DROER	P54624 drosophila	662	325.5	15.8	261	1	DER3_DERPT	P39675 dermatophag
590	330.5	16.0	269	2	Q6TSP9	Q6tsp9 homo sapien	663	325.5	15.8	492	1	FA10_BOVIN	P00743 bos taurus
591	330.5	16.0	560	2	Q14520	Q14520 homo sapien	664	325.5	15.8	891	2	Q9VV38	Q9vv38 drosophila
592	330.5	16.0	638	2	Q8R0P5	Q8r0P5 mus musculus	665	324.5	15.7	146	2	Q9DDE1	Q9dde1 brachydanio
593	330	16.0	236	2	Q7SIG3	Q7sig3 salmo salar	666	324.5	15.7	228	2	Q7Q153	Q7q153 anopheles g
594	330	16.0	253	2	Q9V5Y3	Q9v5Y3 drosophila	667	324.5	15.7	258	2	Q7YRZ7	Q7yrz7 bos taurus
595	330	16.0	266	2	Q81916	Q8i916 blomia trop	668	324.5	15.7	263	2	Q7PUB9	Q7pub9 anopheles g
596	330	16.0	282	1	FA9_RAT	P16296 rattus norv	669	324.5	15.7	275	1	TRYA_HUMAN	P15157 homo sapien
597	330	16.0	364	2	Q9N8S9	Q9nas9 anopheles g	670	324.5	15.7	312	2	Q7M755	Q7m755 mus musculus
598	330	16.0	365	2	Q7Q1D1	Q7q1d1 anopheles g	671	324.5	15.7	466	1	FA7_HUMAN	P08709 homo sapien
599	330	16.0	4548	1	AP0A_HUMAN	P08519 homo sapien	672	324	15.7	253	1	TRYB_DROME	P35004 drosophila
600	329.5	15.9	248	2	Q8T4P2	Q8t4P2 lepeophthei	673	324	15.7	257	1	GRAM_HUMAN	P51124 homo sapien

820	310.5	15.0	371	2	Q8MRV3	Q8mry3 drosophila	893	304.5	14.7	271	2	Q7Q820	Q7q820 anopheles g
821	310.5	15.0	473	2	Q7P6V3	Q7p6v3 anopheles g	894	304.5	14.7	384	2	Q9XY63	Q9xy63 ctenocephal
822	310.5	15.0	1374	2	Q9VSU0	Q9vsu0 drosophila	895	304.5	14.7	492	1	TMS2 HUMAN	O15393 homo sapien
823	310.5	15.0	1449	2	Q9ULI2	Q9uli2 drosophila	896	304.5	14.7	492	2	Q96T73	Q96t73 homo sapien
824	310.5	15.0	1450	2	O8IQB8	O8iqb8 drosophila	897	304.5	14.7	685	2	Q92338	Q92338 mus musculu
825	310.5	15.0	1462	2	Q9ULI3	Q9uli3 drosophila	898	304	14.7	268	1	CLCR_HUMAN	Q99895 homo sapien
826	310.5	15.0	2382	2	Q9BII19	Q9bii19 drosophila	899	304	14.7	375	2	Q8I7W8	Q8i7w8 dermacentor
827	310.5	15.0	2409	2	Q96G06	Q96g06 drosophila	900	304	14.7	393	2	Q6RX66	Q6rx66 armigeres s
828	310.5	15.0	2786	2	Q9VSU2	Q9vsu2 drosophila	901	304	14.7	400	2	Q9VCJ8	Q9vcj8 drosophila
829	310	15.0	275	1	FA9 RABIT	P16292 oryctolagus	902	304	14.7	423	2	Q8BM10	Q8bmi10 mus musculu
830	310	15.0	315	2	O8IER3	O8ier3 drosophila	903	304	14.7	449	2	Q9VDU8	Q9vdu8 drosophila
831	310	15.0	327	2	Q7Q530	Q7q530 anopheles g	904	304	14.7	543	2	Q9BU99	Q9bu99 homo sapien
832	310	15.0	532	2	Q7P6T3	Q7p6t3 anopheles g	905	304	14.7	562	1	TPA_HUMAN	P00750 homo sapien
833	310	15.0	1111	2	Q8OYN4	Q8oyn4 rattus norv	906	304	14.7	589	2	Q6PJA5	Q6pia5 homo sapien
834	310	15.0	1379	2	Q9V4N6	Q9v4n6 drosophila	907	303.5	14.7	240	2	Q7SYQ8	Q7syq8 xenopus lae
835	310	15.0	1397	2	Q7KQ9	Q7kq9 drosophila	908	303.5	14.7	244	1	MCT2_MOUSE	P15119 mus musculu
836	309.5	15.0	246	2	Q9EP90	Q9ep90 mus musculu	909	303.5	14.7	246	1	MCT4_MOUSE	P97592 rattus norv
837	308.5	15.0	265	2	Q9VVT3	Q9vvt3 drosophila	910	303.5	14.7	259	2	Q6JPG5	Q6jpg5 neodiprion
838	309.5	15.0	284	2	Q7Q493	Q7q493 anopheles g	911	303.5	14.7	309	2	Q27083	Q27083 tachyples
839	309.5	15.0	468	2	Q9U0G3	Q9u0g3 pacifastacu	912	303.5	14.7	352	2	Q6UWB4	Q6uwb4 homo sapien
840	309.5	15.0	471	2	Q8O4X6	Q8o4x6 gallus gall	913	303.5	14.7	603	1	CFAI_MOUSE	Q61129 mus musculu
841	309.5	15.0	698	2	Q6GPF9	Q6gpf9 xenopus lae	914	303.5	14.7	761	2	Q99JC8	Q99jc8 rattus norv
842	309.5	15.0	868	2	Q9Y1V3	Q9y1v3 polyandroca	915	303	14.7	255	1	CATG_HUMAN	P08311 homo sapien
843	309	15.0	285	2	Q8CG42	Q8cg42 rattus norv	916	302.5	14.7	119	2	Q9NR68	Q9nr68 homo sapien
844	308.5	14.9	240	2	Q6IE06	Q6ie06 rattus norv	917	302.5	14.6	223	2	Q9VBV4	Q9vby4 drosophila
845	308.5	14.9	246	1	MCT9_MOUSE	O35164 mus musculu	918	302.5	14.6	273	1	TRY6_ANOGA	P35040 anopheles g
846	308.5	14.9	260	2	Q6VP06	Q6vp06 sarcopites s	919	302.5	14.6	394	2	P91817	P91817 tachyples
847	308.5	14.9	272	2	Q9XYV6	Q9xyv6 rhzyopertha	920	302.5	14.6	394	2	Q91817	Q92319 mus musculu
848	308.5	14.9	317	1	BSS4_HUMAN	Q9gzn4 homo sapien	921	302	14.6	1113	1	CORI_MOUSE	Q92319 mus musculu
849	308.5	14.9	334	2	Q6UXE0	Q6uxed0 homo sapien	922	302	14.6	247	2	Q6T376	Q6t376 eisenia foe
850	308.5	14.9	1004	2	P79953	P79953 drosophila	923	302	14.6	255	1	TRY4_LUCCU	P35044 lucilia cup
851	308	14.9	125	2	Q8O4G0	Q8o4g0 sphoeroides	924	302	14.6	268	2	Q9W7Q2	Q9w7q2 paralichthy
852	308	14.9	301	2	Q8I9P4	Q8i9p4 aurelia aur	925	302	14.6	269	2	Q7PWL7	Q7pwl7 anopheles g
853	308	14.9	321	2	Q6MZL2	Q6mzl2 homo sapien	926	302	14.6	280	2	Q8WR11	Q8wr11 paralithode
854	308	14.9	335	2	Q86PB3	Q86pb3 drosophila	927	302	14.6	281	2	Q76898	Q76898 drosophila
855	308	14.9	377	2	Q9VB68	Q9vnb68 drosophila	928	302	14.6	284	2	Q8IRX5	Q8irx5 drosophila
856	308	14.9	408	2	Q8MR95	Q8mr95 drosophila	929	302	14.6	291	2	Q8IQ89	Q8iq89 drosophila
857	308	14.9	417	1	HEPS_HUMAN	P05981 homo sapien	930	302	14.6	394	1	URTG_DESRO	P49150 desmodus ro
858	307.5	14.9	255	2	Q7PFI6	Q7pfi6 anopheles g	931	302	14.6	424	2	Q9VA88	Q9va88 drosophila
859	307.5	14.9	676	2	Q6DUJ6	Q6duj6 cyprinus ca	932	301.5	14.6	477	1	URT2_DESRO	P15638 desmodus ro
860	307	14.9	135	2	Q62284	Q62284 mus musculu	933	301.5	14.6	241	2	Q8BW11	Q8bw11 m mus muscu
861	307	14.9	250	2	Q17036	Q17036 anopheles g	934	301.5	14.6	257	2	O19023	O19023 macaca mula
862	307	14.9	259	1	CTRI_ANOGA	Q17036 anopheles g	935	301.5	14.6	273	2	Q7JYN3	Q7jyn3 drosophila
863	307	14.9	318	2	Q7Q9W4	Q7q9w4 anopheles g	936	301.5	14.6	433	2	Q8MHY7	Q8mhy7 oryctolagus
864	307	14.9	726	2	Q7OBP4	Q7obp4 anopheles g	937	301.5	14.6	433	2	Q8MIL0	Q8mil0 oryctolagus
865	307	14.9	728	2	Q96RS4	Q96rs4 anopheles g	938	301.5	14.6	505	2	Q7QCV2	Q7qcv2 anopheles g
866	306.5	14.8	308	2	Q9W454	Q9w454 drosophila	939	301	14.6	698	2	Q9PU71	Q9pu71 xenopus lae
867	306.5	14.8	362	2	Q9W453	Q9w453 drosophila	940	301	14.6	255	2	O34289	O34289 salvelinus
868	306.5	14.8	365	2	Q7QGL1	Q7qgl1 anopheles g	941	301	14.6	268	2	Q7P030	Q7p030 anopheles g
869	306.5	14.8	375	1	PCE TACTR	P21902 tachyples	942	301	14.6	279	2	Q7PX39	Q7px39 anopheles g
870	306.5	14.8	418	2	Q8SZK2	Q8szk2 drosophila	943	301	14.6	279	2	Q7TNX3	Q7tnx3 mus musculu
871	306.5	14.8	685	2	Q91WP0	Q91wp0 mus musculu	944	301	14.6	283	2	Q9SV22	Q9sv22 lumbricus b
872	306	14.8	162	2	Q6UEM2	Q6uem2 homo sapien	945	301	14.6	417	2	Q8VHK8	Q8vbk8 mus musculu
873	306	14.8	247	2	Q8NID2	Q8nid2 homo sapien	946	301	14.6	417	2	Q8VDV1	Q8vdl1 mus musculu
874	306	14.8	266	2	Q6AZC0	Q6azc0 brachydanio	947	301	14.6	431	1	URTB_DESRO	P98121 desmodus ro
875	306	14.8	433	2	Q9QWF2	Q9qwf2 rattus sp.	948	300.5	14.5	442	1	URTK_PIG	P04185 sus scrofa
876	305.5	14.8	228	2	Q9XY49	Q9xy49 ctenocephal	949	300.5	14.5	239	2	Q7T2H1	Q7t2h1 xenopus lae
877	305.5	14.8	246	1	MCT2_SHEEP	P79204 ovis aries	950	300.5	14.5	276	2	P91894	P91894 arenicola m
878	305.5	14.8	246	2	Q91VB1	Q91vb1 mus musculu	951	300.5	14.5	278	2	Q68FN6	Q68fn6 brachydanio
879	305.5	14.8	254	1	HYPA_HYPLI	P35587 hypoderma l	952	300.5	14.5	314	2	Q8RUT2	Q8rut2 mus musculu
880	305.5	14.8	274	2	Q6GNF0	Q6gnf0 xenopus lae	953	300.5	14.5	318	2	Q8OUR4	Q8our4 mus musculu
881	305.5	14.8	278	2	Q7Q492	Q7q492 anopheles g	954	300.5	14.5	369	2	Q6AXZ6	Q6axz6 rattus norv
882	305.5	14.8	383	2	Q77102	Q77102 manduca sex	955	300.5	14.5	386	2	Q81924	Q81924 bombyx mori
883	305.5	14.8	418	2	Q9VA87	Q9va87 drosophila	956	300	14.5	562	2	Q8SQ23	Q8sq23 sus scrofa
884	305.5	14.8	435	1	SNAK_DROME	P05049 drosophila	957	300	14.5	245	1	GILX_HELHO	P43685 heloderma h
885	305.5	14.8	441	2	Q8O4X2	Q8o4x2 fugu rubrip	958	300	14.5	417	2	Q8VHJ4	Q8vhj4 rattus norv
886	305	14.8	247	1	GRAB_HUMAN	P10144 h granzyme	959	299.5	14.5	433	1	UROK_MOUSE	P08869 mus musculu
887	305	14.8	281	2	Q67BC3	Q67bc3 homo sapien	960	299.5	14.5	241	2	Q63637	Q63637 rattus norv
888	305	14.8	307	2	Q64ID2	Q64id2 anthonomus	961	299.5	14.5	246	1	MCTX_MOUSE	Q00356 mus musculu
889	305	14.8	391	2	Q7P6J5	Q7p6j5 anopheles g	962	299.5	14.5	254	2	Q6DBS8	Q6db88 brachydanio
890	305	14.8	395	2	Q9BZW1	Q9bzw1 homo sapien	963	299.5	14.5	258	1	CTR2_ANOGA	Q17025 anopheles g
891	305	14.8	733	2	Q9VTX9	Q9vtx9 drosophila	964	299.5	14.5	272	2	Q7Q9W5	Q7q9w5 anopheles g
892	304.5	14.7	258	2	Q9XY53	Q9xy53 ctenocephal	965	299.5	14.5	282	2	Q7PT16	Q7pt16 anopheles g
										325	2	O15944	O15944 sarcophaga

966	299.5	14.5	372	2	Q9W2C8	Q9W2C8 drosophila	1039	293	14.2	246	2	Q9R2C8	Q9R2C8 rattus norv
967	299.5	14.5	615	2	Q8IZZ5	Q8izz5 homo sapien	1040	293	14.2	247	1	MCT3 RAT	P50339 rattus norv
968	299.5	14.5	974	2	Q9W0D8	Q9W0d8 bufo japoni	1041	293	14.2	247	1	SER1_DROME	P17205 drosophila
969	299.5	14.5	1069	1	ENTK_MOUSE	P97435 mus musculu	1042	293	14.2	268	2	Q16900	Q16900 aedes aegyp
970	299	14.5	256	2	Q6VIQ1	Q6viq1 verticilliu	1043	293	14.2	268	2	Q8NUR8	Q8n0r8 aedes aegyp
971	299	14.5	421	1	ACRO_HUMAN	P10323 homo sapien	1044	293	14.2	277	2	Q9VFN8	Q9vfn8 drosophila
972	299	14.5	219	2	Q8T3A3	Q8t3a3 ciona intes	1045	293	14.2	278	2	Q8MQQ2	Q8mq02 drosophila
973	298.5	14.4	535	2	Q81004	Q91004 gecko gecko	1046	293	14.2	301	2	Q7Q6U2	Q7q6u2 anopheles g
974	298.5	14.4	248	2	Q9VQ98	Q9vq98 drosophila	1047	293	14.2	427	2	Q6Y2X4	Q6y2x4 manduca sex
975	298.5	14.4	249	1	MCT1_CANFA	P21842 canis famil	1048	293	14.2	433	1	UROK_PAPCY	P16227 papio cynoc
976	298.5	14.4	350	2	Q7QKY0	Q7qky0 anopheles g	1049	293	14.2	777	2	Q8CAN9	Q8can9 mus musculu
977	298.5	14.4	407	1	FAT7_BOVIN	P22457 bos taurus	1050	293	14.2	855	1	STI14_MOUSE	P36677 mus musculu
978	298.5	14.4	433	2	Q8T3A2	Q8t3a2 ciona intes	1051	292.5	14.2	235	2	Q90387	Q90387 cynops pyrr
979	298	14.4	235	2	Q28731	Q28731 oryctolagus	1052	292.5	14.2	236	2	Q9Z1H1	Q9z1h1 mus musculu
980	298	14.4	255	2	Q18435	Q18435 helicoverpa	1053	292.5	14.2	317	2	Q8K4D1	Q8k4d1 mus musculu
981	298	14.4	268	2	Q8T4T4	Q8t4t4 aedes aegyp	1054	292.5	14.2	390	2	Q8MP08	Q8mp08 bombyx mori
982	298	14.4	348	2	Q86WS5	Q86ws5 homo sapien	1055	292.5	14.2	469	2	Q9GMD9	Q9gmd9 ornithorhyn
983	298	14.4	421	2	Q61CK2	Q61ck2 homo sapien	1056	292	14.1	257	2	Q8T639	Q8t639 aedes aegyp
984	297.5	14.4	254	2	Q76520	Q76520 stomoxys ca	1057	292	14.1	268	1	CLCR RAT	P50091 rattus norv
985	297.5	14.4	256	2	Q6WJY6	Q6wjy6 bdellovibri	1058	292	14.1	270	2	Q8T4A8	Q8t4a8 drosophila
986	297.5	14.4	269	2	Q6NZF9	Q6azf9 xenopus lae	1059	292	14.1	276	2	Q9Y398	Q9y398 phaedon coc
987	297.5	14.4	277	2	Q8IQ10	Q8iq10 drosophila	1060	292	14.1	332	2	Q8YSX8	Q8ysx8 drosophila
988	297.5	14.4	293	2	Q7Q8F9	Q7q8f9 anopheles g	1061	291.5	14.1	216	1	CTR2_VESOR	P00768 vespa orien
989	297.5	14.4	408	2	Q9VM19	Q9vm19 drosophila	1062	291.5	14.1	238	2	Q9Z1D3	Q9z1d3 rattus norv
990	297.5	14.4	472	2	Q7Q182	Q7q182 anopheles g	1063	291.5	14.1	255	2	Q9NBC9	Q9nbc9 glossina mo
991	297.5	14.4	486	2	Q7PX74	Q7px74 anopheles g	1064	291.5	14.1	264	2	Q7Q290	Q7q290 anopheles g
992	297.5	14.4	616	2	Q8Y507	Q8y507 sus scrofa	1065	291.5	14.1	270	2	Q7Q5A6	Q7q5a6 anopheles g
993	297	14.4	237	1	TRYP_ASTFL	P00765 astacus flu	1066	291.5	14.1	678	2	Q9JJS8	Q9jj58 rattus norv
994	297	14.4	247	1	MCT5_MOUSE	P21844 mus musculu	1067	291	14.1	239	2	Q6LCU4	Q6lcu4 lumbricus r
995	297	14.4	256	2	Q9XY51	Q9xy51 ctenocephal	1068	291	14.1	271	2	Q54213	Q54213 streptomyce
996	297	14.4	268	2	Q9BIG0	Q9big0 aedes aegyp	1069	291	14.1	410	2	Q7QJ44	Q7qj44 anopheles g
997	297	14.4	454	1	TWS3_HUMAN	P57727 homo sapien	1070	291	14.1	415	1	ACRO_PIG	P08001 sus scrofa
998	297	14.4	477	1	URT1_DESRO	P98119 desmodus ro	1071	291	14.1	415	1	Q29015	Q29015 sus sp. pre
999	296.5	14.4	248	1	GRAP_MOUSE	P08861 mus musculu	1072	291	14.1	436	1	HEPS_MOUSE	Q35453 mus musculu
1000	296.5	14.4	270	1	ELJ3_HUMAN	P08861 homo sapien	1073	291	14.1	730	2	Q5Q1Q8	Q5q1q8 gallus gall
1001	296.5	14.4	272	2	Q9V5X6	Q9v5x6 drosophila	1074	290.5	14.0	483	2	Q7PKJ7	Q7pkj7 anopheles g
1002	296.5	14.4	279	2	Q9QZ74	Q9qz74 rattus norv	1075	290	14.0	149	2	Q6DTY8	Q6dty8 hypophthalm
1003	296.5	14.4	283	2	Q25394	Q25394 lumbricus r	1076	290	14.0	256	1	HYPB_HYPLI	P35588 hypoderma l
1004	296.5	14.4	283	2	Q8ITU7	Q8itu7 lumbricus r	1077	290	14.0	257	2	Q72440	Q72440 aedes aegyp
1005	296.5	14.4	581	2	Q96015	Q96015 drosophila	1078	290	14.0	390	2	Q81927	Q81927 hyphantria
1006	296.5	14.4	1047	2	Q9VZH2	Q9vzh2 drosophila	1079	290	14.0	472	2	Q61GB2	Q61gb2 drosophila
1007	296	14.3	265	2	Q74696	Q74696 phaenocphaer	1080	289.5	14.0	246	2	Q9BLI7	Q9bli7 lumbricus r
1008	296	14.3	553	2	Q6P719	Q6p719 xenopus lae	1081	289.5	14.0	248	1	GRAG_MOUSE	P13366 mus musculu
1009	295.5	14.3	239	2	Q9QME0	Q9qme0 ornithorhyn	1082	289.5	14.0	257	2	Q6R560	Q6r560 ostrinia nu
1010	295.5	14.3	239	2	Q91218	Q91218 oncorhynch	1083	289.5	14.0	339	2	Q9QX91	Q9qx91 rattus norv
1011	295.5	14.3	270	2	Q9VRS4	Q9vrs4 drosophila	1084	289.5	14.0	366	2	Q9QX85	Q9qx85 rattus norv
1012	295.5	14.3	453	2	Q6ZWC3	Q6zmc3 homo sapien	1085	289.5	14.0	541	2	Q9QX90	Q9qx90 rattus norv
1013	295	14.3	260	2	Q9V6P6	Q9v6p6 drosophila	1086	289.5	14.0	623	2	Q9JJP3	Q9jjp3 rattus norv
1014	295	14.3	267	2	Q6DGM4	Q6dgm4 brachydantio	1087	289.5	14.0	643	2	Q9QX84	Q9qx84 rattus norv
1015	295	14.3	268	2	Q8T4T5	Q8t4t5 aedes aegyp	1088	289	14.0	278	2	Q7RTY3	Q7rty3 homo sapien
1016	295	14.3	269	2	Q95KW7	Q95kw7 bos taurus	1089	289	14.0	278	2	Q7QHS0	Q7qhs0 anopheles g
1017	295	14.3	358	2	Q45029	Q45029 drosophila	1090	289	14.0	376	1	FA10_TROCA	P81428 tropidechis
1018	295	14.3	681	2	Q7Q554	Q7q554 anopheles g	1091	289	14.0	377	2	P79343	P79343 bos taurus
1019	295	14.3	688	2	Q868H6	Q868h6 branchiost	1092	289	14.0	441	2	Q9XXV0	Q9xxv0 bombyx mori
1020	294.5	14.3	244	2	Q816N3	Q816n3 eisenia foe	1093	289	14.0	583	1	CFAL_HUMAN	P05156 homo sapien
1021	294.5	14.3	413	2	Q8T9T2	Q8t9t2 aedes aegyp	1094	288.5	14.0	255	2	Q9XY62	Q9xy62 ctenocephal
1022	294.5	14.3	575	2	Q81RB8	Q81rb8 drosophila	1095	288.5	14.0	438	2	Q6ZWK6	Q6zwk6 homo sapien
1023	294	14.2	247	2	Q61E57	Q61e57 rattus norv	1096	288.5	14.0	442	2	Q804X1	Q804x1 fugu rubrip
1024	294	14.2	259	2	Q9X161	Q9xy61 ctenocephal	1097	288.5	14.0	1047	2	Q24019	Q24019 drosophila
1025	294	14.2	257	2	Q9VHF8	Q9vnh8 drosophila	1098	288	13.9	257	2	Q9NB49	Q9nb49 aedes aegyp
1026	294	14.2	271	2	Q9GTK2	Q9gtk2 culex quinq	1099	288	13.9	261	2	Q8IRE1	Q8ire1 drosophila
1027	294	14.2	293	2	Q725A4	Q725a4 homo sapien	1100	288	13.9	405	2	Q9MZM7	Q9mzm7 anopheles g
1028	294	14.2	303	2	Q76900	Q76900 drosophila	1101	288	13.9	405	2	Q7PGY0	Q7pgy0 anopheles t
1029	293.5	14.2	246	2	Q61E10	Q61e10 rattus norv	1102	287.5	13.9	234	2	Q90244	Q90244 acipenser t
1030	293.5	14.2	256	2	Q9XY11	Q9xyy1 rhyzopertha	1103	287.5	13.9	244	2	Q6T375	Q6t375 eisenia foe
1031	293.5	14.2	257	2	Q7Z0G1	Q7z0g1 phlebotomus	1104	287.5	13.9	249	2	Q7KR00	Q7krd0 drosophila
1032	293.5	14.2	302	2	Q8SYZ7	Q8syz7 drosophila	1105	287.5	13.9	382	2	Q76HL1	Q76hl1 mus musculu
1033	293.5	14.2	302	2	Q9W586	Q9w586 drosophila	1106	287.5	13.9	603	1	FA12_CAVPO	Q04962 cavia porce
1034	293.5	14.2	317	2	Q8K4I7	Q8k4i7 mus musculu	1107	287.5	13.9	845	2	Q63ZQ6	Q63zq6 xenopus lae
1035	293.5	14.2	425	2	Q7P285	Q7p285 anopheles g	1108	287	13.9	204	2	Q6S9W8	Q6s9w8 homo sapien
1036	293.5	14.2	431	1	UROK_HUMAN	P00749 homo sapien	1109	287	13.9	244	2	Q6LAM0	Q6lam0 homo sapien
1037	293.5	14.2	475	2	Q804W9	Q804w9 fugu rubrip	1110	287	13.9	256	2	Q25081	Q25081 hypoderma l
1038	293.5	14.2	845	2	Q6GR54	Q6gr54 xenopus lae	1111	287	13.9	268	2	Q8T4T3	Q8t4t3 aedes aegyp

1112	287	13.9	273	2	Q9VEM5	Q9vem5 drosophila	1185	280	13.6	248	2	Q920S1	Q920s1 mus musculus
1113	287	13.9	291	2	Q8MLC5	Q8mlc5 drosophila	1186	280	13.6	254	1	TRYP_SARBU	P51388 sarcophaga
1114	287	13.9	416	2	Q86T26	Q86t26 homo sapien	1187	280	13.6	267	2	Q8SYK8	Q8syk8 drosophila
1115	287	13.9	422	1	DE51_HUMAN	Q9ul52 homo sapien	1188	280	13.6	271	2	Q9V4W5	Q9v4w5 drosophila
1116	287	13.9	423	1	Q6UW31	Q6uw31 homo sapien	1189	280	13.6	282	2	Q25395	Q25395 lumbricus r
1117	287	13.9	481	1	FA10_MOUSE	Q88947 mus musculus	1190	280	13.6	336	2	Q7RTY5	Q7rtty5 homo sapien
1118	287	13.9	581	2	Q819Z5	Q81925 hyphantria	1191	280	13.6	420	2	Q7Q235	Q7q235 anopheles g
1119	287	13.9	667	2	Q9BUM1	Q9bjm1 trichnella	1192	280	13.6	420	2	Q61E14	Q61e14 rattus norv
1120	286.5	13.9	210	1	CTR2_VESCR	P07669 vespa crabr	1193	279.5	13.5	330	2	Q61E62	Q61e62 rattus norv
1121	286.5	13.9	220	2	Q7QM61	Q7qm61 anopheles g	1194	279.5	13.5	330	2	Q9FVY3	Q9fvy3 cyprinus ca
1122	286.5	13.9	376	2	Q7PTP7	Q7ptp7 anopheles g	1195	279	13.5	242	2	Q6T374	Q6t374 eisenia foe
1123	286	13.8	235	2	Q6XGZ4	Q6xgz4 homo sapien	1196	279	13.5	267	2	Q9VA67	Q9va67 drosophila
1124	286	13.8	254	1	CTPL_HALRU	P35003 halicoris ru	1197	279	13.5	280	1	TRYZ_DROME	P42280 drosophila
1125	286	13.8	272	2	Q7O483	Q7q483 anopheles g	1198	279	13.5	280	2	Q9V5X8	Q9v5x8 drosophila
1126	286	13.8	398	2	Q8MKP4	Q8mkp4 drosophila	1199	279	13.5	385	2	Q25101	Q25101 herdmania m
1127	286	13.8	416	2	Q8BZ13	Q8bz13 mus musculus	1200	279	13.5	694	2	Q8R099	Q8r099 mus musculus
1128	286	13.8	416	2	Q8BZ30	Q8bz30 mus musculus	1201	279	13.5	694	2	Q6P6T1	Q6p6t1 rattus norv
1129	286	13.8	443	2	Q8JHC9	Q8jhc9 brachydanio	1202	279	13.5	717	2	Q8AXR1	Q8axr1 xenopus lae
1130	285.5	13.8	175	2	Q6FLJ9	Q6flj9 squilla ora	1203	279	13.5	721	2	Q7ZT69	Q7zt69 lampetra ja
1131	285.5	13.8	248	1	MCT8_RAT	P97594 rattus norv	1204	278.5	13.5	269	2	Q7PWT2	Q7pwt2 anopheles g
1132	285.5	13.8	270	1	EL3A_HUMAN	P09093 homo sapien	1205	278.5	13.5	326	2	Q7ZZ80	Q7zz80 brachydanio
1133	285.5	13.8	270	2	Q96QL8	Q96ql8 homo sapien	1206	278.5	13.5	432	1	UROK_RAT	P29598 rattus norv
1134	285.5	13.8	270	2	Q91039	Q91039 gadus morhu	1207	278.5	13.5	593	1	FA12_BOVIN	P98140 bos taurus
1135	285.5	13.8	289	2	Q8MR67	Q8mr67 drosophila	1208	278	13.5	239	2	Q9NKC5	Q9nkc5 drosophila
1136	285.5	13.8	290	2	Q9VRT2	Q9vrt2 drosophila	1209	278	13.5	474	2	Q7PZH7	Q7pzh7 anopheles g
1137	285	13.8	424	2	Q6R558	Q6r558 ostrinia nu	1210	278	13.5	488	1	FA10_HUMAN	P00742 homo sapien
1138	285	13.8	470	2	Q8T3A1	Q8t3a1 ciona intes	1211	278	13.5	501	2	Q7QCVO	Q7qcvo anopheles g
1139	285	13.8	688	2	Q868H4	Q868h4 branchiosteo	1212	277.5	13.4	245	2	Q8BLI8	Q8bli8 lumbricus r
1140	284.5	13.8	172	2	Q6T776	Q6t776 homo sapien	1213	277.5	13.4	266	2	Q24091	Q24091 drosophila
1141	284.5	13.8	245	2	Q6DKQ3	Q6dkq3 eisenia foe	1214	277.5	13.4	271	2	Q76519	Q76519 stomoxys ca
1142	284.5	13.8	253	1	CAC3_BOVIN	P05805 bos taurus	1215	277.5	13.4	272	2	Q82XG0	Q82xg0 streptomyce
1143	284.5	13.8	564	2	Q7RTZ1	Q7rtz1 homo sapien	1216	277.5	13.4	845	2	Q9DGR1	Q9dgr1 xenopus lae
1144	284.5	13.8	686	2	Q6Q1Q9	Q6qlq9 gallus gall	1217	277	13.4	252	2	Q76498	Q76498 diaprepes a
1145	284	13.7	235	2	Q6B4R4	Q6b4r4 bos taurus	1218	277	13.4	254	1	PRN3_MOUSE	Q61096 mus musculus
1146	284	13.7	243	2	O01309	O01309 botryllus s	1219	277	13.4	1629	2	Q9V5I3	Q9v5i3 drosophila
1147	284	13.7	247	1	TRYP_SIMVI	P35048 simulium vi	1220	277	13.4	1674	2	Q8SY35	Q8sy35 drosophila
1148	284	13.7	257	2	Q86FL8	Q86fl8 aedes aegyp	1221	276.5	13.4	257	2	Q97099	Q97099 anopheles d
1149	283.5	13.7	268	2	Q9XY56	Q9xy56 ctenocephal	1222	276.5	13.4	262	2	Q9V5J2	Q9v5j2 drosophila
1150	283.5	13.7	707	2	Q8QGV0	Q8qgv0 cyprinus ca	1223	276	13.4	257	2	Q818E4	Q818e4 ochlerotatu
1151	283	13.7	258	2	Q9GME1	Q9gme1 ornithorhyn	1224	276	13.4	271	1	S24D_ANOGA	Q17004 anopheles g
1152	283	13.7	273	2	Q9VKA8	Q9vka8 drosophila	1225	276	13.4	300	2	Q7Q6U1	Q7q6u1 anopheles g
1153	283	13.7	320	2	Q7QKL3	Q7qkl3 anopheles g	1226	276	13.4	302	2	Q9VCJ0	Q9vcj0 drosophila
1154	283	13.7	424	2	Q6R559	Q6r559 ostrinia nu	1227	276	13.4	376	1	FA10_HOPST	P83370 hoptocephal
1155	283	13.7	490	1	FA10_RABIT	O19045 oryctolagus	1228	275.5	13.3	246	2	Q6DKQ2	Q6dkq2 eisenia foe
1156	282.5	13.7	245	2	Q7BPJ0	Q7bpj0 anopheles g	1229	275.5	13.3	256	2	Q818E5	Q818e5 ochlerotatu
1157	282.5	13.7	246	2	Q817P0	Q817p0 lumbricus b	1230	275.5	13.3	258	2	Q6NLM5	Q6nlm5 drosophila
1158	282.5	13.7	267	2	Q9VLF5	Q9vlf5 drosophila	1231	275.5	13.3	262	2	Q9V5X9	Q9v5x9 drosophila
1159	282.5	13.7	269	2	Q9V929	Q9v929 drosophila	1232	275.5	13.3	265	2	Q17800	Q17800 caenorhabdi
1160	282.5	13.7	319	2	Q9VRS5	Q9vrs5 drosophila	1233	275.5	13.3	296	2	Q8T9U6	Q8t9u6 aedes aegyp
1161	282.5	13.7	687	2	Q69DK8	Q69dk8 sus scrofa	1234	275	13.3	237	2	Q17035	Q17035 anopheles g
1162	282	13.6	258	2	Q6JKF3	Q6jkf3 neodiprion	1235	275	13.3	256	2	Q25082	Q25082 hypoderma l
1163	282	13.6	259	2	O18600	O18600 drosophila	1236	275	13.3	260	2	Q9V5J1	Q9v5j1 drosophila
1164	282	13.6	263	2	Q9N892	Q9nb92 agrotis ips	1237	275	13.3	262	2	Q7Z0G3	Q7z0g3 phlebotomus
1165	282	13.6	416	1	HERS_RAT	Q05511 rattus norv	1238	275	13.3	284	2	Q8AXQ8	Q8axq8 xenopus lae
1166	282	13.6	496	2	Q8CHP7	Q8chp7 cavia porce	1239	275	13.3	317	2	Q7Q619	Q7q619 anopheles g
1167	281.5	13.6	249	2	Q8C1Q8	Q8clq8 mus musculus	1240	275	13.3	467	2	Q6IT09	Q6it09 pseudonaja
1168	281.5	13.6	258	2	Q9NGY6	Q9ngy6 aedes aegyp	1241	275	13.3	492	2	Q7Z155	Q7z155 chiromantes
1169	281.5	13.6	329	2	Q7QB72	Q7qb72 anopheles g	1242	275	13.3	688	1	C1S_HUMAN	P09871 homo sapien
1170	281.5	13.6	388	2	Q7Z1F0	Q7z1f0 cotesia rub	1243	275	13.3	707	2	Q7QW31	Q7qw31 oncorhynch
1171	281.5	13.6	430	2	Q7PNQ4	Q7pnq4 anopheles g	1244	275	13.3	717	2	Q8AXR0	Q8axr0 xenopus lae
1172	281	13.6	262	2	Q7Z0G5	Q7z0g5 phlebotomus	1245	274.5	13.3	695	1	CASP_MESAU	P15156 mesocricetu
1173	281	13.6	267	2	Q9VA66	Q9va66 drosophila	1246	274	13.3	87	2	Q9CQ78	Q9cq78 m mus muscu
1174	281	13.6	322	2	Q9AGI6	Q9agi6 rhizobium l	1247	274	13.3	254	2	Q8K597	Q8k597 rattus norv
1175	281	13.6	564	2	Q8MKB1	Q8mkb1 oryctolagus	1248	274	13.3	265	2	Q9VHF7	Q9vhf7 drosophila
1176	280.5	13.6	227	2	Q7PHB4	Q7phb4 anopheles g	1249	273	13.2	125	2	Q86V18	Q86v18 homo sapien
1177	280.5	13.6	255	2	Q97100	Q97100 anopheles d	1250	273	13.2	247	1	MCT8_MOUSE	P43430 mus musculus
1178	280.5	13.6	270	2	Q7Q0N6	Q7q0n6 anopheles g	1251	273	13.2	257	2	Q818E3	Q818e3 aedes polyn
1179	280.5	13.6	329	2	Q9GL10	Q9gl10 ovis aries	1252	273	13.2	258	1	TRYU_DROER	P54629 drosophila
1180	280.5	13.6	365	2	Q9Y1K7	Q9y1k7 anopheles g	1253	273	13.2	288	2	Q9VEM8	Q9vem8 drosophila
1181	280.5	13.6	366	2	Q7O170	Q7o170 mus musculus	1254	272.5	13.2	262	1	TRYU_DROME	P42379 drosophila
1182	280.5	13.6	439	2	Q8BHM9	Q8bhm9 m mus muscu	1255	272.5	13.2	282	2	Q7PX30	Q7px30 anopheles g
1183	280.5	13.6	494	2	Q9VJD7	Q9vjd7 drosophila	1256	272.5	13.2	287	2	Q9VTV2	Q9vtv2 drosophila
1184	280	13.6	241	2	Q7PQB3	Q7pqb3 anopheles g	1257	272.5	13.2	375	2	Q9NAS8	Q9nas8 anopheles g

1258	272.5	13.2	389	2	Q7QGN4	Q7qgn4 anopheles g	1331	265	12.8	362	2	Q6LU71	Q6lu71 photobacter
1259	272.5	13.2	537	2	Q804W8	Q804w8 fugu rubrip	1332	264.5	12.8	247	1	Q7PFF5	Q7pff5 anopheles g
1260	272.5	13.2	688	2	Q8CFG8	Q8cf98 mus musculus	1333	264.5	12.8	248	1	TRYP_FUSOX	Q7pff5 fusarium ox
1261	272.5	13.2	978	2	Q91777	P91777 pacifastacu	1334	264.5	12.8	251	1	CAP7_HUMAN	P20160 homo sapien
1262	272	13.2	243	2	Q01310	Q01310 botryllus s	1335	264.5	12.8	256	1	TRYA_MANSE	P35045 manduca sex
1263	272	13.2	262	1	TRYT_DROME	P42278 drosophila	1336	264.5	12.8	264	1	VDP_BOMMO	Q07943 bombyx mori
1264	272	13.2	262	2	Q9V5Y0	Q9v5y0 drosophila	1337	264.5	12.8	369	2	Q6QES3	Q6q6s3 callinectes
1265	272	13.2	288	2	Q8SX49	Q8sx49 drosophila	1338	264.5	12.8	719	2	Q9PVY2	Q9pvy2 triakis scy
1266	272	13.2	475	1	FA10_CHICK	P25155 gallus gall	1339	264	12.8	176	2	Q15098	Q15098 homo sapien
1267	271.5	13.1	250	2	Q7PWE3	Q7pwe3 anopheles g	1340	264	12.8	180	2	Q96A30	Q96a30 homo sapien
1268	271.5	13.1	257	2	Q8IS83	Q8is83 aedes albop	1341	264	12.8	301	2	Q7PXG5	Q7pxg5 anopheles g
1269	271.5	13.1	262	2	Q9NB91	Q9nb91 agrotis ips	1342	264	12.8	459	2	Q9V4W7	Q9v4w7 brachydanio
1270	271.5	13.1	267	2	Q9V942	Q9v942 drosophila	1343	264	12.8	504	2	Q6PGW7	Q6pgw7 drosophila
1271	271.5	13.1	272	2	Q9VRS3	Q9vrs3 drosophila	1344	264	12.8	522	2	Q8MQM9	Q8mqm9 drosophila
1272	271.5	13.1	322	2	Q6BD03	Q6bd03 drosophila	1345	263.5	12.8	256	2	Q8R561	Q8r561 ostrinia nu
1273	271.5	13.1	332	2	Q6BD03	Q6bd03 strongyloce	1346	263.5	12.8	258	2	Q9VMX9	Q9vmx9 drosophila
1274	271.5	13.1	833	2	Q96442	Q96442 bombyx mori	1347	263.5	12.8	281	1	TRYZ_DROER	P54630 drosophila
1275	271.5	13.1	1801	2	Q8WSJ2	Q8wsj2 mesocricetu	1348	263.5	12.8	300	2	Q6T775	Q6t775 homo sapien
1276	271	13.1	247	2	Q70164	Q70164 stomoxys ca	1349	263	12.7	180	2	Q7Q5E4	Q7q5e4 anopheles g
1277	271	13.1	253	2	Q9XY50	Q9xy50 stomoxys ca	1350	263	12.7	241	2	Q9VZT0	Q9vzt0 anopheles g
1278	270.5	13.1	275	2	Q7J0B4	Q7j0b4 anopheles g	1351	263	12.7	272	2	Q7QIH5	Q7qih5 phytophthor
1279	270.5	13.1	219	2	Q7PJ75	Q7pj75 rattus norv	1352	263	12.7	289	2	Q945T9	Q945t9 heliothor z
1280	270.5	13.1	245	2	Q6IE56	Q6ie56 rattus norv	1353	263	12.7	295	2	Q9N6C6	P35047 manduca sex
1281	270.5	13.1	248	1	GRAD_MOUSE	P11033 mus musculus	1354	262.5	12.7	256	1	TRIC_MANSE	Q818e2 aedes trise
1282	270.5	13.1	256	1	PRN3_HUMAN	P24158 homo sapien	1355	262.5	12.7	271	2	Q9VRS6	Q9vrs6 drosophila
1283	270	13.1	253	2	Q184J0	P35046 manduca sex	1356	262.5	12.7	279	2	Q7QEA1	Q7qe41 anopheles g
1284	270	13.1	297	2	Q7Q6U4	O18440 helicoverpa	1357	262.5	12.7	281	2	Q8SVB5	Q8sby5 drosophila
1285	270	13.1	694	2	Q70542	Q70542 anopheles g	1358	262.5	12.7	324	2	Q6BD16	Q6bd16 drosophila
1286	269.5	13.0	248	1	GRZ2_RAT	Q70542 rattus norv	1359	262.5	12.7	778	2	Q9V519	Q9v519 drosophila
1287	269.5	13.0	339	2	Q6BDA8	Q6bd06 rattus norv	1360	262	12.7	108	2	Q9CVU2	Q9cvu2 mus musculu
1288	269	13.0	235	2	Q9GTX7	Q9gtx7 aedes albop	1361	262	12.7	183	2	Q6PLJ7	Q6plj7 fenneropena
1289	269	13.0	244	2	Q8MWR5	Q8mwr5 dermatophag	1362	262	12.7	245	2	Q9VQ97	Q9vq97 drosophila
1290	269	13.0	326	2	Q7RTY6	Q7rty6 homo sapien	1363	262	12.7	265	2	Q9VMX7	Q9vmx7 drosophila
1291	269	13.0	405	2	Q8S260	Q8s260 drosophila	1364	262	12.7	282	2	Q8MJD1	Q8mjd1 canis famil
1292	269	13.0	445	2	Q7Q956	Q7q956 anopheles g	1365	262	12.7	324	2	Q6BD11	Q6bd11 drosophila
1293	269	13.0	2616	1	NDL_DROME	P98159 drosophila	1366	262	12.7	390	2	Q7PQV3	Q7pqv3 anopheles g
1294	268.5	13.0	245	2	Q6DF10	Q6df10 xenopus tro	1367	262	12.7	427	2	Q7Q6T1	Q7qt61 anopheles g
1295	268.5	13.0	249	2	Q6IE63	Q6ie63 rattus norv	1368	262	12.7	259	2	Q45048	O45048 anopheles g
1296	268.5	13.0	256	2	Q9Y842	Q9y842 metarhizium	1369	262	12.7	262	2	Q7PX38	Q7px38 anopheles g
1297	268.5	13.0	260	2	Q7Z0G4	Q7z0g4 phlebotomus	1370	261.5	12.7	297	2	Q7QNM1	Q7qnm1 anopheles g
1298	268.5	13.0	261	2	Q00344	P54628 drosophila	1371	261.5	12.7	669	2	Q7PWE1	Q7pwe1 anopheles g
1299	268.5	13.0	262	1	TRYT_DROER	Q66ud0 culicoides	1372	261.5	12.7	239	2	Q9T595	P97595 rattus norv
1300	268.5	13.0	275	2	Q6GUD0	Q6gud0 culicoides	1373	261	12.6	246	2	Q9T611	P97611 rattus norv
1301	268.5	13.0	523	2	Q9V819	Q9v819 drosophila	1374	261	12.6	262	2	Q7QFW4	Q7qfw4 anopheles g
1302	268.5	13.0	524	2	Q8MR00	Q8mr00 drosophila	1375	261	12.6	316	2	Q9VAQ2	Q9vaq2 drosophila
1303	268	13.0	182	2	Q6PLJ6	Q6plj6 penaeus jap	1376	261	12.6	242	1	FIBC_LUMRU	P83298 lumbricus r
1304	268	13.0	270	2	Q6WN60	Q6wn60 drosophila	1377	260.5	12.6	242	2	Q966E7	O966e7 lumbricus b
1305	268	13.0	463	2	Q6IT10	Q6it10 pseudonaja	1378	260.5	12.6	242	2	Q8MX72	Q8mx72 eisenia foe
1306	268	13.0	255	2	O44332	O44332 manduca sex	1380	260.5	12.6	242	2	Q6T373	Q6t373 eisenia foe
1307	267.5	12.9	280	2	Q6GLK1	Q6glk1 xenopus lae	1381	260.5	12.6	245	2	Q7PFF6	Q7pff6 anopheles g
1308	267.5	12.9	324	2	Q6BD05	Q6bd05 drosophila	1382	260.5	12.6	264	2	Q9VT25	Q9vt25 drosophila
1309	267.5	12.9	324	2	Q6BD05	Q6bd05 neocardinia	1383	260.5	12.6	298	2	Q7PZ90	Q7p290 anopheles g
1310	267	12.9	182	2	Q6PLJ5	Q6slx7 drosophila	1384	260.5	12.6	688	2	Q9PVY4	Q9pvy4 xenopus lae
1311	267	12.9	262	2	Q8SZQ7	Q8szq7 anopheles g	1385	260	12.6	282	2	Q7PVP7	Q7pvp7 anopheles g
1312	267	12.9	271	2	Q7PIA2	Q7pia2 anopheles g	1386	260	12.6	302	2	Q8I1G9	Q8i1g9 drosophila
1313	267	12.9	272	2	Q8SZG4	Q8szg4 drosophila	1387	260	12.6	309	2	Q6DHH4	Q6dhn4 brachydanio
1314	267	12.9	273	2	Q8MTU7	Q8mtu7 drosophila	1388	260	12.6	252	2	Q61388	Q61388 mus musculu
1315	267	12.9	388	2	Q8I926	Q8i926 hyphantria	1389	259.5	12.6	254	2	Q97098	Q97098 anopheles a
1316	266.5	12.9	464	2	Q9NK82	Q9nk82 drosophila	1390	259.5	12.6	275	2	Q66UC8	Q66uc8 culicoides
1317	266	12.9	222	2	Q7S1G2	Q7s1g2 solenopsis	1391	259.5	12.6	324	2	Q6BD06	Q6bd06 drosophila
1318	266	12.9	248	2	Q8IRE2	Q8ire2 drosophila	1392	259.5	12.6	511	2	Q9VZHS	Q9vzhs drosophila
1319	266	12.9	252	1	TRVI_DROME	Q9xyy0 rhizopertha	1393	259.5	12.6	248	1	Q8SXG6	P08884 mus musculu
1320	266	12.9	254	2	Q9XYV0	Q9xyv0 mus musculu	1394	259.5	12.6	546	2	Q8SXX6	Q8sxx6 drosophila
1321	266	12.9	255	2	Q8C1L4	Q8c1l4 mus musculu	1395	259	12.5	263	2	Q9V5X7	Q9v5x7 drosophila
1322	266	12.9	277	2	Q9VBM9	Q9vbm9 drosophila	1396	259	12.5	327	2	Q8MS77	Q8ms77 drosophila
1323	266	12.9	286	2	Q8MLC4	Q8mlc4 tenebrio mo	1397	259	12.5	167	2	Q6URK9	Q6urk9 bothrops ja
1324	266	12.9	400	2	Q9GRG2	Q9grg2 anopheles g	1398	258.5	12.5	248	2	Q6IES8	Q6ies8 rattus norv
1325	266	12.9	506	2	Q7PR64	Q7pr64 anopheles g	1399	258.5	12.5	285	2	Q69997	Q69997 streptomyce
1326	265.5	12.9	334	2	Q6BD08	Q6bd08 drosophila	1400	258.5	12.5	286	2	Q96900	Q96900 scolopendra
1327	265.5	12.9	434	2	Q9V7S7	Q9v7s7 drosophila	1401	258.5	12.5	1089	2	Q8T3A0	Q8t3a0 ciona intes
1328	265.5	12.9	444	2	Q9V4W6	Q9v4w6 drosophila	1402	258.5	12.5	265	2	Q7QCB3	Q7qcb3 anopheles g
1329	265	12.8	251	2	Q9VQ99	Q9vq99 drosophila	1403	258	12.5				
1330	265	12.8	277	2	Q7QKR3	Q7qkr3 anopheles g							

1404	258	12.5	267	2	Q9GP27	Q9gp27 drosophila	1477	251.5	12.2	520	2	Q8INGO	Q8ing0 drosophila
1405	258	12.5	269	2	Q7Q515	anopheles g	1478	251.5	12.2	556	2	Q8DEK7	Q8dek7 brachydanio
1406	258	12.5	277	2	Q7PG95	anopheles g	1479	251	12.1	268	2	Q7Z0G0	Q7z0g0 phlebotomus
1407	258	12.5	295	2	O18445	helioverpa	1480	251	12.1	285	2	Q7Q5K4	Q7q5k4 anopheles g
1408	258	12.5	300	2	Q7Q6U0	anopheles g	1481	251	12.1	716	1	HGFL MOUSE	P26928 mus musculus
1409	258	12.5	352	2	Q7KVM3	drosophila	1482	250.5	12.1	226	2	Q6XHU4	Q6xhu4 drosophila
1410	258	12.5	387	2	Q7RTY4	homo sapien	1483	250.5	12.1	240	2	Q7PYJ1	Q7pyj1 anopheles g
1411	257.5	12.5	196	2	Q6VFC8	anopheles g	1484	250.5	12.1	268	2	Q9VT24	Q9vt24 drosophila
1412	257.5	12.5	248	2	Q6IB09	anopheles g	1485	250	12.1	124	2	Q8C6G5	Q8c6g5 mus musculus
1413	257.5	12.5	254	2	Q01136	rattus norv	1486	250	12.1	203	2	Q9NB77	Q9nb77 heliothis z
1414	257.5	12.5	255	2	Q97107	galleria me	1487	250	12.1	274	2	Q8MUQ0	Q8mug0 glossina fu
1415	257.5	12.5	259	2	Q97097	anopheles a	1488	249.5	12.1	253	2	O18442	O18442 helioverpa
1416	257.5	12.5	274	2	Q6DHC9	brachydanio	1489	249.5	12.1	254	2	O18447	O18447 helioverpa
1417	257.5	12.5	418	2	Q7Q529	anopheles g	1490	249.5	12.1	258	2	Q7Q2P0	Q7q2p0 anopheles g
1418	257	12.4	237	2	Q6LBN2	homo sapien	1491	249.5	12.1	269	2	Q7PWL5	Q7pwl5 anopheles g
1419	257	12.4	256	2	O18441	helioverpa	1492	249.5	12.1	274	2	Q9VRS7	Q9vrs7 drosophila
1420	257	12.4	284	2	Q8MLV8	drosophila	1493	249.5	12.1	282	2	O18655	O18655 plodia inte
1421	257	12.4	417	2	Q6JE90	homo sapien	1494	249.5	12.1	381	2	Q8MQY4	Q8mqy4 drosophila
1422	256.5	12.4	196	2	Q6VFD0	anopheles g	1495	249.5	12.1	464	2	O6L7Z5	O6l7z5 haemaphysal
1423	256.5	12.4	235	1	TR1D_HUMAN	homo sapien	1496	249.5	12.1	520	2	Q8SY93	Q8sy93 drosophila
1424	256.5	12.4	242	2	Q6NTB8	homo sapien	1497	249	12.1	253	2	Q9NGY5	Q9ngy5 heliothis v
1425	256.5	12.4	827	2	Q7PZ88	anopheles g	1498	249	12.1	388	2	Q966V2	Q966v2 halocynthia
1426	256	12.4	245	2	Q9XY47	ctenocephal	1499	249	12.1	714	2	Q7PWES	Q7pwe5 anopheles g
1427	256	12.4	265	2	Q9XY55	ctenocephal	1500	249	12.1	716	2	Q91XG8	Q91xg8 mus musculus
1428	256	12.4	267	2	Q9VRU0	drosophila							
1429	256	12.4	282	2	Q7QCX2	anopheles g							
1430	256	12.4	403	2	Q9K5Q6	vibrio chol							
1431	256	12.4	421	2	Q6ZMR5	homo sapien							
1432	255.5	12.4	220	2	O6X143	drosophila							
1433	255.5	12.4	254	2	O18436	helioverpa							
1434	255.5	12.4	273	2	Q7Z163	dermatophag							
1435	255.5	12.4	324	2	Q6BD09	drosophila							
1436	255.5	12.4	334	2	Q9VEA0	drosophila							
1437	255.5	12.4	431	2	Q7PVO5	anopheles g							
1438	255	12.3	292	2	Q7PVO5	anopheles g							
1439	255	12.3	367	2	Q7O169	mus musculus							
1440	255	12.3	374	2	Q8OYD5	mus musculus							
1441	255	12.3	405	2	Q7PNQ3	anopheles g							
1442	254.5	12.3	254	2	O18434	helioverpa							
1443	254.5	12.3	278	2	P91893	arenicola m							
1444	254.5	12.3	357	2	Q7Q092	anopheles g							
1445	254.5	12.3	357	2	Q7QXK6	anopheles g							
1446	254.5	12.3	392	2	Q9VMZ3	drosophila							
1447	254.5	12.3	493	2	Q7PVE2	anopheles g							
1448	254	12.3	305	2	Q8MLR2	drosophila							
1449	254	12.3	323	2	Q7G920	drosophila							
1450	253.5	12.3	282	2	O641D4	anthonomus							
1451	253.5	12.3	405	2	Q8MQS8	apis mellif							
1452	253	12.2	242	2	Q9XY59	ctenocephal							
1453	253	12.2	251	2	Q9VXC9	drosophila							
1454	253	12.2	253	2	Q6W741	pediculus h							
1455	253	12.2	258	2	Q9VS86	drosophila							
1456	253	12.2	272	1	SEB3_DROME	drosophila							
1457	253	12.2	287	2	Q675S0	oikopleura							
1458	253	12.2	288	2	Q8T9T5	aedes aegypt							
1459	252.5	12.2	245	2	Q7Q2Q8	anopheles g							
1460	252.5	12.2	254	2	Q76954	laccanobia o							
1461	252.5	12.2	291	2	Q6V1Y9	lygus lineo							
1462	252.5	12.2	401	2	O6LH17	photobacter							
1463	252	12.2	235	2	Q7PRK6	anopheles g							
1464	252	12.2	295	2	O18450	helioverpa							
1465	252	12.2	301	2	Q7Q6T0	anopheles g							
1466	252	12.2	400	2	Q27081	tachyples							
1467	251.5	12.2	186	2	Q6X655	marmota mon							
1468	251.5	12.2	266	2	Q8MLC2	drosophila							
1469	251.5	12.2	267	2	Q9VGB8	drosophila							
1470	251.5	12.2	276	2	O18443	helioverpa							
1471	251.5	12.2	291	2	Q8WPE4	lygus lineo							
1472	251.5	12.2	291	2	O6V1Y7	lygus lineo							
1473	251.5	12.2	291	2	O6V1Z0	lygus lineo							
1474	251.5	12.2	298	2	Q8T4N4	rhinoccephal							
1475	251.5	12.2	305	2	Q7Q6S4	anopheles g							
1476	251.5	12.2	318	2	Q7QC37	anopheles g							

ALIGNMENTS

RESULT 1

KLKC_HUMAN STANDARD; PRT; 248 AA.

ID KLKC_HUMAN Q9UKR0; Q9UKR1;
AC Q9UKR0; Q9UKR1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein 5)
DE (KLK-L5) (UNQ669/PRO1303).

GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

SEQUENCE FROM N.A. (ISOFORM 1).
RP MEDLINE=20118156; PubMed=10652563;
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
RT "Identification of novel human kallikrein-like genes on chromosome
19q13.3-q13.4.";
RL Anticancer Res. 19:2843-2852(1999).

[2]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP Yousef G.M., Magklara A., Scorilas A., Diamandis E.P.;
RT "Cloning of new alternatively spliced forms of the kallikrein-like
gene 5 (KLK-L5).";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

[3]
SEQUENCE FROM N.A. (ISOFORM 1).
RP PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Paepers B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).

[4]
SEQUENCE FROM N.A. (ISOFORM 1).
RP MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Jin Y., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jun Q., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wieda J., Woods K., Xie M.-H., Yansura D.,

QY 841 ATCCGATGATCATCAGGACAC 864
Db 241 IieArgMetilleMetArgaAen 248
RESULT 2
Q9CV76 PRELIMINARY; PRT; 234 AA.
AC Q9CV76;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus adult male tongue cDNA, RIKEN full-length enriched
DE library, clone:231008B01 product:similar to KALLIKREIN 12 (EC
DE 3.4.21.-) (KALLIKREIN-LIKE PROTEIN 5) (KUK-L5) (fragment).
GN Name=K1k12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA "RIKEN FANTOM Consortium";
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA The FANTOM Consortium;
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [4]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDAJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AK009217; BAB26143.1; -.
DR HSSP; P00760; IEZX.
DR MEROPS; S01.020; -.
DR MGD; MG1:1916761; K1k12.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON_TER 1
SQ SEQUENCE 234 AA; 25888 MW; 6D81E609EDD39110 CRC64;
Alignment Scores:
Pred. No.: 3,096-52 Length: 234
Score: 952.50 Matches: 166
Percent Similarity: 82.13% Conservative: 27
Best Local Similarity: 70.64% Mismatches: 41
Query Match: 46.10% Indels: 1
DB: 2 Gaps: 1
US-10-015-385A-193 (1-1091) x Q9CV76 (1-234)
QY 160 CTCAGCCAGGAGCCACACCCAGAGATTTTCATGGCAGTGTGGGGTAACTCAG 219
Db 1 LeuSerGlnAlaAapArgGluLysIleTyraenglyValGluCysVallysAsnSerGln 20
QY 220 CGTGGCAGGTGGGGCTGTTCAGGGGACCCAGCCCTGCGTGGGGGGTGTCTTATTGAC 279
Db 21 ProTrGlnValGlyLeuPheHisGlyLysTyLeuArgCysGlyValLeuValAsp 40
QY 280 CACAGTGGGTCTCACAGCGCTCAGTCAGCGGAGGAGTGTGGTGGCTGGCTGGGG 339
Db 41 ArglystPvalLeuThrAlaAlaHisCysArg---AspLysTyValValArgLeuGly 59
QY 340 GAACACAGCTCAGCAGCTCGACTGGACCGAGCAGATCCCGCAGCGGCTTCTGTG 399
Db 60 GluHisSerLeuThrLysLeuAspTrpThrGluGlnLeuArgHisThrPheSerIle 79
QY 400 ACCATCCCGGTACTCTGGAGCTTCGACGAGCCACGAGCAGACCTCCGGCTGTGGCG 459
Db 80 ThrHisProSerTyGlnGlyAlaTyGlnAenHisGluHisAspLeuArgLeuArg 99
QY 460 CTGGCGCTCCCGTCCGGTAAACAGCAGCGTTCACCCCTCCCTCCCAATGACTGT 519
Db 100 LeuAsnArgProIleHisLeuThrArgAlaValArgProValAlaLeuProSerCys 119
QY 520 GCAACCGTGGCAGCGAGTGCACCTCTCAGGCTGGGGCATCCACCAACCCACCGGAAC 579
Db 120 ValThrThrGlyAlaMetCysHisValSerGlyTyGlyThrThrAsnLysProTrpAsp 139
QY 580 CAATTCCCGGTCTCTCAGTGTCTCACTCTCACTCTCTCACTCTCTCCCATGCCATGCCAT 639
Db 140 ProPheProAspArgLeuGlnCysLeuAsnLeuSerThrValSerAsnGluThrCysArg 159
QY 640 GGTGTGTATCCCGGAGATCACGAGCAGACATGGTGTGTGGCAGGCGGTCCCGGGGAG 699
Db 160 AlaValPheProGlyArgValThrGluAsnMetLeuCysAlaGlyGlyGluAlaGlyLys 179

QY 700 GATCGCTGCAGGCTGATTCTGGGGGCCCCCTGCTGTGTGGGGAGCTCCTTCAGGCTCG 759
Db 180 AspalacysGlnGlyAspSerGlyGlyProLeuValCysGlyGlyValLeuGlnGlyLeu 199
QY 760 GTGTCCTGGGGCTGTGGGGCCCTGTGGCAAGATGCATCCCTGGAGTCTACACCTAT 819
Db 200 ValSerTrpGlySerValGlyProCysGlyGlnGlyProGlyValTyThrLys 219
QY 820 ATTCGAGTATGTGAGTCCGATCCGGATGATCATGAGGAACAAC 864
Db 220 ValCysLysTyThrAspTrpIleArgIleValIleArgAsnAsn 234
RESULT 3
ID KX8 HUMAN STANDARD; PRT; 260 AA.
AC O60259; O9HC83; Q9U1L9; Q9UQ47;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Ovasin) (Serine
DE protease TADG-14) (tumor-associated differentially expressed gene-14
DE protein) (UNQ283/PRO322).
GN Name=KLK8; Synonyms=NRPN, PRSS19, TADG14;
OS Homo sapiens (Human).
OC Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Hippocampus;
RX MEDLINE=99203457; PubMed=10102990;
RA Mitsu S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.;
RT "A novel form of human neuropsin, a brain-related serine protease, is
RT generated by alternative splicing and is expressed preferentially in
RT human adult brain."
RL Eur. J. Biochem. 260:627-634 (1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=99203457; PubMed=10102990;
RA Mitsu S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.;
RT "A novel form of human neuropsin, a brain-related serine protease, is
RT generated by alternative splicing and is expressed preferentially in
RT human adult brain."
RL Eur. J. Biochem. 260:627-634 (1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Ovary;
RX MEDLINE=99413504; PubMed=10485494;
RA Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H.,
RA O'Brien T.J.;
RT "Cloning of tumor-associated differentially expressed gene-14, a novel
RT serine protease overexpressed by ovarian carcinoma."
RL Cancer Res. 59:4435-4439 (1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Gan L., Gelinias R., Gown A.M., Moss P., Smith R., Wang K.;
RT "Molecular cloning and characterization of a novel serine protease,
RT ovasin, a potential molecular marker for ovarian carcinomas."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Pieper B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region."
RL Gene 257:119-130 (2000).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.B., Abaya E., Baker K., Baldwin D., Brueh J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandien R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270 (2003).
RN [7]
RP SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).
RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Skilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Andreise T., Frankheim M., Attix C., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carraro A.V.;
RT "Sequence analysis of chromosome 19q13.4";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
CC hippocampal plasticity.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O60259-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O60259-2; Sequence=VSP_005401;
CC -!- TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in the
CC pancreas while isoform 2 is expressed in adult brain and
CC hippocampus. Both forms are also found in fetal brain and
CC placenta. Not detected in kidney, spleen, liver and lung.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB009849; BAA28673.1; -
CC EMBL; AB012761; BAA28676.1; -
CC EMBL; AB010780; BAA88684.1; -
CC EMBL; AB008390; BAA82665.1; -
CC EMBL; AB008927; BAA82666.1; -
CC EMBL; AF055982; AAD56050.1; -
CC EMBL; AF095742; AAD25979.1; -
CC EMBL; AF095743; AAD29574.1; -
CC EMBL; AF243527; AAG33361.1; -
CC EMBL; AY359036; AAQ89395.1; -
CC EMBL; AC011473; AAG23254.1; -
CC HSSP; P00760; 1EZK.
CC MEROPS; S01.244; -
CC Genew; HGNC:6369; KLK8.
CC MIM; 605644; -
CC GO; GO:0008236; F:serine-type peptidase activity; TAS.
CC GO; GO:0007399; P:neurogenesis; TAS.
CC InterPro; IPR009003; Pept_Ser_Cys.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00089; Trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
KW

KW Signal; Zymogen. 28
 FT SIGNAL 1
 FT PROPEP 29
 FT CHAIN 33
 FT ACT_SITE 73
 FT ACT_SITE 120
 FT ACT_SITE 212
 FT ACT_SITE 212
 FT DISULFID 39
 FT DISULFID 58
 FT DISULFID 145
 FT DISULFID 152
 FT DISULFID 184
 FT DISULFID 208
 FT DISULFID 223
 FT CARBOHYD 110
 FT VARSPLIC 23
 FT
 FT
 SQ SEQUENCE 260 AA; 28048 MW; EF43955B8C3B660 CRC64;

Alignment Scores:
 Pred. No.: 5.8e-32 Length: 260
 Score: 632.50 Matches: 125
 Percent Similarity: 58.08% Conservativity: 26
 Best Local Similarity: 48.08% Mismatches: 96
 Query Match: 30.61% Indels: 13
 DB: 1 Gaps: 4

US-10-015-385A-193 (1-1091) x KLK8_HUMAN (1-260)

QY 88 CCCTTTTCCCGAGACTTGGAGTGGACCCACCATGGGGCTGAGTCTTTTGGCTCTG 147
 DB : : : : :
 6 ProArgAlaAlaLysThrTrp-----MetPheLeuLeuLeu 17

QY 148 -----TGTGTTCTTGGGCTCAGCGAGCGAGCCACACCGAAGATTTCATGGCACT 198
 DB : : : : :
 18 LeuGlyGlyAlaTrpAlaGlyHisSerArgAlaGlnGluAspLysValLeuGlyGlyHis 37

QY 199 GAGTGTGGCGPACTCAGCGGTGGAGGTGGGGCTGTTTGGAGCGACCGCTGGCG 258
 DB : : : : :
 38 GluGlyGlnProHisSerGlnProTrpGlnAlaAlaLeuPheGlnGlyGlnLeuLeu 57

QY 259 TGGGGGGTGTCTATTGACACACAGTGGGTCTTCCAGCGGCTCACTGGAGCGGCGAGC 318
 DB : : : : :
 58 CysGlyGlyValLeuValGlyGlyAsnTrpValLeuThrAlaAlaHisCysLysLysPro 77

QY 319 AGTACTGGTGGCTGGGGAAACACAGCCCTCAGCGCTGAGTGGACCGAGCATC 378
 DB : : : : :
 78 LysTyrThrValArgLeuGlyAspHisSerLeuGlnAsnLysAspGlyProGluGlnGlu 97

QY 379 CGGCACAGCGGTTCTGTGACCCATCCCGGCTACCTGGGAGCGCTCGACG---AGCCAC 435
 DB : : : : :
 98 IleProValValGlnSerIleProHisProCysTyrAsnSerSerAspValGluAspHis 117

QY 436 GAGCAGCGACTCCGCTGCTGGCGTGGCGTGGCGTCCCGGTAAACAGCAGCGTTCAA 495
 DB : : : : :
 118 AsnHisAspLeuMetLeuGlnLeuLysArgAspGlnAlaSerLeuGlySerLysValLys 137

QY 496 CCCCTGCCCTGCCAATGACTGTGCAACCGCTGCACCGAGTGCACGCTCTCAGGCTGG 555
 DB : : : : :
 138 ProIleSerLeuAlaAspHisCysThrGlnProGlyGlnLysCysThrValSerGlyTyr 157

QY 556 GGCATCACCAACCCACCGAACCATTCCCGGATCTGCTCCAGTCCCTCAACCTCC 615
 DB : : : : :
 158 GlyThrValThrSerProArgGluAsnPheProAspThrLeuAsnCysAlaGluValLys 177

QY 616 ATCGTCTCCATGCCACCTGCCATGGTGTGATCCGGAGAGATCAGCAGCAACATGGTG 675
 DB : : : : :
 178 IlePheProGlnLysCysGluAspAlaTyrProGlyGlnIleThrAspGlyMetVal 197

QY 676 TGTGAGCGCGCTCCCGGCGAGCATGCTGCCAGGTGATTCTGGGGGCCCCCTGGTG 735
 DB : : : : :
 198 CysAlaGlySerSerLysGlyAlaAspThrCysGlnGlyAspSerGlyGlyProLeuVal 217

QY 736 TGTGGGGAGTCTCTCAAGGTCTGTGCTGGGGTCTGTGGGGCCCTGTGGACAAGAT 795
 DB : : : : :
 218 CysAspGlyAlaLeuGlnGlyIleThrSerTrpGlySer---AspProCysGlyArgSer 236

QY 796 GGCATCCCTGGAGTCTACACCTATATTGCAAGTATGTGACTGGATCGGATGATCATG 855
 DB : : : : :
 237 AspLysProGlyValThrAsnIleCysArgTyrLeuAspIleLysLysIleIle 256

RESULT 4
 Q8IW69 PRELIMINARY; PRT; 260 AA.
 AC Q8IW69;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Kallikrein 8, isoform 1 preproprotein.
 GN Name=KLK8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshikiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.E., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Hellon K., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBSJ databases.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 DR EMBL; BC040887; AAH40887.1; -;
 DR HSSP; P00760; 1EXX.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase_S1a.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 SW HydroLase; Protease; Serine protease.
 SQ SEQUENCE 260 AA; 28090 MW; EF5934EB96295660 CRC64;

Alignment Scores:
 Pred. No.: 8.99e-32 Length: 260
 Score: 629.50 Matches: 125
 Percent Similarity: 58.08% Conservativity: 26

Best Local Similarity:	48.08%	Mismatches:	96
Query Match:	30.47%	Indels:	13
DB:	2	Gaps:	4

US-10-015-385A-193 (1-1091) x Q8IM69 (1-260)

QY	88	CCCTTTTCCCAGACACTTTGGAAGTGACCCACCATTGGGGCTCAGCATCTTTTGTCTCTCG	147
Db	6	ProArgAlaIalysThrTrp-----MetPheLeuLeuLeu	17
QY	148	-----TGTGTTCTTGGGCTCAGCCAGGCAGCCACACGGAAGATTTCAATGGCACT	198
Db	18	LeuGlyGlyAlaTrpAlaGlyHisSerArgAlaGlnGluAspLysValLeuGlyGlyHis	37
QY	199	GAGTGTGGGGCTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGGAGGCCAGCAGCTCGGC	258
Db	38	GluCysGlnProHisSerGlnProTrpGlnAlaAlaLeuPheGlnGlyGlnGlnLeuLeu	57
QY	259	TGGGGGGGTGTCCTTAATTGACACAGGTGGGTCTCTCAGCGGCTCATCGNAGCGGCAGC	318
Db	58	CysGlyGlyValLeuValGlyGlyAsnTrpValLeuThrAlaAlaHisCysLysIysPro	77
QY	319	AGGTACTGGGTGGCGCTGGGGGAACACAGCTCTCAGCCAGCTCGACTGGACCGAGCAGATC	378
Db	78	LysTrpThrValArgLeuGlyAspHisSerLeuGlnAsnLysAspGlyProGlnGlnGlu	97
QY	379	CGGCACAGCGGCTTCTCTGTCACCCATCCCCGCTACCTGGGAGCCTCGACG---AGCCAC	435
Db	98	IleProValValGlnSerIleProHisProCysTyrAsnSerSerAspValgluAspHis	117
QY	436	GAGCACAGCTCTCGGCTGCTCGGCTGCGCTGCCGCTCCCGCTCCCGGTAAACCAGCAGCTTCAA	495
Db	118	AsnHisAspLeuMetLeuLeuGlnLeuArgAspGlnAlaSerLeuGlySerLysVallys	137
QY	496	CCCTGTCCTGCCCAATGACTGTCACACCGCTGGCACCGAGTGCCAGTGCACGTCTCAGGCTGG	555
Db	138	ProIleSerLeuAlaAspHisCysThrGlnProGlyGlnLysCysThrValSerGlyTrp	157
QY	556	GGCATCACCAACCCACAGCAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCC	615
Db	158	GlyThrValThrSerProArgGluAsnPheProaspThrLeuAsnCysAlaGluVallys	177
QY	616	ATCGTCTCCCATGCCATCGCATGGTGTATCCCGGAGAATCACGAGCAACATGTGTG	675
Db	178	IlePheProGlnLysLysCysGluAspAlaTyrProGlyGlnIleThrAspValMetVal	197
QY	676	TGTCAGCGCGCTCCCGGGCAGGATCGCTCCAGGGTGATCTGGGGCCCCCTGGTG	735
Db	198	CysAlaGlySerSerLysGlyAlaAspThrCysGlnGlyAspSerGlyGlyProLeuVal	217
QY	736	TGTGGGGAGTCCCTCAAGTCTGTGTCTGGGGTCTGTGGGGCCCTGTGCAACAAGAT	795
Db	218	CysaspGlyAlaLeuGlnGlyIleThrSerTrpGlySer--AspProCysGlyargSer	236
QY	796	GGCATCCCTGGAGTCTACACCTATATTTGCAAGTAGTGGAGCTGGATCOGGATGATCATG	855
Db	237	AspLysProGlyValTyrThrAsnIleCysArgTyrLeuAspTrpIleLysLysIlelle	256

RESULT 5

ID	NRPN	RAT	STANDARD;	PRT;	260 AA.
AC	O88780;				
DT	15-JUL-1999	(Rel. 38, Created)			
DT	15-JUL-1999	(Rel. 38, Last sequence update)			
DT	25-OCT-2004	(Rel. 45, Last annotation update)			
DE	Neurosin precursor (EC 3.4.21.-) (NP)	(Kallikrein 8) (Brain serine protease 1).			
GN	Name=Kl8; Synonyms=Bspl, Nrpn, Prss19;				
OS	Rattus norvegicus (Rat)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				
NCBI_TaxID=10116;					
RN	[1]				


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QY 280 CACAGTGGTCTCTCACAGCGCTCACTGACCGGACGACGAGTACTGGTGGCTGGCGCTGGGG 339
Db 65 AspAgtTpValLeuThraAlaHisCysLysAspLysSerValArgLeuGly 84
QY 340 GAACACGCTCAGCAGCTCGACTCGAGCGGACGAGCAGATCCGGCAGCGGCTTCTCTG 399
Db 85 AspHisSerLeuGlnlyArgAspLupProGluGlnGluileGlnValAlaArgSerIle 104
QY 400 ACCATCCCGGCTACCTGGGAGCTCG---ACGAGCCACGACGACGACCTCCGGTCTGCTG 456
Db 105 GlnHisProCysPheAsnSerSerAsnProGluAspHisSerHisAspIleMetLeuIle 124
QY 457 CGGCTGGCGCTCCCGTGGCGTACACGACGCGTTCACCCCTCCCTCCCGTCCCGATGAC 516
Db 125 ArgLeuGlnAsnSerAlaAsnLeuGlyAspLysValysProIleGluLeuAlaAsnLeu 144
QY 517 TGTGCAACCGCTGGCAGCGAGTCCAGCTCTCAGGCTGGGATCACCACACCCACCG 576
Db 145 CysProLysValGlyGlnLysCysIleIleSerGlyTrpGlyThrValThrSerProGln 164
QY 577 AACCCATTCCCGGATCTGCTCAGTGCCTCAACCTCTCCATGCTCCCATGCCACCTGC 636
Db 165 GluAsnPheProAsnThrLeuAsnCysAlaGluValLysIleTyrSerGlnAsnLysCys 184
QY 637 CATGCTGTATCCCGGAGATACAGAGCAACATGCTGTGTGCGAGCGGCTCCCGGG 696
Db 185 GluArgAlaTyrProGlyLysIleThrGluGlyMetValCysAlaGlySerSerAsnGly 204
QY 697 CAGGATGCTCCGAGGTATCTCGGGGCGCCCTGTGTGTGGGGAGTCTTCAAGT 756
Db 205 AlaAspThrCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlyValLeuGlnGly 224
QY 757 CTGGTGTCTCGGGGCTGTGTGGGCGCTGTGACAGATGCGATCCCTGGAGTCTACACC 816
Db 225 IleThrThrTrpGlySer---AspProCysGlyLysProGluLysProGlyValThr 243
QY 817 TATATTCAAGTATGTGAGTCCGATCCGATGATCATG 855
Db 244 LysIleCysArgTyrThrAsnTrpIleLysThrMet 256

RESULT 6
NRPN_MOUSE STANDARD; PRT; 260 AA.
AC Q61955;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neuropilin precursor (EC 3.4.21.-) (NP) (Kallikrein 8).
GN Name=Klk8; Synonyms=Nrpn, Prs619;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hippocampus;
RX MEDLINE=95348817; PubMed=7623137;
RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
RA Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.;
RT "Expression and activity-dependent changes of a novel limbic-serine
RT protease gene in the hippocampus."
RL J. Neurosci. 15:5088-5097(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Yoshida S., Hirata A., Inoue N., Shiosaka S.;
RT "Cloning and assignment of mouse neuropilin gene, Prs619 to chromosome
RT 7B4."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.I., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RN [4]
RP SEQUENCE OF N-TERMINUS, CHARACTERIZATION, AND MASS SPECTROMETRY.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=9825202; PubMed=9556608; DOI=10.1074/jbc.273.18.11189;
RA Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,
RA Shiosaka S., Morikawa R., Kamachi T., Kawabe A., Shiosaka S.;
RT "Characterization of recombinant and brain neuropilin, a plasticity-
RT related serine protease."
RL J. Biol. Chem. 273:11189-11196 (1998).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
RC TISSUE=Hippocampus;
RX MEDLINE=99134351; PubMed=9933620; DOI=10.1074/jbc.274.7.4220;
RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
RA Shiosaka S., Hakoshima T.;
RT "Crystal structure of neuropilin, a hippocampal protease involved in
RT kindling epileptogenesis."
RL J. Biol. Chem. 274:4220-4224 (1999).
CC -!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
CC hippocampal plasticity. Has a strong proteolytic activity against
CC fibronectin.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
CC -!- ENZYME REGULATION: Strongly inhibited by diisopropyl
CC fluorophosphate, leupeptin and (4-aminodiphenyl)methanesulfonyl 1-
CC fluoride.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed specifically in the limbic system of
CC mouse brain and is localized at highest concentration in pyramidal
CC neurons of the hippocampal CA1-3 subfields.
CC -!- MASS SPECTROMETRY: MW=26613; METHOD=MALDI; RANGE=29-260;
CC NOTE=Ref.4.
CC -!- MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260;
CC NOTE=Ref.4.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D30785; BAA06451.1; -.
CC EMBL; AB032202; BAA92435.1; -.
CC EMBL; BC055895; AAB55895.1; -.
CC PIR; I56559; I56559.
CC PDB; 1NPM; X-ray; A/B=33-256.
CC MEROPS; S01.244; -.
CC MGD; MGI:992018; Klx8.
CC InterPro; IPR009003; Pept_Ser_Cys.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
```

DR Pfam: PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW 3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;
KW Serine protease; Signal; Zymogen.

FT SIGNAL 1 28 Potential.
FT PROPEP 29 32
FT CHAIN 33 260
FT ACT SITE 73 73 Neuropsin.
FT ACT SITE 120 120 Charge relay system (By similarity).
FT ACT SITE 212 212 Charge relay system (By similarity).
FT DISULFID 39 173 Charge relay system (By similarity).
FT DISULFID 58 74
FT DISULFID 145 246
FT DISULFID 152 218
FT DISULFID 184 198
FT DISULFID 208 233
FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
FT STRAND 34 34
FT STRAND 37 38
FT TURN 41 42
FT TURN 45 46
FT STRAND 47 52
FT TURN 53 54
FT STRAND 55 64
FT TURN 65 66
FT STRAND 67 70
FT HELIX 72 74
FT STRAND 80 83
FT STRAND 87 87
FT TURN 88 89
FT STRAND 96 98
FT STRAND 100 105
FT TURN 107 108
FT TURN 114 115
FT TURN 118 119
FT STRAND 122 126
FT STRAND 140 141
FT TURN 148 149
FT STRAND 151 156
FT STRAND 170 170
FT STRAND 172 178
FT HELIX 181 187
FT TURN 189 191
FT TURN 194 195
FT STRAND 196 200
FT TURN 202 203
FT STRAND 206 206
FT TURN 209 210
FT TURN 212 213
FT STRAND 215 218
FT TURN 219 220
FT STRAND 221 228
FT STRAND 235 235
FT TURN 236 237
FT STRAND 238 238
FT STRAND 240 244
FT HELIX 245 256

SQ SEQUENCE 260 AA; 28523 MW; BESF6G6BE37CD60E CRC64;

Alignment Scores:
Pred. No.: 2,49e-31 Length: 260
Score: 622.50 Matches: 121
Percent Similarity: 60.32% Conservative: 28
Best Local Similarity: 48.99% Mismatches: 93
Query Match: 30.13% Indels: 5
DB: 1 Gaps: 3

US-10-015-385A-193 (1-1091) x NRPN_MOUSE (1-260)

QY 133 APTTTTTTCTCTGTGTGT-----CTTGGGCTCAGCCAGCCACACCGAAG 183

Db 13 ILELEULEULEULEUPHEMETGLYALATRPALAGLYLEUTHRALAGALAGLNGLYSERLYS 32
QY 184 ATTTTCATATGCACTAGTGTGGCGGTAACTCACAGCGGTGGCGGTGGGTGGTGGTTCAG 243
Db 33 ILELEUGLIYARGGLUCYILEPROHISERGLNPROFIRGLNALAALALEUPHEGLIN 52
QY 244 GGCACACGCTGCGTGGCGGGTGTCTCTATTGACACACAGTGGGTCTCACACGCGCT 303
Db 53 GLYGLUARGLEULILECYSGLYGLYVALLEUVALGLYASPAAGTRPVALLEUTHRALALA 72
QY 304 CACTGACGCGGACAGAGTACTGGGTGCGCTGGGGGAACACAGCTCAGCAGCTCCAG 363
Db 73 HISCYSLYSLYSGLNLYSYRYSERVALARGLEUGLYASPGLNGLNGLNGLNGLNGLN 92
QY 364 TGGACCGAGCAGATCCGCGCGGTCTCTGTGACCCATCCGCGGTCTCTGACCGGCC 423
Db 93 GLNPROGLUGLNGLIULEGLNVALALAGLNSERILEGLNGLNGLNGLNGLNGLNGLN 112
QY 424 TCG---ACGAGCCACGACGACCTCCGCGGTCTGTGCGGTGCGGTGCGGTCTCCGCGTA 480
Db 113 ASNPROGLUASPGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLN 132
QY 481 ACCAGACGCTTCAACCCCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 540
Db 133 GLYASPLYSVALYSVALGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLN 152
QY 541 CACGTCTCAGGCTGGGCGCATCACCAACCCAGGACCCATCCCGGATCTGCTCCAG 600
Db 153 ILEILESERGLYTRPGLYTHRVALTHRSEPRGLNGLNGLNGLNGLNGLNGLNGLNGLN 172
QY 601 TGCCTCAACCTCTCCATCGTCTCCCATGCTCCCATGCTCCCATGCTCCCATGCTCCG 660
Db 173 CYSALAGLUVALYILETYRSERGLNASNLYSCYSGLUARGALATYRPROGLYLYSILE 192
QY 661 ACAGAACATGCTGTGTGCGAGCGCGCTCCCGGGGAGGATGCTGCGAGGCTGATCT 720
Db 193 THRGLUGLYMETVALCYALAGLYSERSEASNGLYALASPTHRCYSGLNGLYASPSER 212
QY 721 GGGGGCCCCCTGCTGTGGGGAGTCTCTCAAGTCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 213 GLYGLYPROLEUVALCYASPGLYMETLEUGLNGLYILETHRSETRPGLYSER---ASP 231
QY 781 CCTGTGGACAAAGATGCGATCCCTGAGTCTACACCTATATTTGCAAGTATGAGCTGG 840
Db 232 PROCYSGLYSPROGLULYSPROGLYVALTYRTHRYSILECYSEARGTYRTHRTRTP 251
QY 841 ATCCGGATGATCATGAGGAAC 861
Db 252 ILELYSLYSTRMETHASPSN 258

RESULT 7

KLKB_HUMAN
ID KLKB_HUMAN STANDARD; PRT; 250 AA.
AC Q9UBX7; O75837; Q9NS65;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Kallikrein 11 precursor (EC 3.4.21.-) (Hippotaasin) (Trypsin-like
protease) (UNQ649/PRO1279).
GN Name=KLK11; Synonyms=PRSS20, TLSP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Hippocampus;
RX MEDLINE=98438738; PubMed=9765601; DOI=10.1016/S0167-4781(98)00116-X;
RA Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiosaka S.;
FT "cDNA cloning and expression of a novel serine protease, TLSP";
RL Biochim. Biophys. Acta 1399:225-228(1998).
RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=hippocampus, and Prostate;
RX MEDLINE=20329229; PubMed=10872828; DOI=10.1006/bbr.2000.2761;
RA Mitui S., Yamada T., Okui A., Kominami K., Uemura H., Yamaguchi N.;
RT "A novel isoform of a kallikrein-like protease, TLSP/hike proteasin,
RL (PRSS20), is expressed in the human brain and prostate.";
RN Biochem. Biophys. Res. Commun. 272:205-211(2000).
[3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20130117; PubMed=10662548; DOI=10.1006/geno.1999.6072;
RA Yusef G.M., Scorilas A., Diamandis E.P.;
RT "Genomic organization, mapping, tissue expression, and hormonal
RT regulation of trypsin-like serine protease (TLSP PRSS20), a new member
RT of the human kallikrein gene family.";
RL Genomics 63:88-96(2000).
[4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paepel B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
[5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Weiland D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
[6]
RP SEQUENCE FROM N.A.
RX PubMed=15057824; DOI=10.1038/nature02399;
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
RA Canepael S., Carrano A.V., Caciile C., Chan Y.M., Christensen M.,
RA Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Deter J.C.,
RA Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,
RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
RA Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
RA Malfatti S., Martinez D., McCreedy P.M., Medina C., Morgan J.,
RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
RA Popkie A.P., Predki P., Qian G., Ramirez L., Rash S., Retterer J.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
RA Furey T.S., DeJong P., Dickinson M., Gordon D., Eichler E.E.,
RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
RA Rubin E.M., Lucas S.M.;
RT "The DNA sequence and biology of human chromosome 19.";
RL Nature 428:529-535(2004).
[7]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Shen M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Xie H., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavento T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Sutterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Possible multifunctional protease. Efficiently cleaves
CC bz-Phe-Arg-4-methylcoumaryl-7-amide, a kallikrein substrate, and
CC weakly cleaves other substrates for kallikrein and trypsin.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9UBX7-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9UBX7-2; Sequence=VSP 005402;
CC -!- TISSUE SPECIFICITY: Expressed in brain, skin and prostate. Isoform
CC 1 is expressed preferentially in brain; isoform 2 in prostate.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.

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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch)

CC EMBL; AB012917; BAA33404.1; ALT_INIT.
DR EMBL; AB013730; BAA88713.1; -.
DR EMBL; AB041036; BAA96797.1; -.
DR EMBL; AF164623; AAD47815.1; -.
DR EMBL; AF243527; AAG33364.1; -.
DR EMBL; AY359014; AAQ9373.1; -.
DR EMBL; AC011473; AAG23257.1; -.
DR EMBL; BC022068; AAG22068.1; -.
DR HSSP; P00760; 1EZX.
DR MEROPS; S01.257; -.
DR Genew; HGNC:6359; KLK11.
DR H-InvDB; HIX0015375; -.
DR MIM; 604434; -.
DR GO; GO:0008236; F:serine-type peptidase activity; TAS.
DR InterPro; IPR009003; Pept Ser Cys.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS02040; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
KW Signal; Zymogen.
FT SIGNAL 1 18 Potential.
FT PROPEP 19 21 Activation peptide (Potential).
FT CHAIN 22 250 Kallikrein 11.
FT ACT_SITE 62 62 Charge relay system (By similarity).
FT ACT_SITE 110 110 Charge relay system (By similarity).
FT ACT_SITE 203 203 Charge relay system (By similarity).
FT DISULFID 28 163 By similarity.
FT DISULFID 47 63 By similarity.
FT DISULFID 135 237 By similarity.
FT DISULFID 142 209 By similarity.
FT DISULFID 174 188 By similarity.
FT DISULFID 199 224 By similarity.
FT CARBOHYD 99 N-linked (GlcNAc...) (Potential).

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FT CARBOHYD 165 165 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 181 181 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 210 210 N-linked (GlcNAc... ) (Potential).
FT VARSPLTC 1 1 M -> MQLRLWRDQKSSGRGLTAKEFGARSSPLQAM
FT (in isoform 2).
FT /FTid=VSP_005402.
SQ SEQUENCE 250 AA; 27466 MW; 192D910BBCDC7A56 CRC64;

Alignment Scores:
Pred. No.: 4.46e-31 Length: 250
Score: 618.50 Matches: 120
Percent Similarity: 62.25% Conservativity: 35
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
DB: 1 Gaps: 4

US-10-015-385A-193 (1-1091) x KLKB_HUMAN (1-250)
QY 127 CTCAGCATCTTTTGTCTCTGTGTCTTGTGGCTCAGCCAGGCAGCCACACCGAAGATT 186
Db 4 LeuGlnLeuLeuLeuAlaLeuAlaThrGlyLeuValGlyGluThr---Argile 22
QY 187 TTCATGCACTAGTGTGGCGTAACACACAGCGTGGCGAGTGGGGCTGTTGAGGGC 246
Db 23 IleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLys 42
QY 247 ACCAGCTCGCTGGGGGGTGTCTTATTGACACAGTGGGTCTTACACAGCGGCTCAC 306
Db 43 ThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHis 62
QY 307 TGCAGCGGCAGCAGTACTGGTGGCGCTTGGGGGAACACACAGCTCAGCAGCTCGACTGG 366
Db 63 CysLeuLysProArgTyrlleValHisLeuGlyGlnHisAsnLeuGlnLysGluGly 82
QY 367 ACCGAGCAGATCCGCACAGCGGTCTCTGTGTGACCCATCCCGGTACTCTGGAGCC--- 423
Db 83 CysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeu 102
QY 424 ---TCGACGAGCCAGCAGCAGCAGCTCCGGTGTGCGGTGCGGTGCGCTCCGCTCGCGTA 480
Db 103 ProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSerile 122
QY 481 ACCAGCAGCTTCAACCCCTGCGCCCTGCGCCCAATGACTGTGCAACCGCTGGCACCGAGTGC 540
Db 123 ThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCys 142
QY 541 CAGCTCTAGGCTGGGGATCATCAACACACACACCGAACCCATTCGCGATCTGCTCCAG 600
Db 143 LeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeuArg 162
QY 601 TGCCTCAACCTCTCATGCTCTCCATGCCATGCCATGCTGTGTATCCCGGGAGAAATC 660
Db 163 CysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTyProGlyAsnIle 182
QY 661 ACAGCAACATGCTGTGTGTCAGGC---GGCGTCCCGGGGAGGATCCCTGCCAGGGTGTAT 717
Db 183 ThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGlyAsp 202
QY 718 TGTGGGGGGCCCTGTGTGTGGGGAGTCTTCAAGTCTGGTCTGCTCCCGGGGTCTGTG 777
Db 203 SerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln--- 221
QY 778 GGGCCCTGGGACAGATGCATCCCTGGAGTCTACACCTATATTGGCAAGTATGTGGAC 837
Db 222 AspProCysAlaIleThrArgLysProGlyValTyThrLysValCysLysTyValAsp 241
QY 838 TGGATCCGGATGATCATGAGGAACAC 864
Db 242 TrpIleGlnGluThrMetLysAsnAsn 250

RESULT 8
Q7JIG6
ID Q7JIG6 PRELIMINARY; PRT; 255 AA.
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Q7JIG6;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE K15.
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=9490;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=21094033; PubMed=11177570; DOI=10.1089/10454900750058080;
RA Olsson A.Y., Persson A.M., Valtonen-Andre C., Lundwall A.;
RE "Glandular kallikreins of the cotton-top tamarin: molecular cloning of
RT the gene encoding the tissue kallikrein.";
RL DNA Cell Biol. 19:721-727(2000).
RN [2]
SEQUENCE FROM N.A.
RA Olsson Y., Persson M., Lundwall A.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF173845; AA545302.1; -.
DR HSSP; P00761; IAKS
DR GO; GO:004283; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 255 AA; 28078 MW; A040914ABC8FEC8D CRC64;

Alignment Scores:
Pred. No.: 1.33e-30 Length: 255
Score: 611.00 Matches: 118
Percent Similarity: 62.34% Conservativity: 31
Best Local Similarity: 49.37% Mismatches: 76
Query Match: 29.57% Indels: 14
DB: 2 Gaps: 5

US-10-015-385A-193 (1-1091) x Q7JIG6 (1-255)
QY 191 AAGATTTTCATGTCAGTGTGGCGTAACACAGCGTGGCAGGTGGGCTGTTT 240
Db 20 LysLeuLeuGluGlyGluGluCysAlaProHisSerGlnProTrpGlnValAlaLeuTyr 39
QY 241 GAGGSCACAGCCTCGCTGGGGGTGTCTTATTGACACACAGGTGGGTCTTCACAGC 300
Db 40 GluArgGlyArgPheAsnCysGlyAlaSerLeuIleSerProHisTrpValLeuSerAla 59
QY 301 GCTCATCTCAGCGGCAGCAGTACTGGTGTGGCTGGGGGAACACAGCTCAGCCAGCTC 360
Db 60 AlaHisCysGlnSerArgPheMetArgValArgLeuGlyGluHisAsnLeuArgLysArg 79
QY 361 GACTGACCGAGCAGATCCGGCAGCAGCGCTCTCTGTGACCCATCCCGGTCTACCTGGGA 420
Db 80 AspGlyProGluGlnLeuArgThrAlaSerArgValIleProHisProArgTyr----- 97
QY 421 GCCTCAGCAGCAGCAGCAGCAGCTCCGGTGTGTGCTGCGGTGCGCTGCGCTCCGCTG 480
Db 98 GluAlaArgSerHisArgHisAspIleMetLeuLeuArgLeuValGlnProAlaArgLeu 117
QY 481 ACCAGCAGGTTCAACCCCTGCGCTCCCTGCGCTCCCTGCGCTCCCTGCGCTCCGCTG 540
Db 118 ThrProGlnValArgProValValLeuProThrArgCysProHisProGlyGluAlaCys 137
QY 541 CAGCTCTCAGGTGGGTCATCACCACCAACAC-----CCACGG 576
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Db 138 ValSerGlyTrpGlyLeuValSerHisAsnGluProGlyThrThrGlyArgProGln 157
577 AAC-----CCATCCCGGATCTGCTCCAGTCTCAACCTCTCCATCTCCATGCTCCATGCC 630
::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 158 SerGlnValSerLeuProAspThrLeuHisCysAlaAsnIleSerIleSerAspAla 177
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 631 ACTGTCATGTTGTATCCCGGAGATCAACAGCAACATGTTGTGTGTCAGCGCGCTC 690
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 178 SerCysAspIleSerGlyArgLeuThrAsnThrMetValCysAlaGlyAlaGlu 197
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 691 ---CCGGGCGAGATCCCTGCCAGGTGATCTCGGGGCGCTGTGGCAAGATGCCATCCCTGGA 747
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 198 GlyArgGlyAlaGluSerCysGluGlyAspSerGlyGlyProLeuValCysGlyGlyIle 217
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 748 CTTCAAGTCTGTGTCCTGGGGGCTGTGGGGGCTGTGGGCAAGATGCCATCCCTGGA 807
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 218 LeuGlnGlyIleValSerTrpGlyAspVal---ProCysAspAsnThrThrLysProGly 236
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 808 GTCTACACCTATTTGCAAGTATGTGACTGGATCCGATCCGATGATGATGAGGAACAAC 864
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 237 ValTyrThrLysValCysArgTyrValLysTrpIleArgGluThrMetLysArgAsn 255
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
Q63ZF2 PRELIMINARY; PRT; 250 AA.
AC Q63ZF2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Glandular kallikrein 11 precursor.
GN Name=Klk11;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15203212; DOI=10.1016/j.ygeno.2004.01.009;
RA Olsson A.Y., Lilja H., Lundwall A.;
RT "Taxon-specific evolution of glandular kallikrein genes and
RT identification of a progenitor of prostate-specific antigen.";
RL Genomics 84:147-156(2004).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK001364; DAA05600.1; --
KW Signal.
FT SIGNAL. 1 18 Potential.
FT CHAIN 22 250 Glandular kallikrein 11.
SQ SEQUENCE 250 AA; 27630 MW; 247B29D3F0DEF8F1 CRC64;

Alignment Scores:
Pred. No.: 1,54e-30 Length: 250
Score: 610.00 Matches: 115
Percent Similarity: 61.79% Conservative: 37
Best Local Similarity: 46.75% Mismatches: 90
Query Match: 29.53% Indels: 4
DB: 2 Gaps: 3

US-10-015-385A-193 (1-1091) x Q63ZF2 (1-250)
QY 136 TTTTGTCTCTGTGTCTTCTGGTCTCAGCCAGGCACACCGAAGATTTTCAATGGC 195
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6 PhelleAlaLeuAlaLeuValThrGlyHisValGlyGlyGluThrArgIleIleLysGly 25
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 196 ACTGAGTGTGGGGTAACCAACAGCCGTGGAGGTGGGGCTGTTCAGGGCAACCAAGCTTG 255
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 26 TyrGluCysArgProHisSerGlnProTrpGlnValAlaLeuPheGlnLysThrArgLeu 45
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 256 CGCTGGGGGTGCTCTTATTACACAGGTGGGTCTTCAGCGGCTCACTGCGAGCGGC 315
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 46 LeuCysGlyAlaThrLeuIleAlaProLysTrpLeuLeuThrAlaAlaHisCysArgLys 65
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY 316 AGCAGGTACTGGTGGCGCTGGGGGAACAACAGCCTCAGCCAGCTCAGTCCAGCAGCAG 375
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66 ProHisTyrValIleLeuLeuGlyGluHisAsnLeuGluLysThrArgCysGluGln 85
::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 376 ATCCGGCAGCAGCGGCTTCTCTGTGAGCCATCCGGCTACTCTGGGAGCC-----TCGACG 429
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 86 ArgArgMetAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLys 105
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 430 AGCCAGCAGCAGCAGCCTCGCGTGTCTCGCGCTCGCGCTCGCGCTCGCGCTCGCGCTCG 489
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 106 AspHisArgAsnAspIleMetLeuValLysMetSerSerProAlaPheIleThrArgAla 125
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 490 GTTCAACCCCTGCTGCTCCCAATGACTGTGCAACCGCTGGCAACCGAGTGCCAGCTCTCA 549
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 126 ValArgProLeuThrLeuSerSerLeuCysValThrAlaGlyThrSerCysLeuIleSer 145
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 550 GCGTGGGCGATCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 609
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 146 GlyTrpGlyThrThrSerSerProGlnLeuArgLeuProHisSerLeuArgCysAlaAsn 165
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 610 CTCTCCATCTCTCCCATGCCATGCCATGGTGTGTATCCCGGAGAAATCACAGCAAC 669
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 166 ValSerIleIleGlyHisLysGluCysGluArgAlaTyrProGlyAsnIleThrAspThr 185
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 670 ATGGTGTGTGAGGC---GGCGTCCGGGGGAGGATGCTCCAGCGGTGATTTCTGGGGGC 726
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 186 MetLeuCysAlaSerValArgLysGluLysAspSerCysGlnGlyAspSerGlyGly 205
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 727 CCCCTGGTGTGGGGAGTCTCTCAAGTCTGGTGTCTCTGGGGGTCTGTGGGGCCCTGT 786
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 206 ProLeuValCysAsnGlySerLeuGlnGlyIleIleSerTrpGlyGln---AspProCys 224
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 787 GGACAAGATGGCATCCCTCGAGTCTACACCTATATTGCAAGTATGTGAGTGGATCGCG 846
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 225 AlaValThrArgLysProGlyValThrLysValCysLysTyrPheAspTrpIleHis 244
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 847 ATGATCATGAGGAACAAC 864
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 245 GluValMetArgAsnAsn 250
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RESULT 10
Q8CGR4 PRELIMINARY; PRT; 254 AA.
ID Q8CGR4;
AC Q8CGR4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Prost.
GN Name=Klk15; Synonyms=KLK15;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22325484; PubMed=12437987; DOI=10.1016/S0006-291X(02)02629-3;
RA Olsson A.Y., Lundwall A.;
RT "Organization and evolution of the glandular kallikrein locus in Mus
RT musculus.";
RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M., Mural R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AY152434; AAN78422.1; --
DR HSSP; P00760; 1E2X.
DR MEROPS; S01.297; --
DR MGD; MGI:2447533; Klk15.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

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Db 123 PheAsnAenSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAla 142
Qy 466 CTGCCCGTCCGTAACACAGCAGCGCTTCAACCCCTGCGCCCTCCCAATGACTGTGCAACC 525
Db 143 SerProValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThr 162
Qy 526 GCTGGCACCAGTGCACGCTCTCAGCTGGGGCATCACACACCCACCGAACCACATTC 585
Db 163 AlaGlyThrSerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeu 182
Qy 586 CGGATCTGCTCCAGTGCCTCAACTCTCCATCGCTCCCATGCCACCTGCCATGGTGTG 645
Db 183 ProHisThrLeuArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAla 202
Qy 646 TATCCCGGAGAAATCACAGCAACATGCTGTGTGCGAGC---GGCGTCCCGGGCAGCAT 702
Db 203 TyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAsp 222
Qy 703 GCCTGCCAGGTGATCTGGGGGCCCTCTGTGTGTGGGGAGTCTTCAAGTCTGTGTG 762
Db 223 SerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIle 242
Qy 763 TCCTGGGGTCTGTGGGGCCCTGTGACAGATGCATCCCTGGAGTCTACACCTATATT 822
Db 243 SerTrpGlyGln---AspProCysAlaIleThrArgLysProGlyValThrLysVal 261
Qy 823 TGCAAGTATGTGGACTGATCGGATCGGATGATCATGAGGAACAAC 864
Db 262 CysLysTrpValAspTrpIleGlnGluThrMetLysAsnAsn 275

RESULT 12
Q61S10 PRELIMINARY; PRT; 255 AA.
AC Q61S10;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Kallikrein 15, isoform 4 preproprotein.
GN Name=KLK15;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Director MGC Project;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
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CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; BC069518; AAH69518.1; -.
DR HSSP; P00761; 1AKS.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:peptidolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 255 AA; 28016 MW; 1581B784D4A39C4F CRC64;

Alignment Scores:
Pred. No.: 7.67e-30 Length: 255
Score: 599.00 Matches: 120
Percent Similarity: 59.38% Conservative: 32
Best Local Similarity: 46.88% Mismatches: 86
Query Match: 28.99% Indels: 18
DB: 2 Gaps: 6

US-10-015-385A-193 (1-1091) x Q61S10 (1-255)
Qy 142 CTCCTGTGTGTTCTTGGGCTCAGCCAGCAGCCACA-----CCGAAGATTTC 189
Db 3 LeuLeuLeuThrLeuSerPheLeuLeuAlaSerThrAlaGlnAspGlyAspLysLeuLeu 22
Qy 190 AATGGCACTGAGTGTGGCGCTAACTCACAGCGCTGGCAGGTGGGCTGTGTTGAGGCGACC 249
Db 23 GluGlyAspGluCysAlaProHisSerGlnProTrpGlnValAlaLeuTyrGluArgGly 42
Qy 250 AGCTGCGCTGCGGGGTGTCTTATTGACACACAGGTGGTCTCTCAGCGGCTACTGCG 309
Db 43 ArgPheAsnCysGlyAlaSerLeuIleSerProHisTrpValLeuSerAlaAlaHisCys 62
Qy 310 AGCGCAGCAGGTACTGGGTGGCGCTGGCGGGAACACAGCCTCAGCAGCTCCAGTGGACC 369
Db 63 GlnSerArgPheMetArgValArgLeuGlyGluHisAsnLeuArgLysArgAspGlyPro 82
Qy 370 GAGCAGATCCGCGACAGCGGCTCTCTGTGTGCCCATCCCGCTACTGTGGAGCCCTCGACG 429
Db 83 GluGlnLeuArgThrSerArgValIleProHisProArgTyr-----GluAlaArg 100
Qy 430 AGCCACGACGACGACTCCGCTGCTGCGGTGCGGCTGCGGCTCCGCTCCGCTAACCGACG 489
Db 101 SerHisArgAsnAspIleMetLeuLeuArgLeuValGlnProAlaArgLeuAsnProGln 120
Qy 490 GTTCNAACCCCTGCCCTGCCCAATGACTGTGCACCGCTGGCAGCGAGTGCACCTCTCA 549
Db 121 ValArgProAlaValLeuProThrArgCysProHisProGlyGluAlaCysValValSer 140
Qy 550 GCCTGGGGCATCACCAACCAC-----CCACGGGAAC-----579
Db 141 GlyTrpGlyLeuValSerHisAsnGluProGlyThrAlaGlySerProArgSerGlnVal 160
Qy 580 CCATTCCGGATGTCTCCAGTGCCTCAACCTCTCCATGCTCCCATGCCACCTGCCAT 639
Db 161 SerLeuProAspThrLeuHisCysAlaAsnIleSerIleSerAspThrSerCysAsp 180
Qy 640 GGTGTGTATCCGGGAGAAATCACAGCAACATGTTGTGTGCGAGGGGGCTC---CCGGGG 696
Db 181 LysSerTrpProGlyArgLeuThrAsnThrMetValCysAlaGlyAlaGluGlyArgGly 200
Qy 697 CAGGATGCTCCAGGGTGATTCTGGGGGCCCTCTGGTGTGTGGGGAGTCTCTCAAGT 756
Db 201 AlaGluSerCysGluGlyAspSerGlyGlyProLeuValCysGlyGlyIleLeuGlnGly 220
Qy 757 CTGGTGTCTCTGGGGGTCTGTGGGGCCCTGTGGGCAAGATGGCATCCCTGGAGTCTACACC 816
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Db 83 ProGluGlnLeuArgThrThrSerArgValIleProHisProArgTyr-----GluAla 100
QY 427 AGAGCCACGACAGCAGCTCCGGTGTCTGGCGTCCGCTCCGCTCCGCTACCAACAGC 486
Db 101 ArgSerHisArgAsnAspIleMetLeuLeuArgLeuValGlnProAlaArgLeuAsnPro 120
QY 487 AGCGTTCAACCTCCCTCCGCTCCCAATGACTGCTGCAACCGCTGGCAGCGAGTGCACGTC 546
Db 121 GlnValArgProAlaValLeuProThrArgCysProHisProGlyGluAlaCysValVal 140
QY 547 TCAGCTGGGGGATCACCACCAACAC-----CCACGGGAAC--- 579
Db 141 SerGlyTyrGlyLeuValSerHisAsnGluProGlyThrAlaGlySerProArgSerGln 160
QY 580 ---CCATTCCTCCGATCTGCTCCAGTCTCAACTCTCCATCTCCATGCTCCACCTGC 636
Db 161 ValSerLeuProAspThrLeuHisCysAlaAsnIleSerIleSerAspThrSerCys 180
QY 637 CATGTGTGTATCCCGGAGATCAGGACACATGCTGTGTGCGAGCGGCGTC---CCG 693
Db 181 AspLysSerTyrProGlyArgLeuThrAsnThrMetValCysAlaGlyAlaGluGlyArg 200
QY 694 GGGAGGATGCTGCGAGGCTGATCTGGGGGCCCTGGTGTGTGGGGAGTCTTCAA 753
Db 201 GlyAlaGluSerCysGluGlyAspSerGlyProLeuValCysGlyGlyIleLeuGln 220
QY 754 GGTCTGTGTCTGGGGGCTGTGTGGGGCCCTGTGGACAGATGGCATCTGGAGTCTAC 813
Db 221 GlyIleValSerTyrGlyAspVal---ProCysAspAsnThrThrLysProGlyValTyr 239
QY 814 ACCTATATTGCAAGTATGTGGACTGTGGATCCGGATGATCATGAGGAACAAC 864
Db 240 ThrLysValCysHisTyrLeuGluTrpIleArgGluThrMetLysArgAsn 256

RESULT 14
Q9QYN4
ID Q9QYN4 PRELIMINARY; PRT; 249 AA.
AC Q9QYN4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hippocasin.
GN Name=2310015108Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
OX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
RA Mitsui S., Okui A., Kominami K., Uemura H., Yamaguchi N.;
RT "cDNA cloning and tissue-specific splicing variants of mouse
RT hippocasin/TUSP (PRSS20).";
RL Biochim. Biophys. Acta 1494:206-210(2000).
RL [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Yamaguchi N., Mitsui S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBSJ databases.
CC -! SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AB016226; BAA88825.1; -
DR HSSP; P00760; 1EZX.
DR MEROPS; S01.257; -
DR MGD; MGI:1929977; 2310015108Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW. Hydrolase; Protease; Serine protease.
SQ SEQUENCE 249 AA; 27604 MW; F9PF9CB457D727D5 CRC64;
Alignment Scores:
Pred. No.: 9, 548-30 Length: 249
Score: 597.50 Matches: 118
Percent Similarity: 60.16% Conservative: 33
Best Local Similarity: 47.01% Mismatches: 95
Query Match: 28.92% Indels: 5
DB: 2 Gaps: 4
US-10-015-385A-193 (1-1091) x Q9QYN4 (1-249)
QY 121 ATGGGGCTCAGCATCTTTTGTCTCTGTGTCTTGGGCTCAGCCAGCAGCCACACG 180
Db 1 MetIleLeuArgLeuIleAlaLeuAlaValThrGlyHisValGlyGluThr--- 19
QY 181 AAGATTTCAATGGCACTGAGTGTGGCGTAACCTACAGCCCTGGCAGGTGGGCTGTTT 240
Db 20 ArgIleIleLysGlyTyrGluCysArgProHisSerGlnProTyrGlnValAlaLeuPhe 39
QY 241 GAGGCGACAGCTCGCTCGGGGTGTCTTATTGACACAGGTGGTCTCAGCAGG 300
Db 40 GlnLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProLysTrpLeuLeuThrAla 59
QY 301 GCTCACTCAGCGGCGCAGCAGGTACTGGGTGCGCTGGGGAAACACAGCTCAGCCAGCTC 360
Db 60 AlaHisCysArgLysProHisTyrValIleLeuLeuGlyGluHisAsnLeuGluLysThr 79
QY 361 GACTGGACCGCAGCATCCGCGCTTCTCTGTGACCCATCCCGGCTACCTGGGA 420
Db 80 AspGlyCysGluGlnArgArgMetAlaThrGluSerPheProHisProAspPheAsnAsn 99
QY 421 GCC-----TCGACGAGCAGCAGCAGCTCCCGCTGCTCGCGTGGCGCTGCCCGTC 474
Db 100 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetSerSerProVal 119
QY 475 CGCGTAACCGCAGCGTTCACCCCTCGCTCCCAATGACTGTGTGCAACCCCTGGCACC 534
Db 120 PhePheThrArgAlaValGlnProLeuThrLeuSerProHisCysValAlaAlaGlyThr 139
QY 535 GAGTGCCACGTCTCAGGCTGGGCGATCAACCAACCAACCAACCAACCAACCAACCAAC 594
Db 140 SerCysLeuIleSerGlyTyrGlyThrThrSerSerProGlnLeuArgLeuProHisSer 159
QY 595 CTCAGTGCCTCAACCTCTCCATGCTCCCATGCCACCTGCCATGCTGTGTATCCCGGG 654
Db 160 LeuArgCysAlaAsnValSerIleIleGluHisLysGluCysGluLysAlaTyrProGly 179
QY 655 AGAATCAGCAGCAACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 711
Db 180 AsnIleThrAspThrMetLysCysAlaSerValArgLysGluGlyLysAspSerCysGln 199
QY 712 GGTGATTCTGGGGGCCCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 771
Db 200 GlyAspSerGlyGlyProLeuValCysAsnGlySerLeuGlnGlyIleIleSerTrpGly 219
QY 772 TCTGTGGGGCCTGTGGACAGATGGCATCCCTGAGTCTACACCTATATTGTCAGATAT 831
Db 220 Gln---AspProCysAlaValThrArgLysProGlyValTyrThrLysValCysLysTyr 238
QY 832 GTGGACTGATCCGATCATGAGGAACAAC 864
Db 239 PheAsnTrpIleHisGluValMetArgAsnAsn 249
RESULT 15
Q9QYN3
ID Q9QYN3 PRELIMINARY; PRT; 276 AA.
AC Q9QYN3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)


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QY 595 CTCACGTGCTCAACCTCTCCATCGTCTCCATGCCACCTGCCATGGTGTGTATCCGGG 654
Db |||:|||| |||:|||||:|||| ||| ||| ||| ||| ||| ||| ||| |||
187 LeuArgCysAlaAsnValSerIleIleGluHisLysGluCysGluLysAlaTyrProGly 206
QY 655 AGAATCACGAGCAACATGGTGTGTGCAGGC--GGCGTCCCGGGCGAGGATGCTGCCAG 711
Db ||| ||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
207 AsnIleThrAspThrMetLeuCysAlaSerValArgLysGluGlyLysAspSerCysGln 226
QY 712 GGTGATTCTGGGGCCCCCTGTGTGTGGGGGAGTCTTCAAGGTCTGTGTCTCTGGGG 771
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
227 GlyAspSerGlyGlyProLeuValCysAsnGlySerLeuGlnGlyIleIleSerTrpGly 246
QY 772 TCTGTGGGGCCCTGTGCACAAGATGGCATCCCTGGAGTCTACACCTATATTTCAGATAT 831
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
247 Gln---AspProCysAlaValThrArgLysProGlyValTyrThrLysValCysLysTyr 265
QY 832 GTGACTGGATCCGGATGATCATGAGGAACAAC 864
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
266 PheAsnTrpIleHisGluValMetArgAsnAsn 276
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Search completed: March 5, 2005, 23:17:52
Job time : 251 secs

Run on: March 5, 2005, 23:40:21 ; Search time 183 Seconds
(without alignments)
4611.536 Million cell updates/sec

Title: US-10-015-385A-193
Perfect score: 357
Sequence: 1 caagcaggtcatcccttgg.....aggggcaaaaaaaaaa 1091
Scoring table: OLIGO
Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 3967864
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAB21304	standard;	protein;	248	AA.	
DE	Human KIK-L5	protein #4.				
PN	WO200053776-A2.					
PD	14-SEP-2000.					
PA	(MOUN) MOUNT SINAI HOSPITAL.					
Best Local Similarity:	100.00%					Mismatches: 0
Query Match:	69.47%					Indels: 0
RESULT 2						
ID	AAB24428	standard;	protein;	248	AA.	
DE	Human PRO1303	protein sequence	SEQ ID NO:203.			
PN	WO200032221-A2.					
PD	08-JUN-2000.					
PA	(GETH) GENENTECH INC.					
Best Local Similarity:	100.00%					Mismatches: 0
Query Match:	69.47%					Indels: 0
RESULT 3						
ID	AAB24032	standard;	protein;	248	AA.	
DE	Human PRO1303	protein sequence	SEQ ID NO:33.			
PN	WO200053750-A1.					
PD	14-SEP-2000.					
PA	(GETH) GENENTECH INC.					
Best Local Similarity:	100.00%					Mismatches: 0
Query Match:	69.47%					Indels: 0
RESULT 4						
ID	AAY99393	standard;	protein;	248	AA.	
DE	Human PRO1303 (UNQ669)	amino acid sequence	SEQ ID NO:194.			
PN	WO200012708-A2.					
PD	09-MAR-2000.					
PA	(GETH) GENENTECH INC.					
Best Local Similarity:	100.00%					Mismatches: 0
Query Match:	69.47%					Indels: 0
RESULT 5						
ID	AAM231994	standard;	protein;	248	AA.	
DE	Human EST encoded	protein	SEQ ID NO: 1519.			
PN	WO200154477-A2.					
PD	02-AUG-2001.					
PA	(HYSE-) HYSEQ INC.					
Best Local Similarity:	100.00%					Mismatches: 0
Query Match:	69.47%					Indels: 0
RESULT 6						
ID	AAB66142	standard;	protein;	248	AA.	
DE	Protein of the invention	#54.				
PN	WO200078961-A1.					
PD	28-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Best Local Similarity:	100.00%					Mismatches: 0
Query Match:	69.47%					Indels: 0

RESULT 7

ID ABO33635 standard; protein; 248 AA.
DE Novel human secreted and transmembrane protein PRO1303.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.47% Indels: 0

RESULT 8

ID ABO44488 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.47% Indels: 0

RESULT 9

ID ABO33512 standard; protein; 248 AA.
DE Novel human secreted and transmembrane protein PRO1303.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.47% Indels: 0

RESULT 10

ID ADC18063 standard; protein; 248 AA.
DE Human PRO polypeptide #54.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.47% Indels: 0

RESULT 11

ID ADD70709 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.47% Indels: 0

RESULT 12

ID ADD39786 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.47% Indels: 0

RESULT 13

ID ADD70232 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.47% Indels: 0

RESULT 14

ID ADD38353 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.47% Indels: 0

RESULT 15

ID ADD39309 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.47% Indels: 0

RESULT 16

ID ADD39309 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.47% Indels: 0

ID	ADD38832 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2003092061-A1.		
PD	15-MAY-2003.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 17			
ID	ADD40263 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2003082627-A1.		
PD	01-MAY-2003.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 18			
ID	ADE50484 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2003069179-A1.		
PD	10-APR-2003.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 19			
ID	ADE20096 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2003092883-A1.		
PD	15-MAY-2003.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 20			
ID	ADE50007 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2003082626-A1.		
PD	01-MAY-2003.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 21			
ID	ADE21565 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2003082628-A1.		
PD	01-MAY-2003.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 22			
ID	ADF29990 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2003204053-A1.		
PD	30-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 23			
ID	ADF55883 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2003204054-A1.		
PD	30-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 24			
ID	ADH99387 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2003065142-A1.		
PD	03-APR-2003.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 25			
ID	ADE96567 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2003195347-A1.		
PD	16-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 26			
ID	ADP25878 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2003199675-A1.		
PD	23-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 27			
ID	ADF24777 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2003198993-A1.		
PD	23-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 28			
ID	ADF29513 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2003203401-A1.		
PD	30-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 29			
ID	ADP97044 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2003195334-A1.		
PD	16-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 30			
ID	ADH03082 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2003216562-A1.		
PD	20-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 31			
ID	ADH04036 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2003220471-A1.		
PD	27-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 32			
ID	ADH03559 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2003224478-A1.		
PD	04-DEC-2003.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 33			
ID	ADH04513 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		
PN	US2004005626-A1.		
PD	08-JAN-2004.		
PA	(GETH) GENENTECH INC.		
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.47%	Indels:	0
RESULT 34			
ID	ADH61514 standard; protein; 248 AA.		
DE	Human secreted/transmembrane protein PRO1303.		

PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.47% Indels: 0
RESULT 35
ID ADN10927 standard; protein; 248 AA.
DE Human kallikrein 12, marker of endocrine cancer.
PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.47% Indels: 0
RESULT 36
ID ADL94713 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.47% Indels: 0
RESULT 37
ID ADT94373 standard; protein; 248 AA.
DE Human PRO1303 protein.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.47% Indels: 0
RESULT 38
ID AAB21303 standard; protein; 254 AA.
DE Human KIK-L5 protein #3.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 65.83% Indels: 0
RESULT 39
ID ABG66676 standard; protein; 254 AA.
DE Human novel polypeptide #11.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 65.83% Indels: 0
RESULT 40
ID ADN10926 standard; protein; 254 AA.
DE Human kallikrein 12, marker of endocrine cancer.
PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 65.83% Indels: 0
RESULT 41
ID ADP56174 standard; protein; 254 AA.
DE Human PRO protein sequence SEQ ID NO:2150.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 65.83% Indels: 0
RESULT 42
ID AAB21301 standard; protein; 184 AA.
DE Human KIK-L5 protein #1.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 51.54% Indels: 0
RESULT 43
ID AAO29516 standard; protein; 248 AA.
DE Human kallikrein-like protein 5 (18817).
PN WO2003039475-A2.

PD 15-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.98% Indels: 0
RESULT 44
ID AAY28642 standard; protein; 162 AA.
DE Human secreted protein from cDNA clone HKAFV61.
PN WO9940183-A1.
PD 12-AUG-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.05% Indels: 0
RESULT 45
ID AAB21302 standard; protein; 111 AA.
DE Human KIK-L5 protein #2.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.21% Indels: 0
RESULT 46
ID ADN10928 standard; protein; 111 AA.
DE Human kallikrein 12, marker of endocrine cancer.
PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.21% Indels: 0
RESULT 47
ID ADR72141 standard; peptide; 16 AA.
DE Common protein epitope tag, PET, for human kallikrein 4.
PN US2004180380-A1.
PD 16-SEP-2004.
PA (ENGE-) ENGINEOS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.48% Indels: 0
RESULT 48
ID AAP70474 standard; protein; 562 AA.
DE Sequence of tissue plasminogen (TPA) analogue.
PN WO8703906-A.
PD 02-JUL-1987.
PA (UPJO) UPJOHN CO.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.92% Indels: 0
RESULT 49
ID AAB08953 standard; protein; 30 AA.
DE Human secreted protein sequence encoded by gene 22 SEQ ID NO:110.
PN WO200017222-A1.
PD 30-MAR-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 50
ID AAU76373 standard; protein; 70 AA.
DE Human Marcov Model trypsin consensus protein sequence.
PN WO200206455-A2.
PD 24-JAN-2002.
PA (FARB) BAYER AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 51
ID ABP09500 standard; protein; 107 AA.
DE Human ORFX protein sequence SEQ ID NO:18982.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 52
ID ADC31388 standard; protein; 113 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1470.
PN WO2003029271-A2.

PD 10-APR-2003.
PA (HYSE-) HYSEQ INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:
RESULT 53
ID AAP1986 standard; protein; 117 AA.
DE Chain 2 of modified tissue plasminogen activator.
PN EP253582-A.
PD 20-JAN-1988.
PA (NOVO) NOVO IND AS. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:
RESULT 54
ID AAY72094 standard; protein; 187 AA.
DE Human serine protease #5 encoded by clone HHFBJ67.
PN WO200088247-A2.
PD 16-NOV-2000.
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:
RESULT 55
ID ABG30791 standard; protein; 187 AA.
DE Human serine protease #4.
PN US2002119925-A1.
PD 29-AUG-2002.
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:
RESULT 56
ID AAEE17922 standard; protein; 187 AA.
DE Human gene 4 encoded serine protease, HHFBJ67.
PN WO200198476-A1.
PD 27-DEC-2001.
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:
RESULT 57
ID AAU77550 standard; protein; 199 AA.
DE Membrane-type serine protease #1.
PN WO200212461-A2.
PD 14-FEB-2002.
PA (FARB) BAYER AG. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:
RESULT 58
ID AAY28590 standard; protein; 212 AA.
DE Human Factor D.
PN WO9942133-A1.
PD 26-AUG-1999.
PA (TANO-) TANOX INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:
RESULT 59
ID AAG79215 standard; protein; 214 AA.
DE Consensus sequence of trypsin serine protease-like protein domain.
PN WO200173074-A2.
PD 04-OCT-2001.
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:
RESULT 60
ID ADI17277 standard; protein; 217 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 813.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:
RESULT 61
ID ADI17269 standard; protein; 217 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 805.
PN WO200268649-A2.
PD 06-SEP-2002.

PA (CURA-) CURAGEN CORP. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:
RESULT 62
ID ABO00751 standard; protein; 217 AA.
DE Polypeptide encoded by novel human contig #2.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:
RESULT 63
ID ADI21707 standard; protein; 217 AA.
DE Novel human polypeptide #186.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:
RESULT 64
ID ADJ83076 standard; protein; 217 AA.
DE Trypsin protein which is related to human NOVX protein - SEQ ID 67.
PN US2003170830-A1.
PD 11-SEP-2003.
PA (ALSO-) ALSOBROOK J P. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:
RESULT 65
ID AAE21442 standard; protein; 226 AA.
DE Human trypsin domain consensus protein #2.
PN WO200226802-A2.
PD 04-APR-2002.
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:
RESULT 66
ID ABG75786 standard; protein; 226 AA.
DE Trypsin domain consensus sequence, SMART.
PN US2002165152-A1.
PD 07-NOV-2002.
PA (KAPE-) KAPELLER-LIBERMANN R. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:
RESULT 67
ID AAE14342 standard; protein; 227 AA.
DE Human protease PR7S-7 protein.
PN WO200183775-A2.
PD 08-NOV-2001.

PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 68
ID ABG75785 standard; protein; 227 AA.
DE Trypsin domain consensus sequence, PFAM.
PN US2002165152-A1.
PD 07-NOV-2002.
PA (KAPE/) KAPELLE-LIBERMANN R.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 69
ID AAE39994 standard; protein; 228 AA.
DE Human adipisin protein #3.
PN US2003092620-A1.
PD 15-MAY-2003.
PA (GEST) GENSET SA.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 70
ID ADN041134 standard; protein; 228 AA.
DE Antipsoriatic protein sequence #262.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 71
ID ADP03097 standard; protein; 228 AA.
DE Human insulin resistance-related adipisin protein.
PN JF2004041208-A.
PD 12-FEB-2004.
PA (SANY) SANKYO CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 72
ID ADP23853 standard; protein; 228 AA.
DE PRO polypeptide SEQ ID NO:1031.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 73
ID ADI17268 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 804.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 74
ID ADI17276 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 812.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 75
ID ADJ83075 standard; protein; 230 AA.
DE Trypsin-like serine protease protein - SEQ ID 66.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERRHUSEN B D.
PA (PATT/) PATURAJAN M.
PA (LEPL/) LEPLY D M.
PA (BURG/) BURGESS C E.
PA (SHTM/) SHIMKETS R A.

PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 76
ID AAE06932 standard; protein; 235 AA.
DE Human membrane-type serine protease (WTSP) 4.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 77
ID ADI10375 standard; protein; 235 AA.
DE Human cell surface protease #3.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 78
ID ADJ46899 standard; protein; 235 AA.
DE Human transmembrane serine protease (WTSP) polypeptide #3.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 79
ID AAB11695 standard; protein; 238 AA.
DE Mouse serine protease BSSP2 (mBSSP2), SEQ ID NO:2.
PN WO200031272-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 80
ID ADA50474 standard; protein; 238 AA.
DE Human protease SEQ ID NO:72.
PN WO2003040393-A2.
PD 15-MAY-2003.
PA (DECO-) DECODE GENETICS EHF.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 81
ID AAR07241 standard; protein; 245 AA.
DE t-PA(Del296-302).
PN WO9010649-A.
PD 20-SEP-1990.
PA (TEXA) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 82
ID AAE21441 standard; protein; 249 AA.
DE Human trypsin domain consensus protein #1.
PN WO200226802-A2.
PD 04-APR-2002.
PA (MILL-) MILLENNIUM PHARM INC.

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 83
ID AAR05772 standard; protein; 250 AA.
DE Human adipsin gene product from the clone phg31.
PN WO9006365-A.
PD 14-JUN-1990.
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.
PA (DANA-) DANA-PARBER CANCER INST.
PA (META-) METABOLIC BIOSYSTEMS INC.
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 84
ID AAR05421 standard; protein; 250 AA.
DE Human adipsin/D encoded by a cDNA.
PN WO9001540-A.
PD 22-FEB-1990.
PA (CALB-) CALIF BIOTECHN INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 85
ID AAR07239 standard; protein; 252 AA.
DE t-PA(R304->S).
PN WO9010649-A.
PD 20-SEP-1990.
PA (TEXA-) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 86
ID AAR07240 standard; protein; 252 AA.
DE t-PA(R304->E).
PN WO9010649-A.
PD 20-SEP-1990.
PA (TEXA-) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 87
ID AAR07242 standard; protein; 252 AA.
DE t-PA(R298->E).
PN WO9010649-A.
PD 20-SEP-1990.
PA (TEXA-) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 88
ID AAR07244 standard; protein; 252 AA.
DE t-PA(K296,R298,R299->E,E,E).
PN WO9010649-A.
PD 20-SEP-1990.
PA (TEXA-) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 89
ID AAR07243 standard; protein; 252 AA.
DE t-PA(R299->E).
PN WO9010649-A.
PD 20-SEP-1990.
PA (TEXA-) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 90
ID AAY08025 standard; protein; 253 AA.
DE Mouse protease-related protein (FVP).
PN DE19736198-Cl.
PD 24-DEC-1998.
PA (DEXR-) DEUT KREBSFORSCHUNGSZENTRUM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 91
ID AAB98506 standard; protein; 253 AA.
DE Human tissue plasminogen activator serine protease catalytic domain.
PN WO200129056-A1.

PD 26-APR-2001.
PA (UYAR-) UNIV ARKANSAS.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 92
ID ADA50481 standard; protein; 253 AA.
DE Human protease SEQ ID NO:79.
PN WO2003040393-A2.
PD 15-MAY-2003.
PA (DECO-) DECODE GENETICS EHF.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 93
ID AAE39993 standard; protein; 253 AA.
DE Human adipsin protein #2.
PN US2003092620-A1.
PD 15-MAY-2003.
PA (GEST) GENSET SA.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 94
ID AAE39992 standard; protein; 253 AA.
DE Human adipsin protein #1.
PN US2003092620-A1.
PD 15-MAY-2003.
PA (GEST) GENSET SA.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 95
ID ADE58223 standard; protein; 253 AA.
DE Human Protein P00746, SEQ ID NO 4094.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 96
ID AAY50873 standard; protein; 265 AA.
DE Vampire bat saliva plasminogen activator protein fragment.
PN WO9957251-A2.
PD 11-NOV-1999.
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 97
ID AAY9592 standard; protein; 266 AA.
DE Vampire bat salivary plasminogen activator DSPA.
PN WO200032759-A1.
PD 08-JUN-2000.
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 98
ID AAE24189 standard; protein; 268 AA.
DE Human native K2S heterologous protein fragment (260-527).
PN WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 99
ID AAE24195 standard; protein; 268 AA.
DE Human K2S heterologous protein fragment (260-527) mutant #2.
PN WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 100
ID AAE25043 standard; protein; 268 AA.
DE Human kringle 2 serine protease protein fragment (residues 260-527).
PN WO200240650-A2.

PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 101
ID AAE24194 standard; protein; 272 AA.
DE Human K2S heterologous protein fragment (260-527) mutant #1.
PD WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 102
ID AAB11696 standard; protein; 273 AA.
DE Mouse serine protease BSSP2 (mBSSP2), SEQ ID NO:4.
PD WO200031272-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 103
ID AAE24196 standard; protein; 274 AA.
DE Human K2S heterologous protein fragment (260-527) mutant #3.
PD WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 104
ID AAE24198 standard; protein; 308 AA.
DE Human native K2S heterologous protein fragment (220-527).
PD WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 105
ID AAE24192 standard; protein; 308 AA.
DE Human K2S heterologous protein fragment (220-527) mutant #2.
PD WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 106
ID AAE25042 standard; protein; 308 AA.
DE Human Kringle 2 serine protease protein fragment (residues 220-527).
PD WO200240650-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 107
ID AAB11697 standard; protein; 311 AA.
DE Mouse serine protease BSSP2 (mBSSP2), SEQ ID NO:6.
PD WO200031272-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 108
ID AAE24191 standard; protein; 312 AA.
DE Human K2S heterologous protein fragment (220-527) mutant #1.
PD WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 109
ID AAE24193 standard; protein; 314 AA.
DE Human K2S heterologous protein fragment (220-527) mutant #3.
PD WO200240696-A2.
PD 23-MAY-2002.

PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 110
ID AAB03159 standard; protein; 321 AA.
DE Mouse trypsin family serine protease Tespec PRO-3.
PD WO200026352-A1.
PD 11-MAY-2000.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 111
ID ADP29456 standard; protein; 324 AA.
DE Human secreted protein SEQ ID #223.
PD WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 112
ID AAP70450 standard; protein; 329 AA.
DE Human tissue plasminogen activator (tPA) analogue comprising the B domain
DE of Protein A linked to a catalytic fragment of tPA.
PD WO8705934-A.
PD 08-OCT-1987.
PA (CREA/) CREA R.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 113
ID AAE24198 standard; protein; 331 AA.
DE Human K2S heterologous protein fragment (197-527) mutant #2.
PD WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 114
ID AAE24183 standard; protein; 331 AA.
DE Human native K2S heterologous protein fragment (197-527).
PD WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 115
ID AAE25037 standard; protein; 331 AA.
DE Human Kringle 2 serine protease protein fragment (residues 197-527).
PD WO200240650-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 116
ID AAE24197 standard; protein; 335 AA.
DE Human K2S heterologous protein fragment (197-527) mutant #1.
PD WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 117
ID AAE24185 standard; protein; 335 AA.
DE Human K2S heterologous protein fragment (193-527) mutant #2.
PD WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 118
ID AAE25047 standard; protein; 335 AA.
DE Human K2S protein fragment (residues 197-527) mutant #2.
PD WO200240650-A2.
PD 23-MAY-2002.

PA (BOEH) BOHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 119
ID AAE25039 standard; protein; 335 AA.
DE Human K2S protein fragment (residues 193-527) mutant #2.
PN WO200240650-A2.
PD 23-MAY-2002.
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 120
ID AAE25046 standard; protein; 335 AA.
DE Human K2S protein fragment (residues 197-527) mutant #1.
PN WO200240650-A2.
PD 23-MAY-2002.
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 121
ID AAE24200 standard; protein; 337 AA.
DE Human K2S heterologous protein fragment (197-527) mutant #4.
PN WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 122
ID AAE24201 standard; protein; 337 AA.
DE Human K2S heterologous protein fragment (191-527) mutant #3.
PN WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 123
ID AAE24199 standard; protein; 337 AA.
DE Human K2S heterologous protein fragment (197-527) mutant #3.
PN WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 124
ID AAE25049 standard; protein; 337 AA.
DE Human K2S protein fragment (residues 197-527) mutant #4.
PN WO200240650-A2.
PD 23-MAY-2002.
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 125
ID AAE25048 standard; protein; 337 AA.
DE Human K2S protein fragment (residues 197-527) mutant #3.
PN WO200240650-A2.
PD 23-MAY-2002.
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 126
ID AAE24184 standard; protein; 339 AA.
DE Human K2S heterologous protein fragment (193-527) mutant #1.
PN WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 127
ID AAE25038 standard; protein; 339 AA.
DE Human K2S protein fragment (residues 193-527) mutant #1.
PN WO200240650-A2.
PD 23-MAY-2002.
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 128
ID AAE24187 standard; protein; 343 AA.
DE Human K2S heterologous protein fragment (191-527) mutant #2.
PN WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 129
ID AAE24186 standard; protein; 343 AA.
DE Human K2S heterologous protein fragment (191-527) mutant #1.
PN WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 130
ID AAE25041 standard; protein; 343 AA.
DE Human K2S protein fragment (residues 191-527) mutant #2.
PN WO200240650-A2.
PD 23-MAY-2002.
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 131
ID AAE25040 standard; protein; 343 AA.
DE Human K2S protein fragment (residues 191-527) mutant #1.
PN WO200240650-A2.
PD 23-MAY-2002.
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 132
ID AAP94414 standard; protein; 345 AA.
DE Sequence of coding region in plasmid pUttTtrp.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 133
ID AAP94415 standard; protein; 345 AA.
DE Sequence of coding region in plasmid pthTtrp.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 134
ID AAR35404 standard; protein; 348 AA.
DE tPA-8.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 135
ID AAR35401 standard; protein; 348 AA.
DE tPA-2.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 136
ID AAP70641 standard; protein; 354 AA.
DE Modified tissue plasminogen activator.
PN AU8661804-A.
PD 05-MAR-1987.
PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 3.64% Indels: 0
RESULT 137
ID AAR41024 standard; protein; 354 AA.
DE Modified tissue plasminogen activator #2.
PN US244806-A.
PD 14-SEP-1993.
PA (ELIL ) LILLY & CO ELI.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 138
ID AAE24182 standard; protein; 354 AA.
DE Human native K2S heterologous protein fragment (174-527).
PN WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 139
ID AAE25036 standard; protein; 354 AA.
DE Human Kringle 2 serine protease protein fragment (residues 174-527).
PN WO200240650-A2.
PD 23-MAY-2002.
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 140
ID ABU62712 standard; protein; 354 AA.
DE Human plasminogen activating enzyme.
PN CN1380416-A.
PD 20-NOV-2002.
PA (UYFU-) UNIV FUDAN.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 141
ID AAP94407 standard; protein; 355 AA.
DE Sequence encoded by plasmid pTRKPA delta trp.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 142
ID AAP94411 standard; protein; 355 AA.
DE Sequence of coding region in plasmid pSTTKtrp.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 143
ID AAR06417 standard; protein; 355 AA.
DE Tissue plasminogen activator deriv.
PN EP382174-A.
PD 16-AUG-1990.
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 144
ID AAR44836 standard; protein; 355 AA.
DE Human truncated tPA-1 mutein.
PN JP05304992-A.
PD 19-NOV-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 145
ID AAR44835 standard; protein; 355 AA.
DE Human truncated tPA-6' mutein.
PN JP05304992-A.
PD 19-NOV-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 146
ID AAR35407 standard; protein; 355 AA.
DE tPA-13.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 147
ID AAR35409 standard; protein; 355 AA.
DE tPA-15.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 148
ID AAR35406 standard; protein; 355 AA.
DE tPA-12.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 149
ID AAR35400 standard; protein; 355 AA.
DE tPA-1.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 150
ID AAR35411 standard; protein; 355 AA.
DE tPA-17.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 151
ID AAR35413 standard; protein; 355 AA.
DE tPA-5.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 152
ID AAR35414 standard; protein; 355 AA.
DE tPA-6.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 153
ID AAR35408 standard; protein; 355 AA.
DE tPA-14.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 154
ID AAR35410 standard; protein; 355 AA.
DE tPA-16.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 155
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ID AAR35412 standard; protein; 355 AA.
DE tPA-18.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 156
ID AAR35402 standard; protein; 355 AA.
DE tPA-6.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 157
ID AAR35403 standard; protein; 355 AA.
DE tPA-7.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 158
ID AAR35405 standard; protein; 355 AA.
DE tPA-11.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 159
ID AAR34667 standard; protein; 355 AA.
DE Thrombolytically active protein KIX2P, based on human t-PA.
PN US5676947-A.
PD 14-OCT-1997.
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 160
ID AAW28536 standard; protein; 355 AA.
DE mt-PA6-E.
PN US5658788-A.
PD 19-AUG-1997.
PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 161
ID AAW14431 standard; protein; 355 AA.
DE Tissue plasminogen activator derivative, mt-PA6-E.
PN US5595736-A.
PD 21-JAN-1997.
PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 162
ID ADN02588 standard; protein; 355 AA.
DE Human recombinant tissue-type plasminogen activator (r-PA).
PN CN1429909-A.
PD 16-JUL-2003.
PA (SHAN-) SHANGHAI XINSHENGYUAN MEDICINE RES CO LT.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 163
ID ADN02590 standard; protein; 355 AA.
DE Recombinant tissue-type plasminogen activator (r-PA) Leu346Pro mutant.
PN CN1429909-A.
PD 16-JUL-2003.
PA (SHAN-) SHANGHAI XINSHENGYUAN MEDICINE RES CO LT.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 164
ID AAW28537 standard; protein; 356 AA.
DE mt-PA9.
PN US5658788-A.
PD 19-AUG-1997.
PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 165
ID AAW28535 standard; protein; 356 AA.
DE mt-PA6-D.
PN US5658788-A.
PD 19-AUG-1997.
PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 166
ID AAW14430 standard; protein; 356 AA.
DE Tissue plasminogen activator derivative, mt-PA6-D.
PN US5595736-A.
PD 21-JAN-1997.
PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 167
ID AAW1432 standard; protein; 356 AA.
DE Tissue plasminogen activator derivative, mt-PA9.
PN US5595736-A.
PD 21-JAN-1997.
PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 168
ID ADF32668 standard; protein; 356 AA.
DE Mutant tissue plasminogen activator.
PN CN1381460-A.
PD 27-NOV-2002.
PA (AIRF-) AIR FORCE GEN HOSPITAL.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 169
ID AAR05123 standard; protein; 358 AA.
DE Bat-PA(L).
PN EP352119-A.
PD 24-JAN-1990.
PA (MERI) MERCK & CO INC.
PA (SCHD) SCHERING AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 170
ID AAR22502 standard; protein; 371 AA.
DE [GARSYQ]-[Plasminogen 443-541]-[t-PA 262-527] hybrid.
PN WO9204450-A.
PD 19-MAR-1992.
PA (BERC) BEECHAM GROUP PLC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 171
ID AAW87770 standard; protein; 372 AA.
DE Human tissue plasminogen activator.
PN WO9854199-A1.
PD 03-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 172
ID AAE25034 standard; protein; 377 AA.
DE OmpA-X2S fusion protein.
PN WO200240650-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 173
ID AAB11399 standard; protein; 378 AA.

DE E. coli expression plasmid pET20b(+)-rPA encoded protein.
PN EP1048732-A1.
PD 02-NOV-2000.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 174
ID AAB74200 standard; protein; 378 AA.
DE FelB-rPA fusion protein.
PN EP1077262-A1.
PD 21-FEB-2001.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 175
ID AAB70770 standard; protein; 378 AA.
DE Expression plasmid pET20b(+)-rPA protein.
PN EP1077263-A1.
PD 21-FEB-2001.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 176
ID AAY72021 standard; protein; 378 AA.
DE E. carotovora FelB-rPA fusion protein encoded by pET20b(+)-rPA.
PN EP1054063-A2.
PD 22-NOV-2000.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 177
ID AAR41796 standard; protein; 383 AA.
DE CD4/Tissue-type plasminogen activator (tPA) fusion protein.
PN WO9318162-A1.
PD 16-SEP-1993.
PA (CREA-) CREAGEN INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 178
ID AAY42788 standard; protein; 383 AA.
DE Human CD4-tPA fusion protein.
PN US5961973-A.
PD 05-OCT-1999.
PA (CREA/) CREA R.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 179
ID AAU10702 standard; protein; 383 AA.
DE Human CD4-tPA fusion protein.
PN US6287561-B1.
PD 11-SEP-2001.
PA (CREA/) CREA R.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 180
ID AAP70640 standard; protein; 387 AA.
DE Modified tissue plasminogen activator.
PN AU8661804-A.
PD 05-MAR-1987.
PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 181
ID AAR41023 standard; protein; 387 AA.
DE Modified tissue plasminogen activator.
PN US5244806-A.
PD 14-SEP-1993.
PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 182
ID AAP94417 standard; protein; 389 AA.
DE Sequence of coding region in plasmid pmSTK.

PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 183
ID AAP94418 standard; protein; 389 AA.
DE Sequence of coding region in plasmid pmSTK.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 184
ID AAU75907 standard; protein; 389 AA.
DE Human epidermis-specific serine protease #2.
PN WO200200702-A2.
PD 03-JAN-2002.
PA (FARB) BAYER AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 185
ID AAP82587 standard; protein; 390 AA.
DE Modified tissue plasminogen activator lacking F and G region and kringles
DE region 2 and Q-96, I-98 and S-119 substd for N, T and M resp.
PN JP63230084-A.
PD 26-SEP-1988.
PA (EISA) EISAI CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 186
ID AAP82588 standard; protein; 390 AA.
DE Modified tissue plasminogen activator lacking F and G region and kringles
DE region 1 and G-183 and S-186 substd for S and T resp.
PN JP63230084-A.
PD 26-SEP-1988.
PA (EISA) EISAI CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 187
ID AAP70021 standard; protein; 393 AA.
DE Sequence of tissue plasminogen activator (tPA) deriv. with AAs 45-179
DE deleted.
PN EP242836-A.
PD 28-OCT-1987.
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 188
ID AAP70019 standard; protein; 393 AA.
DE Recombinant plasminogen-activator.
PN EP242835-A.
PD 28-OCT-1987.
PA (MATT/) MATTES R.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 189
ID AAR06486 standard; protein; 394 AA.
DE V-PA gamma.
PN EP383417-A.
PD 22-AUG-1990.
PA (SCHD) SCHERING AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 190
ID AAR05125 standard; protein; 395 AA.
DE Modified Bat-PA(H).
PN EP352119-A.
PD 24-JAN-1990.
PA (MERI) MERCK & CO INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0

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Query Match: 3.64% Indels: 0
RESULT 191
ID AAG78109 standard; protein; 395 AA.
DE Human thrombolytic enzyme NTA.
PN CN1287174-A.
PD 14-MAR-2001.
PA (DOUD/) DOU D.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 192
ID AAR25190 standard; protein; 396 AA.
DE mt-PA6.
PN EP493037-A2.
PD 01-JUL-1992.
PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 193
ID ADA56816 standard; protein; 413 AA.
DE Human secreted protein #99.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 194
ID ADA57353 standard; protein; 413 AA.
DE Human secreted protein #99.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 195
ID ADC74423 standard; protein; 413 AA.
DE Human secreted protein - SEQ ID 1056.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 196
ID ADC74063 standard; protein; 413 AA.
DE Human secreted protein - SEQ ID 696.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 197
ID ADD37850 standard; protein; 413 AA.
DE Human secreted protein #33.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 198
ID ADD38017 standard; protein; 413 AA.
DE Human secreted protein #200.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 199
ID AAB08912 standard; protein; 414 AA.
DE Human secreted protein sequence encoded by gene 22 SEQ ID NO:69.
PN WO200017222-A1.
PD 30-MAR-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 200
ID ABG76907 standard; protein; 418 AA.
DE Human spinesin-like protein.
PN WO200233087-A2.
PD 25-APR-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 201
ID ABR57427 standard; protein; 418 AA.
DE Human NOV11 protein SEQ ID NO:32.
PN WO200294870-A2.
PD 28-NOV-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 202
ID ADJ38447 standard; protein; 418 AA.
DE Human novel protein NOV10b.
PN US2003212256-A1.
PD 13-NOV-2003.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (SMIT/) SMITHSON G.
PA (MULL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (STON/) STONE D J.
PA (GUNT/) GUNTHER E.
PA (ELLE/) ELLERMAN K.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (TAUP/) TAUPIER R J.
PA (BURG/) BURGESS C E.
PA (ZERH/) ZERHUSEN B D.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (GORM/) GORMAN L.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 203
ID ABM84894 standard; protein; 422 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5143.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 204
ID AAR13922 standard; protein; 434 AA.
DE Delta(92-179) and delta(466-470) tPA variant.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 205
ID AAP94412 standard; protein; 437 AA.
DE Sequence of coding region in plasmid pSTQktrp.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 206
ID AAP94410 standard; protein; 437 AA.
DE Sequence of coding region in plasmid pTO1PA delta trp.
PN EP302456-A.
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PD 08-FEB-1989.
PA (FUJII) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 207
ID AAP94413 standard; protein; 437 AA.
DE Sequence of coding region in plasmid pSTQ1trp.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJII) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 208
ID AAP94409 standard; protein; 438 AA.
DE Sequence of coding region in plasmid pTQkPA delta trp.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJII) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 209
ID AAR09259 standard; protein; 439 AA.
DE t-PA variant d92-179, I210R, G211A, K212R, V213R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 210
ID AAR09260 standard; protein; 439 AA.
DE t-PA variant d92-179, N184D, I210R, G211A, K212R, V213R, T252R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 211
ID AAR09261 standard; protein; 439 AA.
DE t-PA variant d92-179, I210R, G211A, K212R, V213R, T252R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 212
ID AAR09258 standard; protein; 439 AA.
DE t-PA variant d92-179, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 213
ID AAR68851 standard; protein; 439 AA.
DE Delta 2-89 tissue plasminogen activator.
PN US5376547-A.
PD 27-DEC-1994.
PA (AMHP) AMERICAN HOME PROD CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 214
ID AAP70643 standard; protein; 441 AA.
DE Modified tissue plasminogen activator.
PN AU8661804-A.
PD 05-MAR-1987.
PA (LILLY) LILLY & CO ELI.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 215
ID AAB11698 standard; protein; 445 AA.
DE Mouse serine protease BSSP2 (mBSSP2), SEQ ID NO:8.
PN WO200031272-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 216
ID AAR08150 standard; protein; 446 AA.
DE Non-glycosylated tPA deriv. lacking finger- and EGF-domains.
PN EP400545-A.
PD 05-DEC-1990.
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 217
ID AAB11699 standard; protein; 457 AA.
DE Human serine protease BSSP2 (hBSSP2), SEQ ID NO:10.
PN WO200031272-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 218
ID AAU82752 standard; protein; 457 AA.
DE Amino acid sequence of novel human protease #51.
PN WO200200860-A2.
PD 03-JAN-2002.
PA (SUGE-) SUGEN INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 219
ID AAR22499 standard; protein; 467 AA.
DE (GARSYQ)-[Plasminogen 347-541]-[t-PA 262-527] hybrid.
PN WO9204450-A.
PD 19-MAR-1992.
PA (BEEC) BEECHAM GROUP PLC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 220
ID AAP94416 standard; protein; 472 AA.
DE Sequence of coding region in plasmid pmTQk112.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJII) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 221
ID ABG76906 standard; protein; 472 AA.
DE Human hepsin/plasma transmembrane serine protease-like protein.
PN WO200233087-A2.
PD 25-APR-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 222
ID ADJ38445 standard; protein; 472 AA.
DE Human novel protein NOV10a.
PN US2003212256-A1.
PD 13-NOV-2003.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (STON/) STONE D J.
PA (GUNT/) GUNTHER E.
PA (ELLE/) ELLERMAN K.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (TAUP/) TAUPIER R J.
PA (BURG/) BURGESS C E.
PA (ZERH/) ZERHUSEN B D.

PA (KEKU/) KERUDA R.
PA (SPVT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (PERN/) FERNANDES E R.
PA (GORM/) GORMAN L.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 223
ID ADH41503 standard; protein; 472 AA.
DE Novel human protein NOV4b.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 224
ID AAP70642 standard; protein; 473 AA.
DE Modified tissue plasminogen activator.
PN AU8661804-A.
PD 05-MAR-1987.
PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 225
ID ADM99257 standard; protein; 475 AA.
DE Environmentally sourced protease protein SeqID 140.
PN WO2004033668-A2.
PD 22-APR-2004.
PA (DIVE-) DIVERSA CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 226
ID AAR03004 standard; protein; 476 AA.
DE Tissue plasminogen activator (t-PA) deriv.
PN EP352710-A.
PD 31-JAN-1990.
PA (BOBF) BOEHRINGER MANNHEIM GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 227
ID ADD05463 standard; protein; 476 AA.
DE Desmodus rotundus urokinase protein.
PN WO2003037363-A2.
PD 08-MAY-2003.
PA (PAJO-) PAJON GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 228
ID AAR05122 standard; protein; 477 AA.
DE Bat-PA(H).
PN EP352119-A.
PD 24-JAN-1990.
PA (MERI) MERCK & CO INC.
PA (SCHD) SCHERING AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 229
ID AAR06458 standard; protein; 477 AA.
DE v-PA alpha2.
PN EP383417-A.
PD 22-AUG-1990.
PA (SCHD) SCHERING AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 230
ID AAR06457 standard; protein; 477 AA.
DE v-PA alpha1.
PN EP383417-A.
PD 22-AUG-1990.
PA (SCHD) SCHERING AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 231
ID AAR09247 standard; protein; 482 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 910.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 232
ID AAR09250 standard; protein; 483 AA.
DE t-PA variant d1-44, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 233
ID AAR09246 standard; protein; 483 AA.
DE t-PA variant d1-44, N184D, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 234
ID AAR08950 standard; protein; 480 AA.
DE Human secreted protein sequence encoded by gene 22 SEQ ID NO:107.
PN WO20017222-A1.
PD 30-MAR-2000.
PA (HUNA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 235
ID AAP60613 standard; protein; 482 AA.
DE Polypeptide with plasminogen activator activity.
PN JP61139386-A.
PD 26-JUN-1986.
PA (TOYJ) TOYO SODA MFG CO LTD.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (CENG) CENTRAL GLASS CO LTD.
PA (HODO) HODOGAYA CHEM IND CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 236
ID ADQ39247 standard; protein; 482 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 910.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 237
ID AAR09250 standard; protein; 483 AA.
DE t-PA variant d1-44, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 238
ID AAR09246 standard; protein; 483 AA.
DE t-PA variant d1-44, N184D, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 239
ID AAR09248 standard; protein; 483 AA.
DE t-PA variant d1-44, I210R, G211A, K212R, V213R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 240
ID AAR09249 standard; protein; 483 AA.
DE t-PA variant d1-44, I210R, G211A, K212R, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 241
ID AAR09254 standard; protein; 483 AA.
DE t-PA variant d1-44, I210R, G211H, K212Q, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 242
ID AAR09257 standard; protein; 483 AA.
DE t-PA variant d1-44, N184D, I210R, G211A, K212R, V213R, T252R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 243
ID AAR09247 standard; protein; 483 AA.
DE t-PA variant d1-44, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 244
ID AAR09251 standard; protein; 483 AA.
DE t-PA variant d1-44, T252R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 245
ID AAR09263 standard; protein; 483 AA.
DE t-PA variant Y67N, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 246
ID AAR09252 standard; protein; 483 AA.
DE t-PA variant d1-44, V213K, T252R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 247
ID AAR09233 standard; protein; 483 AA.
DE t-PA variant d1-44, I210K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 248
ID AAR70851 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N67, D184, E275, I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0

Query Match: 3.64% Indels: 0
RESULT 249
ID AAR70855 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N67, K210, E275, I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 250
ID AAR70879 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N103, S184, E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 251
ID AAR70883 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N103, K210, E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 252
ID AAR70845 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N67, S184, E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 253
ID AAR70848 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N67, R252, E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 254
ID AAR70884 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N103, E275, I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 255
ID AAR70886 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N103, S184, E275, I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 256
ID AAR70849 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N67, K210, E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 257
ID AAR70854 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N67, R252, E275, I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0

RESULT 258
ID AAR70878 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,D184,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 259
ID AAR70843 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 260
ID AAR70877 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 261
ID AAR70846 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,K213,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 262
ID AAR70887 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,K213,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 263
ID AAR79144 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,S184,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 264
ID AAR70850 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 265
ID AAR70852 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,K213,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 266
ID AAR70881 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,R210,A211,R212,R213,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 267

ID AAR70882 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,R252,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 268
ID AAR70885 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,D184,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 269
ID AAR70889 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,R252,E275,O277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 270
ID AAR70844 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,D184,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 271
ID AAR70888 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,R210,A211,R212,R213,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 272
ID AAR70890 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,K210,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 273
ID AAR70880 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,K213,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 274
ID AAR70847 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,R210,A211,R212,R213,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 275
ID AAR70853 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,R210,A211,R212,R213,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 276
ID ABM83143 standard; protein; 495 AA.

DE Human diagnostic and therapeutic pprotein SEQ ID NO:3392.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 277
ID ABM81142 standard; protein; 508 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3391.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 278
ID ADH41501 standard; protein; 513 AA.
DE Novel human protein NOV4a.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 279
ID ADH41511 standard; protein; 513 AA.
DE Novel human protein NOV4f.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 280
ID ADH41517 standard; protein; 513 AA.
DE Novel human protein NOV4i.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 281
ID ADH41515 standard; protein; 513 AA.
DE Novel human protein NOV4h.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 282
ID ADH41507 standard; protein; 513 AA.
DE Novel human protein NOV4d.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 283
ID ADH41513 standard; protein; 513 AA.
DE Novel human protein NOV4g.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 284
ID ADH41505 standard; protein; 513 AA.
DE Novel human protein NOV4c.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 285
ID ADH41519 standard; protein; 513 AA.
DE Novel human protein NOV4j.

PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 286
ID ADH41509 standard; protein; 513 AA.
DE Novel human protein NOV4e.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 287
ID ADH41521 standard; protein; 513 AA.
DE Novel human protein NOV4k.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 288
ID AAP60614 standard; protein; 516 AA.
DE Plasmid pDAP3 encoded sequence.
PN JP61139386-A.
PD 26-JUN-1986.
PA (TOYJ) TOYO SODA MFG CO LTD.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (CENG) CENTRAL GLASS CO LTD.
PA (HODO) HODOGAYA CHEM IND CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 289
ID AAP70257 standard; protein; 516 AA.
DE Sequence of human tissue plasminogen activator (TPA) and leader.
PN EP231883-A.
PD 12-AUG-1987.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (NIPS) NIPPON SODA CO.
PA (CENG) CENTRAL GLASS CO LTD.
PA (TOYJ) TOYO SODA MFG CO LTD.
PA (NISC) NISSAN CHEM IND LTD.
PA (NISC) NISSAN CHEMICAL INDS KK.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 290
ID ADN03787 standard; protein; 516 AA.
DE Antipsooriatic protein sequence #90.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 291
ID ABM80985 standard; protein; 516 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81669, SEQ:2539.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 292
ID ADQ39246 standard; protein; 516 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 909.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 293
ID AAP91961 standard; protein; 518 AA.
DE Sequence of des 1-44E275 t-PA mutant.
PN WO8909266-A.

PD 05-OCT-1989.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 294
ID AAR09237 standard; protein; 518 AA.
DE t-PA deletion variant d297-305.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 295
ID AAR74684 standard; protein; 518 AA.
DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by DPVDQ).
PN CN1082111-A.
PD 16-FEB-1994.
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 296
ID AAR74681 standard; protein; 518 AA.
DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by TSRNR).
PN CN1082111-A.
PD 16-FEB-1994.
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 297
ID AAR74686 standard; protein; 518 AA.
DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by DSSRW).
PN CN1082111-A.
PD 16-FEB-1994.
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 298
ID AAR74679 standard; protein; 518 AA.
DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by TIANK).
PN CN1082111-A.
PD 16-FEB-1994.
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 299
ID AAR09236 standard; protein; 519 AA.
DE t-PA deletion variant d297-304.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 300
ID AAR74680 standard; protein; 519 AA.
DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by KPIAEK).
PN CN1082111-A.
PD 16-FEB-1994.
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 301
ID AAR74687 standard; protein; 519 AA.
DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by DPHEAT).
PN CN1082111-A.
PD 16-FEB-1994.
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 302
ID AAR68852 standard; protein; 519 AA.
DE Delta 55-62 tissue plasminogen activator.
PN US5376547-A.
PD 27-DEC-1994.

PA (AMHP) AMERICAN HOME PROD CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 303
ID AAR09235 standard; protein; 520 AA.
DE t-PA deletion variant d297-303.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 304
ID AAR74689 standard; protein; 520 AA.
DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by QRLASQA).
PN CN1082111-A.
PD 16-FEB-1994.
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 305
ID AAR74688 standard; protein; 520 AA.
DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by DNCRRPG).
PN CN1082111-A.
PD 16-FEB-1994.
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 306
ID ADL00357 standard; protein; 520 AA.
DE Human tissue type plasminogen activator (h-TPA) mutant polypeptide.
PN CN1397564-A.
PD 19-FEB-2003.
PA (LIBB/) LI B.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 307
ID AAP50400 standard; protein; 521 AA.
DE TPA- (13-527).
PN JP60041697-A.
PD 05-MAR-1985.
PA (ASAH) ASAH CHEM IND CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 308
ID AAR09242 standard; protein; 521 AA.
DE t-PA deletion variant d300-305.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 309
ID AAR09234 standard; protein; 521 AA.
DE t-PA deletion variant d297-302.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 310
ID AAR74682 standard; protein; 521 AA.
DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by ERHVSQVT).
PN CN1082111-A.
PD 16-FEB-1994.
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 311
ID AAR74678 standard; protein; 521 AA.
DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by ESKPEAE).
PN CN1082111-A.
PD 16-FEB-1994.
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 312
 ID AAR09241 standard; protein; 522 AA.
 DE t-PA deletion variant d300-304.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 313
 ID AAR09233 standard; protein; 522 AA.
 DE t-PA deletion variant d297-301.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 314
 ID AAR13921 standard; protein; 522 AA.
 DE Delta (466-470) tPA variant with H432A and R434A substns.
 PN WO9113149-A.
 PD 05-SEP-1991.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 315
 ID AAR13918 standard; protein; 522 AA.
 DE Delta (466-470) tPA variant with K416A, H417A and E418A substns.
 PN WO9113149-A.
 PD 05-SEP-1991.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 316
 ID AAR14486 standard; protein; 522 AA.
 DE Delta (466-470) tPA variant with Y67N substitution.
 PN WO9113149-A.
 PD 05-SEP-1991.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 317
 ID AAR13917 standard; peptide; 522 AA.
 DE Delta (466-470) tPA variant with K296A, H297A, R298A and R299A substitutions.
 PN WO9113149-A.
 PD 05-SEP-1991.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 318
 ID AAR13919 standard; protein; 522 AA.
 DE Delta (466-470) tPA variant with E426A, R427A, K429A and E430A substitutions.
 PN WO9113149-A.
 PD 05-SEP-1991.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 319
 ID AAR13920 standard; protein; 522 AA.
 DE Delta (466-470) tPA variant with R339A and R342A substns.
 PN WO9113149-A.
 PD 05-SEP-1991.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 320
 ID AAR74685 standard; protein; 522 AA.
 DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by QPLQTPSS).
 PN CN1082111-A.
 PD 16-FEB-1994.

PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 321
 ID AAR74683 standard; protein; 522 AA.
 DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by YAYSQRDQ).
 PN CN1082111-A.
 PD 16-FEB-1994.
 PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 322
 ID AAR09232 standard; protein; 523 AA.
 DE t-PA deletion variant d297-300.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 323
 ID AAR09240 standard; protein; 523 AA.
 DE t-PA deletion variant d300-303.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 324
 ID AAP82584 standard; protein; 524 AA.
 DE Modified tissue plasminogen activator lacking the G region and with G-183 DE and S-186 substd for S and T resp.
 PN JP63230084-A.
 PD 26-SEP-1988.
 PA (EISA) EISAI CO LTD.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 325
 ID AAP82585 standard; protein; 524 AA.
 DE Modified tissue plasminogen activator lacking F and G region and with S- DE 119 substd for M.
 PN JP63230084-A.
 PD 26-SEP-1988.
 PA (EISA) EISAI CO LTD.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 326
 ID AAR09231 standard; protein; 524 AA.
 DE t-PA deletion variant d297-299.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 327
 ID AAR09239 standard; protein; 524 AA.
 DE t-PA deletion variant d300-302.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 328
 ID AAR99136 standard; protein; 524 AA.
 DE Mutant human tissue plasminogen activator for fibrin clot lysis.
 PN US5501853-A.
 PD 26-MAR-1996.
 PA (BEHW) BEHRINGERWERKE AG.
 PA (CHIR) CHIRON CORP.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 329
 ID AAR99138 standard; protein; 524 AA.
 DE Mutant human tissue plasminogen activator for fibrin clot lysis.

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PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW) BEHRINGWERKE AG.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match:
RESULT 330
ID AAR99134 standard; protein; 524 AA.
DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW) BEHRINGWERKE AG.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match:
RESULT 331
ID AAR99137 standard; protein; 524 AA.
DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW) BEHRINGWERKE AG.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match:
RESULT 332
ID AAR99132 standard; protein; 524 AA.
DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW) BEHRINGWERKE AG.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match:
RESULT 333
ID AAR99135 standard; protein; 524 AA.
DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW) BEHRINGWERKE AG.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match:
RESULT 334
ID AAR99133 standard; protein; 524 AA.
DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW) BEHRINGWERKE AG.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match:
RESULT 335
ID AAR99131 standard; protein; 524 AA.
DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW) BEHRINGWERKE AG.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match:
RESULT 336
ID AAP90175 standard; peptide; 525 AA.
DE Tissue plasminogen activator mutant 2K2.
PN W08907146-A.
PD 10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match:
RESULT 337
ID AAP93540 standard; protein; 525 AA.
DE Tissue plasminogen activator (t-PA) variant MB1018.
PN EP311589-A.
PD 12-APR-1989.

PA (MONS) MONSANTO CO.
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match:
RESULT 338
ID AAR09230 standard; protein; 525 AA.
DE t-PA deletion variant d297-298.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match:
RESULT 339
ID AAR09245 standard; protein; 525 AA.
DE t-PA deletion variant d297, d305.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match:
RESULT 340
ID AAR09238 standard; protein; 525 AA.
DE t-PA deletion variant d300-301.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match:
RESULT 341
ID AAR09244 standard; protein; 525 AA.
DE t-PA deletion variant d297, d300.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match:
RESULT 342
ID AAR09243 standard; protein; 525 AA.
DE t-PA deletion variant d304-305.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match:
RESULT 343
ID AAR09222 standard; protein; 526 AA.
DE t-PA deletion variant d298.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match:
RESULT 344
ID AAR09229 standard; protein; 526 AA.
DE t-PA deletion variant d305.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match:
RESULT 345
ID AAR09224 standard; protein; 526 AA.
DE t-PA deletion variant d300.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match:
RESULT 346
ID AAR09221 standard; protein; 526 AA.
DE t-PA deletion variant d297.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 347
ID AAR09223 standard; protein; 526 AA.
DE t-PA deletion variant d299.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 348
ID AAR09225 standard; protein; 526 AA.
DE t-PA deletion variant d301.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 349
ID AAR09226 standard; protein; 526 AA.
DE t-PA deletion variant d302.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 350
ID AAR09227 standard; protein; 526 AA.
DE t-PA deletion variant d303.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 351
ID AAR09228 standard; protein; 526 AA.
DE t-PA deletion variant d304.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 352
ID AAR09229 standard; protein; 527 AA.
DE Thrombolytic proteins 1-9-1-11 having t-PA activity and R275 is deleted
DE or replaced and containing a modified N-linked glycosylation site.
PN W08704722-A.
PD 13-AUG-1987.
PA (GEMY) GENETICS INST INC.
PA (LARS/) LARSEN G R.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 353
ID AAP1747 standard; protein; 527 AA.
DE Gln(117)-substituted tissue plasminogen activator.
PN EP238304-A.
PD 23-SEP-1987.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 354
ID AAP1748 standard; protein; 527 AA.
DE Tissue plasminogen activator substituted at positions 117 and 119.
PN EP238304-A.
PD 23-SEP-1987.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 355
ID AAP1749 standard; protein; 527 AA.
DE Tissue plasminogen activator substituted at positions 117 and 118.
PN EP238304-A.
PD 23-SEP-1987.

PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 356
ID AAP1750 standard; protein; 527 AA.
DE Tissue plasminogen activator substituted at positions 117 and 275.
PN EP238304-A.
PD 23-SEP-1987.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 357
ID AAP70168 standard; protein; 527 AA.
DE Sequence of wild-type human tissue plasminogen activator (t-PA) from Hela
DE cells.
PN EP225286-A.
PD 10-JUN-1987.
PA (CIBA) CIBA GEIGY AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 358
ID AAP91683 standard; protein; 527 AA.
DE Sequence of tissue plasminogen activator (tPA).
PN W08911531-A.
PD 30-NOV-1989.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 359
ID AAR04186 standard; protein; 527 AA.
DE Plasminogen activator.
PN EP365468-A.
PD 25-APR-1990.
PA (CIBA) CIBA GEIGY AG.
PA (UCPG-) UCP GEN-PHARMA AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 360
ID AAR05806 standard; protein; 527 AA.
DE Thrombolytic protein with secondary structure of human tissue plasminogen
DE activator.
PN JP02145184-A.
PD 04-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 361
ID AAR06236 standard; protein; 527 AA.
DE Novel tissue plasminogen activator (tPA) encoding plasmid pTPA102.
PN EP379890-A.
PD 01-AUG-1990.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 362
ID AAR05489 standard; protein; 527 AA.
DE tPA024 precursor protein.
PN EP373896-A.
PD 20-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
PA (YAMA) NIPPON STEEL CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 363
ID AAR05488 standard; protein; 527 AA.
DE tPA024 precursor protein.
PN EP373896-A.
PD 20-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
PA (YAMA) NIPPON STEEL CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 364

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ID AAR09266 standard; protein; 527 AA.
DE t-PA variant R267A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 365
ID AAR09268 standard; protein; 527 AA.
DE t-PA variant K296A, H297A, R298A, R299A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 366
ID AAR09269 standard; protein; 527 AA.
DE t-PA variant E303A, R304A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 367
ID AAR09277 standard; protein; 527 AA.
DE t-PA variant E426A, R427A, K429A, E430A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 368
ID AAR09255 standard; protein; 527 AA.
DE t-PA variant I210R, G211H, K212Q, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 369
ID AAR09267 standard; protein; 527 AA.
DE t-PA variant D283A, H287A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 370
ID AAR09276 standard; protein; 527 AA.
DE t-PA variant K416A, H417A, E418A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 371
ID AAR09256 standard; protein; 527 AA.
DE t-PA variant I210R, G211A, K212R, V213R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 372
ID AAR09270 standard; protein; 527 AA.
DE t-PA variant H331A, H332A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 373
ID AAR09271 standard; protein; 527 AA.
DE t-PA variant R339A, R342A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 374
ID AAR09275 standard; protein; 527 AA.
DE t-PA variant E410A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 375
ID AAR09274 standard; protein; 527 AA.
DE t-PA variant E408A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 376
ID AAR09272 standard; protein; 527 AA.
DE t-PA variant E347A, E348A, E349A, K351A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 377
ID AAR09281 standard; protein; 527 AA.
DE t-PA variant R449A, D453A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 378
ID AAR09215 standard; protein; 527 AA.
DE t-PA variant F305 H, T, N, K, R, Q.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 379
ID AAR09273 standard; protein; 527 AA.
DE t-PA variant D364A, D365A, D366A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 380
ID AAR09262 standard; protein; 527 AA.
DE t-PA variant Y67N, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 381
ID AAR09280 standard; protein; 527 AA.
DE t-PA variant H445A, R449A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 382
ID AAR09278 standard; protein; 527 AA.
DE t-PA variant H432A, R434A.
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Query Match:	3.64%	Indels:	0
RESULT 400			
ID AAR21593 standard; protein; 527 AA.			
DE tPA variant - E94A.			
PN WO9202612-A.			
PD 20-FEB-1992.			
PA (GENE) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 401			
ID AAR21596 standard; protein; 527 AA.			
DE tPA variant - E94A, D95A, N117Q.			
PN WO9202612-A.			
PD 20-FEB-1992.			
PA (GENE) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 402			
ID AAR21595 standard; protein; 527 AA.			
DE tPA variant - D95G.			
PN WO9202612-A.			
PD 20-FEB-1992.			
PA (GENE) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 403			
ID AAR21597 standard; protein; 527 AA.			
DE tPA variant - E94A, D95A, D236A, K240A.			
PN WO9202612-A.			
PD 20-FEB-1992.			
PA (GENE) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 404			
ID AAR21592 standard; protein; 527 AA.			
DE tPA variant - generic form.			
PN WO9202612-A.			
PD 20-FEB-1992.			
PA (GENE) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 405			
ID AAR22620 standard; protein; 527 AA.			
DE Mutated recombinant tPA.			
PN JP04094684-A.			
PD 26-MAR-1992.			
PA (KANF) KANEKA CORP.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 406			
ID AAR22619 standard; protein; 527 AA.			
DE Mutated recombinant tPA.			
PN JP04094684-A.			
PD 26-MAR-1992.			
PA (KANF) KANEKA CORP.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 407			
ID AAR22617 standard; protein; 527 AA.			
DE Mutated recombinant tPA.			
PN JP04094684-A.			
PD 26-MAR-1992.			
PA (KANF) KANEKA CORP.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 408			
ID AAR22621 standard; protein; 527 AA.			
DE Mutated recombinant tPA.			
PN JP04094684-A.			
PD 26-MAR-1992.			
PA (KANF) KANEKA CORP.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 409			
ID AAR22618 standard; protein; 527 AA.			
DE Mutated recombinant tPA.			
PN JP04094684-A.			
PD 26-MAR-1992.			
PA (KANF) KANEKA CORP.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 410			
ID AAR20221 standard; protein; 527 AA.			
DE t-PA analogue expressed by pCDM8-013.			
PN JP03285680-A.			
PD 16-DEC-1991.			
PA (SUMU) SUMITOMO SEIYAKU KK.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 411			
ID AAR20215 standard; protein; 527 AA.			
DE R462E t-PA analogue.			
PN JP03285680-A.			
PD 16-DEC-1991.			
PA (SUMU) SUMITOMO SEIYAKU KK.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 412			
ID AAR20220 standard; protein; 527 AA.			
DE t-PA analogue expressed by pCDM8-012.			
PN JP03285680-A.			
PD 16-DEC-1991.			
PA (SUMU) SUMITOMO SEIYAKU KK.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 413			
ID AAR20216 standard; protein; 527 AA.			
DE R462G t-PA analogue.			
PN JP03285680-A.			
PD 16-DEC-1991.			
PA (SUMU) SUMITOMO SEIYAKU KK.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 414			
ID AAR20219 standard; protein; 527 AA.			
DE t-PA analogue expressed by pCDM8-011.			
PN JP03285680-A.			
PD 16-DEC-1991.			
PA (SUMU) SUMITOMO SEIYAKU KK.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 415			
ID AAR20222 standard; protein; 527 AA.			
DE t-PA analogue expressed by pCDM8-014.			
PN JP03285680-A.			
PD 16-DEC-1991.			
PA (SUMU) SUMITOMO SEIYAKU KK.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 416			
ID AAR20223 standard; protein; 527 AA.			
DE t-PA analogue expressed by pCDM8-018.			
PN JP03285680-A.			
PD 16-DEC-1991.			
PA (SUMU) SUMITOMO SEIYAKU KK.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 417			
ID AAR20217 standard; protein; 527 AA.			
DE t-PA analogue expressed by pCDM8-009.			
PN JP03285680-A.			
PD 16-DEC-1991.			
PA (SUMU) SUMITOMO SEIYAKU KK.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0
RESULT 418			
ID AAR20216 standard; protein; 527 AA.			
DE t-PA analogue expressed by pCDM8-012.			
PN JP03285680-A.			
PD 16-DEC-1991.			
PA (SUMU) SUMITOMO SEIYAKU KK.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.64%	Indels:	0

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ID AAR20218 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-010.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU ) SUMITOMO SEIYAKU KK.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 419
ID AAR44808 standard; protein; 527 AA.
DE Human tPA variant N50.
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 420
ID AAR44809 standard; protein; 527 AA.
DE Human tPA variant (N65, S67).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 421
ID AAR44811 standard; protein; 527 AA.
DE Human tPA variant N67.
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 422
ID AAR44810 standard; protein; 527 AA.
DE Human tPA variant (N65, T67).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 423
ID AAR44816 standard; protein; 527 AA.
DE Human tPA variant (N67, N103).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 424
ID AAR44813 standard; protein; 527 AA.
DE Human tPA variant (N105, S107).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 425
ID AAR44815 standard; protein; 527 AA.
DE Human tPA variant (N67, A197, A198, A298, A299).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 426
ID AAR44812 standard; protein; 527 AA.
DE Human tPA variant N103.
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 427
ID AAR44817 standard; protein; 527 AA.
DE Human tPA variant (N67, A449, A453).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 428
ID AAR44814 standard; protein; 527 AA.
DE Human tPA variant (N105, T107).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 429
ID AAR70875 standard; protein; 527 AA.
DE Human t-PA variant (N60, N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 430
ID AAR70876 standard; protein; 527 AA.
DE Human t-PA variant (N60, N67, N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 431
ID AAR70907 standard; protein; 527 AA.
DE Human t-PA variant (N103, A460, A462).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 432
ID AAR70863 standard; protein; 527 AA.
DE Human t-PA variant (N67, A364, A365, A366).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 433
ID AAR70865 standard; protein; 527 AA.
DE Human t-PA variant (N67, A410).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 434
ID AAR70903 standard; protein; 527 AA.
DE Human t-PA variant (N103, A432, A434).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 435
ID AAR70864 standard; protein; 527 AA.
DE Human t-PA variant (N67, A408).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 436
ID AAR70871 standard; protein; 527 AA.
DE Human t-PA variant (N67, A449, A453).
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PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 437
ID AAR70857 standard; protein; 527 AA.
DE Human t-PA variant (N67,A283,A287).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 438
ID AAR70866 standard; protein; 527 AA.
DE Human t-PA variant (N67,A416,A417,A418).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 439
ID AAR70894 standard; protein; 527 AA.
DE Human t-PA variant (N103,A303,A304).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 440
ID AAR70896 standard; protein; 527 AA.
DE Human t-PA variant (N103,A339,A342).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 441
ID AAR70898 standard; protein; 527 AA.
DE Human t-PA variant (N103,A364,A365,A366).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 442
ID AAR70901 standard; protein; 527 AA.
DE Human t-PA variant (N103,A416,A417,A418).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 443
ID AAR70904 standard; protein; 527 AA.
DE Human t-PA variant (N103,A440).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 444
ID AAR70858 standard; protein; 527 AA.
DE Human t-PA variant (N67,A296,A297,A298,A299).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 445
ID AAR70861 standard; protein; 527 AA.
DE Human t-PA variant (N67,A339,A342).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 446
ID AAR70897 standard; protein; 527 AA.
DE Human t-PA variant (N103,A347,A348,A349,A351).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 447
ID AAR70874 standard; protein; 527 AA.
DE Human t-PA variant (N67,N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 448
ID AAR70892 standard; protein; 527 AA.
DE Human t-PA variant (N103,A283,A287).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 449
ID AAR70868 standard; protein; 527 AA.
DE Human t-PA variant (N67,A432,A434).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 450
ID AAR70895 standard; protein; 527 AA.
DE Human t-PA variant (N103,A331,A332).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 451
ID AAR70860 standard; protein; 527 AA.
DE Human t-PA variant (N67,A331,A332).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 452
ID AAR70906 standard; protein; 527 AA.
DE Human t-PA variant (N103,A449,A453).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 453
ID AAR70872 standard; protein; 527 AA.
DE Human t-PA variant (N67,A460,A462).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 454
ID AAR70899 standard; protein; 527 AA.
DE Human t-PA variant (N103,A408).
PN US5385732-A.
PD 31-JAN-1995.
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PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 455
ID AAR70900 standard; protein; 527 AA.
DE Human t-PA variant (N103,A410).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 456
ID AAR70862 standard; protein; 527 AA.
DE Human t-PA variant (N67,A347,A348,A349,A351).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 457
ID AAR70870 standard; protein; 527 AA.
DE Human t-PA variant (N67,A445,A449).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 458
ID AAR70842 standard; protein; 527 AA.
DE Wild type tissue plasminogen activator protein.
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 459
ID AAR70856 standard; protein; 527 AA.
DE Human t-PA variant (N67,A267).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 460
ID AAR70859 standard; protein; 527 AA.
DE Human t-PA variant (N67,A303,A304).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 461
ID AAR70893 standard; protein; 527 AA.
DE Human t-PA variant (N103,A296,A297,A298,A299).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 462
ID AAR70905 standard; protein; 527 AA.
DE Human t-PA variant (N103,A445,A449).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 463
ID AAR70902 standard; protein; 527 AA.
DE Human t-PA variant (N103,A426,A427,A429,A430).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 464
ID AAR70867 standard; protein; 527 AA.
DE Human t-PA variant (N67,A426,A427,A429,A430).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 465
ID AAR70869 standard; protein; 527 AA.
DE Human t-PA variant (N67,A440).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 466
ID AAR70891 standard; protein; 527 AA.
DE Human t-PA variant (N103,A267).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 467
ID AAR99130 standard; protein; 527 AA.
DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW) BEHRINGWERKE AG.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 468
ID AAR99125 standard; protein; 527 AA.
DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW) BEHRINGWERKE AG.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 469
ID AAR99126 standard; protein; 527 AA.
DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW) BEHRINGWERKE AG.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 470
ID AAR99128 standard; protein; 527 AA.
DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW) BEHRINGWERKE AG.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 471
ID AAR99129 standard; protein; 527 AA.
DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW) BEHRINGWERKE AG.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 472
ID AAR99124 standard; protein; 527 AA.

DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW) BEHRINGERWERKE AG.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 473
ID AAR99127 standard; protein; 527 AA.
DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW) BEHRINGERWERKE AG.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 474
ID AAW57779 standard; protein; 527 AA.
DE R275E,H417E human tissue-type plasminogen activator protein mutant.
PN WO9821320-A2.
PD 22-MAY-1998.
PA (SCRI) SCRIPPS RES INST.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 475
ID AAW57778 standard; protein; 527 AA.
DE R275E,H417D human tissue-type plasminogen activator protein mutant.
PN WO9821320-A2.
PD 22-MAY-1998.
PA (SCRI) SCRIPPS RES INST.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 476
ID AAW57780 standard; protein; 527 AA.
DE R275E,K429Y human tissue-type plasminogen activator protein mutant.
PN WO9821320-A2.
PD 22-MAY-1998.
PA (SCRI) SCRIPPS RES INST.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 477
ID AAW45907 standard; peptide; 527 AA.
DE Single chain form of the intact t-PA molecule.
PN WO9802454-A2.
PD 22-JAN-1998.
PA (ADPR-) ADPROTECH PLC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 478
ID AAE24190 standard; protein; 527 AA.
DE Human tissue plasminogen activator (tPA) protein.
PN WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 479
ID AAG79362 standard; protein; 527 AA.
DE Human tissue plasminogen activator.
PN WO200243747-A2.
PD 06-JUN-2002.
PA (ISIS-) ISIS INNOVATION LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 480
ID AAE25044 standard; protein; 527 AA.
DE Human tissue plasminogen activator (tPA) protein.
PN WO200240650-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 481

ID ADL92126 standard; protein; 527 AA.
DE Alteplase protein sequence.
PN WO200309862-A1.
PD 04-DEC-2003.
PA (NANO-) APPLIED NANOSYSTEMS BV.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 482
ID AAP71451 standard; protein; 528 AA.
DE Modified human tissue plasminogen activator.
PN EP238304-A.
PD 23-SEP-1987.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 483
ID AAP71449 standard; protein; 528 AA.
DE Modified human tissue plasminogen activator.
PN EP238304-A.
PD 23-SEP-1987.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 484
ID AAP71450 standard; protein; 528 AA.
DE Modified human tissue plasminogen activator.
PN EP238304-A.
PD 23-SEP-1987.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 485
ID AAP90171 standard; peptide; 528 AA.
DE Tissue plasminogen activator mutant 2K1 1K2.
PN WO8907146-A.
PD 10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 486
ID AAR07033 standard; protein; 528 AA.
DE Thrombolytic protein with secondary structure of human tissue plasminogen activator.
PN JP02145184-A.
PD 04-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 487
ID AAR09218 standard; protein; 528 AA.
DE t-PA insertion variant i305 H, T, N, K, R, Q.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 488
ID AAR09216 standard; protein; 528 AA.
DE t-PA insertion variant i304 H, T, N, K, R, Q.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 489
ID AAR25435 standard; protein; 528 AA.
DE T-PA variant R299D.
PN WO9211377-A1.
PD 09-JUL-1992.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 490
ID AAR25435 standard; protein; 528 AA.
DE T-PA variant R299D.
PN WO9211377-A1.
PD 09-JUL-1992.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 490

ID AAR68853 standard; protein; 528 AA.
DE Bifibronection domain-delta 52-94-tissue plasminogen activator.
PN US5376547-A.
PD 27-DEC-1994.
PA (AMHP) AMERICAN HOME PROD CORP. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.64%
RESULT 491
ID AAR09217 standard; protein; 529 AA.
DE t-PA insertion variant i304 HH.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.64%
RESULT 492
ID AAR09220 standard; protein; 529 AA.
DE t-PA insertion variant i304H, i305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.64%
RESULT 493
ID AAR09219 standard; protein; 529 AA.
DE t-PA insertion variant i305 HH.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.64%
RESULT 494
ID AAP61007 standard; protein; 530 AA.
DE Sequence of tissue plasminogen activator (TPA) encoded by PUCH.
PN DE3537176-A.
PD 10-JUL-1986.
PA (ZYMO) ZYMOGENETICS INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.64%
RESULT 495
ID AAP70882 standard; protein; 530 AA.
DE Thrombolytic protein 1-19-1-21 having t-PA activity, deleted or replaced
DE R275 is and containing a modified N-linked glycosylation site.
PN WO8704722-A.
PD 13-AUG-1987.
PA (GEMY) GENETICS INST INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.64%
RESULT 496
ID AAP71659 standard; protein; 530 AA.
DE Thrombolytic protein with t-PA activity where R275 is deleted or replaced
DE and containing a modified N-linked glycosylation site.
PN WO8704722-A.
PD 13-AUG-1987.
PA (GEMY) GENETICS INST INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.64%
RESULT 497
ID AAP70879 standard; protein; 530 AA.
DE Thrombolytic proteins 1-1-1-7 having t-PA activity, where R275 is deleted
DE or replaced.
PN WO8704722-A.
PD 13-AUG-1987.
PA (GEMY) GENETICS INST INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.64%
RESULT 498
ID AAP70881 standard; protein; 530 AA.
DE Thrombolytic protein 1-12-1-18 having t-PA activity, deleted or replaced
DE R275 is and containing a modified N-linked glycosylation site.

PN WO8704722-A.
PD 13-AUG-1987.
PA (GEMY) GENETICS INST INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.64%
RESULT 499
ID AAP70449 standard; protein; 530 AA.
DE Sequence encoded by of synthetic gene for mature human tissue plasminogen
DE activator (tPA).
PN WO8705934-A.
PD 08-OCT-1987.
PA (CREA) CREA R. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.64%
RESULT 500
ID AAP92277 standard; protein; 530 AA.
DE Sequence of modified tPA-type thrombolytic proteins.
PN WO8810119-A.
PD 29-DEC-1988.
PA (GEMY) GENETICS INST INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.64%
RESULT 501
ID AAP60700 standard; protein; 531 AA.
DE Sequence of tissue plasminogen activator (t-PA) encoded by plasmid
DE PTPA25.
PN WO8601538-A.
PD 13-MAR-1986.
PA (BIOJ) BIOGEN NV. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.64%
RESULT 502
ID AAR07034 standard; protein; 531 AA.
DE Thrombolytic protein with secondary structure of human tissue plasminogen
DE activator.
PN JP02145184-A.
PD 04-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.64%
RESULT 503
ID AAP90180 standard; peptide; 534 AA.
DE Tissue plasminogen activator mutant U1t.
PN WO8907146-A.
PD 10-AUG-1989.
PA (INTE) INTEG GENETICS INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.64%
RESULT 504
ID AAR11661 standard; protein; 537 AA.
DE Tissue plasminogen activator deriv.
PN JP03065184-A.
PD 20-MAR-1991.
PA (KANF) KANEGAFUCHI CHEM KK. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.64%
RESULT 505
ID AAR12846 standard; protein; 539 AA.
DE t-PA growth domain deletion mutant.
PN JP03130077-A.
PD 03-JUN-1991.
PA (KANF) KANEGAFUCHI CHEM KK. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.64%
RESULT 506
ID AAP71745 standard; protein; 549 AA.
DE des(Cys51-Asp87)t-PA with extra finger domain.
PN EP241210-A.
PD 14-OCT-1987.
PA (BEEC) BEECHAM GROUP PLC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.64%

RESULT 507
ID AAR11662 standard; protein; 552 AA.
DE Tissue plasminogen activator deriv.
PN JP03061484-A.
PD 20-MAR-1991.
PA (KANF) KANEGAFUCHI CHEM KK.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 508
ID AAR06238 standard; protein; 555 AA.
DE Novel mutant tissue plasminogen activator (tPA) encoded by plasmid
DE pIGNTOFPA.
PN EP379890-A.
PD 01-AUG-1990.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 509
ID AAR23805 standard; protein; 555 AA.
DE t-PA (Del 296-302) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 510
ID AAR13148 standard; protein; 556 AA.
DE T-PA variant contg. fibronectin for thrombosis lysis (2).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 511
ID AAR13020 standard; protein; 557 AA.
DE T-PA variant contg. fibronectin for thrombosis lysis (4).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 512
ID AAR13149 standard; protein; 557 AA.
DE T-PA variant contg. fibronectin for thrombosis lysis (4).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 513
ID AAR13153 standard; protein; 558 AA.
DE T-PA with -ve charged finger and/or kringle domain (8).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 514
ID AAR13150 standard; protein; 558 AA.
DE T-PA with -ve charged finger and/or kringle domain (3).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 515
ID AAR81361 standard; protein; 559 AA.
DE Tissue plasminogen activator analogue.
PN EP293934-A.
PD 07-DEC-1988.
PA (ZYMO) ZYMOGENETICS INC.
PA (NOVO) NOVO IND AS.
PA (EISA) EISA CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 516
ID AAR80654 standard; protein; 559 AA.
DE Tissue plasminogen activator analogue.
PN EP293934-A.
PD 07-DEC-1988.
PA (ZYMO) ZYMOGENETICS INC.
PA (NOVO) NOVO IND AS.
PA (EISA) EISA CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 517
ID AAR94403 standard; protein; 559 AA.
DE Analogue of amino acid sequence of tissue plasminogen activator (t-PA).
PN AU8817430-A.
PD 08-DEC-1988.
PA (NOVO) NOVO IND AS.
PA (ZYMO) ZYMOGENETICS INC.
PA (EISA) EISAI CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 518
ID AAR13283 standard; protein; 559 AA.
DE JMI-229 cell line t-PA.
PN WO9110447-A.
PD 25-JUL-1991.
PA (PORT-) PORTON PROD LTD
PA (PUBL-) PUBLIC HEALTH LAB SERVIC.
PA (UNLO) UNIV COLLEGE LONDON.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 519
ID AAR13152 standard; protein; 559 AA.
DE T-PA with -ve charged finger and/or kringle domain (6).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 520
ID AAR13151 standard; protein; 559 AA.
DE T-PA with -ve charged finger and/or kringle domain (4).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 521
ID AAR13156 standard; protein; 559 AA.
DE T-PA variant having Lys416 substitution (6).
PN JP03061484-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 522
ID AAR13154 standard; protein; 559 AA.
DE T-PA variant having Lys416 substitution (2).
PN JP03061484-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 523
ID AAR12340 standard; protein; 559 AA.
DE T-PA variant contg. fibronectin for thrombosis lysis (1).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 524

ID AAR96222 standard; protein; 559 AA.
 DE Novel plasminogen activator.
 PN US5504001-A.
 PD 02-APR-1996.
 PA (ZYMO) ZYMOGENETICS INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 525

ID AAR96223 standard; protein; 559 AA.
 DE Novel plasminogen activator.
 PN US5504001-A.
 PD 02-APR-1996.
 PA (ZYMO) ZYMOGENETICS INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 526

ID AAW23368 standard; protein; 559 AA.
 DE Human tissue plasminogen activator deletion mutant.
 PN US5656269-A.
 PD 12-AUG-1997.
 PA (CHIR) CHIRON CORP.
 PA (BEHW) BEHRINGERWERKE AG.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 527

ID ABB57034 standard; protein; 559 AA.
 DE Mouse ischaemic condition related protein sequence SEQ ID NO:41.
 PN WO200118188-A2.
 PD 22-NOV-2001.
 PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 528

ID AAR12341 standard; protein; 560 AA.
 DE T-PA variant contg. fibronectin for thrombosis lysis (3).
 PN JP03061482-A.
 PD 18-MAR-1991.
 PA (FUJI) FUJISAWA PHARM CO LTD.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 529

ID AAP50219 standard; protein; 561 AA.
 DE Tissue plasminogen activator encoded by cDNA clone.
 PN EP143081-A.
 PD 29-MAY-1985.
 PA (CIBA) CIBA GEIGY AG.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 530

ID AAP70020 standard; protein; 561 AA.
 DE Sequence of tissue plasminogen activator (tPA).
 PN EP242836-A.
 PD 28-OCT-1987.
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 531

ID AAR12342 standard; protein; 561 AA.
 DE T-PA with -ve charged finger and/or kringle domain (1).
 PN JP03061483-A.
 PD 18-MAR-1991.
 PA (FUJI) FUJISAWA PHARM CO LTD.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 532

ID AAR12367 standard; protein; 561 AA.
 DE T-PA with -ve charged finger and/or kringle domain (7).
 PN JP03061483-A.
 PD 18-MAR-1991.
 PA (FUJI) FUJISAWA PHARM CO LTD.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 533

ID AAP30001 standard; protein; 562 AA.
 DE Sequence of full length tissue plasminogen activator (t-Pa).
 PN EP93619-A.
 PD 09-NOV-1983.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 534

ID AAP50342 standard; protein; 562 AA.
 DE Human tPA.
 PN DK8406107-A.
 PD 16-AUG-1985.
 PA (GEWY) GENENTECH INST INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 535

ID AAP60790 standard; protein; 562 AA.
 DE Sequence of human pre-tissue plasminogen activator (pre-t-Pa).
 PN GB2173804-A.
 PD 22-OCT-1986.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 536

ID AAP60810 standard; protein; 562 AA.
 DE Sequence of modified human tissue plasminogen activator (t-Pa).
 PN FR2581652-A.
 PD 14-NOV-1986.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 537

ID AAP60214 standard; protein; 562 AA.
 DE Sequence of active human uterine tissue plasminogen activator (UTPA).
 PN EP178105-A.
 PD 16-APR-1986.
 PA (INTE-) INTEG GENETICS INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 538

ID AAP70285 standard; protein; 562 AA.
 DE Sequence encoded by human tissue plasminogen activator (t-Pa) cDNA clone.
 PN EP236209-A.
 PD 09-SEP-1987.
 PA (GENE-) GENETICA.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 539

ID AAP81913 standard; protein; 562 AA.
 DE Tissue plasminogen activator encoded by pEMpl-tPA.
 PN WO8800242-A.
 PD 14-JAN-1988.
 PA (DAMO-) DAMON BIOTECH INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 540

ID AAP80655 standard; protein; 562 AA.
 DE Tissue plasminogen activator analogue.
 PN EP293934-A.
 PD 07-DEC-1988.
 PA (ZYMO) ZYMOGENETICS INC.
 PA (NOVO) NOVO IND AS.
 PA (EISA) EISA CO LTD.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 541

ID AAP80656 standard; protein; 562 AA.
 DE Tissue plasminogen activator analogue.
 PN EP293934-A.
 PD 07-DEC-1988.
 PA (ZYMO) ZYMOGENETICS INC.
 PA (NOVO) NOVO IND AS.
 PA (EISA) EISA CO LTD.
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 RESULT 542

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 542
ID AAP94380 standard; protein; 562 AA.
DE Amino acid sequence of tissue plasminogen activator (t-PA) protein.
PN AU8817430-A.
PD 08-DEC-1988.
PA (NOVO) NOVO IND AS.
PA (ZYMO) ZYMOGENETICS INC.
PA (EISA) EISAI CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 543
ID AAP82582 standard; protein; 562 AA.
DE Tissue plasminogen activator with S-119 substd for M and QGI96-98 substd
DE for NGT.
PN JP63230083-A.
PD 26-SEP-1988.
PA (EISA) EISAI CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 544
ID AAP82580 standard; protein; 562 AA.
DE Tissue plasminogen activator with G-183 and S-186 substd for S and T.
PN JP63230083-A.
PD 26-SEP-1988.
PA (EISA) EISAI CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 545
ID AAP94406 standard; protein; 562 AA.
DE Sequence encoded by native tPA of plasmid pST112.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 546
ID AAP93716 standard; protein; 562 AA.
DE Human melanoma t-PA encoded by plasmid pKG12.
PN EP237066-A.
PD 28-DEC-1988.
PA (KABI) KABIGEN AB.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 547
ID AAP90916 standard; protein; 562 AA.
DE Human tissue plasminogen activator.
PN JP01174388-A.
PD 10-JUL-1989.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 548
ID AAP94238 standard; protein; 562 AA.
DE Human tissue plasminogen activator (t-PA) gene.
PN WO8900197-A.
PD 12-JAN-1989.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 549
ID AAR07079 standard; protein; 562 AA.
DE Thrombolytic protein with secondary structure of human tissue plasminogen activator.
PN JP02145184-A.
PD 04-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 550
ID AAR09287 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT6 (Thr 67, Asp 68).

PN WO8912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 551
ID AAR09288 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT11 (Ser 67, Leu 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 552
ID AAR09286 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT5 (Ser 67, Ser 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 553
ID AAR09289 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT12 (Asp 67, Thr 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 554
ID AAR09290 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue GP6 (Leu 66, Asp 67, Thr 68, Gln 117).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 555
ID AAR05388 standard; protein; 562 AA.
DE Thrombolytic protein.
PN JP02119776-A.
PD 07-MAY-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 556
ID AAR09284 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (tPA) mutant Thr 478.
PN WO8912680-A.
PD 28-DEC-1989.
PA (UNIW) UNIV WASHINGTON.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 557
ID AAR06237 standard; protein; 562 AA.
DE Novel tissue plasminogen activator (tPA) encoded by plasmid pST112.
PN EP379890-A.
PD 01-AUG-1990.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 558
ID AAR04700 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA C87S, H420S
DE with altered residues 419 and 420.
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 3.64% Indels: 0
RESULT 559
ID AAR04701 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA K419S with
DE altered residue 419.
PD EP351246-A.
PD 17-JAN-1990.
PA (NOVO ) NOVO-NORDISK AS.
PA (NOVO ) NOVO-NORDISK AS.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 560
ID AAR04702 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA C87S; K419S
DE with altered residues 87 and 419.
PD EP351246-A.
PD 17-JAN-1990.
PA (NOVO ) NOVO-NORDISK AS.
PA (NOVO ) NOVO-NORDISK AS.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 561
ID AAR04699 standard; protein; 562 AA.
DE Native tissue plasminogen activator (t-PA).
PD EP351246-A.
PD 17-JAN-1990.
PA (NOVO ) NOVO-NORDISK AS.
PA (NOVO ) NOVO-NORDISK AS.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 562
ID AAR13727 standard; protein; 562 AA.
DE T-PA67+ mutant with supernumerary N-linked oligosaccharide side chain.
PD US041376-A.
PD 20-AUG-1991.
PA (TEXA ) UNIV TEXAS SYSTEM.
PA (COLD-) COLD SPRING HARBOR LAB.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 563
ID AAR13441 standard; protein; 562 AA.
DE MB1023 t-PA variant.
PD US037752-A.
PD 06-AUG-1991.
PA (MONS ) MONSANTO CO.
PA (MONS ) MONSANTO CO.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 564
ID AAR13442 standard; protein; 562 AA.
DE MB1083 t-PA variant with longer half-life.
PD US037752-A.
PD 06-AUG-1991.
PA (MONS ) MONSANTO CO.
PA (MONS ) MONSANTO CO.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 565
ID AAR12343 standard; protein; 562 AA.
DE T-PA with -ve charged finger and/or kringle domain (2).
PD EP351246-A.
PD 18-MAR-1991.
PA (FUJI ) FUJISAWA PHARM CO LTD.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 566
ID AAR12366 standard; protein; 562 AA.
DE T-PA with -ve charged finger and/or kringle domain (5).
PD EP351246-A.
PD 18-MAR-1991.
PA (FUJI ) FUJISAWA PHARM CO LTD.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 567
ID AAR12425 standard; protein; 562 AA.
DE T-PA variant having Lys416 substitution (5).
PD EP351246-A.
PD 18-MAR-1991.
PA (FUJI ) FUJISAWA PHARM CO LTD.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 568
ID AAR12423 standard; protein; 562 AA.
DE T-PA variant having Lys416 substitution (1).
PD EP351246-A.
PD 18-MAR-1991.
PA (FUJI ) FUJISAWA PHARM CO LTD.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 569
ID AAR12847 standard; protein; 562 AA.
DE T-PA Kringle 1 domain substitution mutant.
PD EP35127987-A.
PD 31-MAY-1991.
PA (KANP ) KANEGAFUCHI CHEM KK.
PA (KANP ) KANEGAFUCHI CHEM KK.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 570
ID AAR23802 standard; protein; 562 AA.
DE Zymogen-like t-PA (Ser 292, His 305).
PD WO9206203-A.
PD 16-APR-1992.
PA (TEXA ) UNIV TEXAS SYSTEM.
PA (TEXA ) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 571
ID AAR23809 standard; protein; 562 AA.
DE t-PA (Glu 299) mutant.
PD WO9206203-A.
PD 16-APR-1992.
PA (TEXA ) UNIV TEXAS SYSTEM.
PA (TEXA ) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 572
ID AAR23803 standard; protein; 562 AA.
DE t-PA (Ser 304) mutant.
PD WO9206203-A.
PD 16-APR-1992.
PA (TEXA ) UNIV TEXAS SYSTEM.
PA (TEXA ) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 573
ID AAR23808 standard; protein; 562 AA.
DE t-PA (Glu 298) mutant.
PD WO9206203-A.
PD 16-APR-1992.
PA (TEXA ) UNIV TEXAS SYSTEM.
PA (TEXA ) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 574
ID AAR23801 standard; protein; 562 AA.
DE Zymogen-like t-PA (His 305).
PD WO9206203-A.
PD 16-APR-1992.
PA (TEXA ) UNIV TEXAS SYSTEM.
PA (TEXA ) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 575
ID AAR23811 standard; protein; 562 AA.
DE t-PA (Glu 296, Glu 298, Glu 299) triple mutant.
PD WO9206203-A.
PD 16-APR-1992.
PA (TEXA ) UNIV TEXAS SYSTEM.
PA (TEXA ) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 576
ID AAR23807 standard; protein; 562 AA.
DE t-PA (Tyr 297) mutant.

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PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 577
ID AAR23806 standard; protein; 562 AA.
DE t-PA (Glu 296) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 578
ID AAR23810 standard; protein; 562 AA.
DE t-PA (Gly 301) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 579
ID AAR23804 standard; protein; 562 AA.
DE t-PA (Glu 304) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 580
ID AAR34426 standard; protein; 562 AA.
DE Sequence of human pre-pro tissue plasminogen activator (t-PA).
PN US5200340-A.
PD 06-APR-1993.
PA (ZYMO) ZYMOGENETICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 581
ID AAR44834 standard; protein; 562 AA.
DE Human tPA (R129W).
PN JP05304992-A.
PD 19-NOV-1993.
PA (TAKE) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 582
ID AAR35399 standard; protein; 562 AA.
DE TPA7.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 583
ID AAR38674 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA).
PN WO9312225-A1.
PD 24-JUN-1993.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 584
ID AAR41545 standard; protein; 562 AA.
DE Modified tPA WB1012 with two K2 kringle domains.
PN US5244676-A.
PD 14-SEP-1993.
PA (MONS) MONSANTO CO.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 585
ID AAR36220 standard; protein; 562 AA.
DE Full-length tissue plasminogen activator.
PN US5504001-A.

PD 02-APR-1996.
PA (ZYMO) ZYMOGENETICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 586
ID AAW47536 standard; protein; 562 AA.
DE Tissue plasminogen activator variant R275E.
PN US5714372-A.
PD 03-FEB-1998.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 587
ID AAW47537 standard; protein; 562 AA.
DE Tissue plasminogen activator variant I276P.
PN US5714372-A.
PD 03-FEB-1998.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 588
ID AAW47535 standard; protein; 562 AA.
DE Tissue plasminogen activator variant R275G.
PN US5714372-A.
PD 03-FEB-1998.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 589
ID AAY50868 standard; protein; 562 AA.
DE Human tissue plasminogen activator protein fragment.
PN WO9957251-A2.
PD 11-NOV-1999.
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 590
ID AAY43397 standard; protein; 562 AA.
DE Human tissue plasminogen activator protein sequence.
PN US5985607-A.
PD 16-NOV-1999.
PA (CANG-) CANGENE CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 591
ID AAM48426 standard; protein; 562 AA.
DE Tissue type plasminogen activator, tPA.
PN KRI41262-B1.
PD 15-JUN-1998.
PA (GLDS) LG CHEM LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 592
ID AAY99590 standard; protein; 562 AA.
DE Human tissue-type plasminogen activator t-PA.
PN WO200032759-A1.
PD 08-JUN-2000.
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 593
ID AAU97700 standard; protein; 562 AA.
DE Human tissue plasminogen activator (t-PA) protein sequence.
PN WO200232446-A2.
PD 25-APR-2002.
PA (PFIZ) PFIZER LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 594
ID AAE317130 standard; protein; 562 AA.
DE Human tissue-type plasminogen activator (tPA) protein.
PN WO2003033009-A2.

PD 24-APR-2003.
PA (OMNI-) OMNIO AB.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 595
ID ABR55851 standard; protein; 562 AA.
DE Human tissue-type plasminogen activator (TPA).
PN WO2003031464-A2.
PD 17-APR-2003.
PA (NEOS-) NEOSE TECHNOLOGIES INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 596
ID ABUS7646 standard; protein; 562 AA.
DE Differentially expressed breast cancer associated protein #33.
PN US2002156263-A1.
PD 24-OCT-2002.
PA (CHEN/) CHEN H.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 597
ID ADN95624 standard; protein; 562 AA.
DE Human BEC/LEC-related protein sequence SeqID547.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 598
ID ADN49698 standard; protein; 562 AA.
DE Human tissue type plasminogen activator TPA protein SeqID 26.
PN WO2004033651-A2.
PD 22-APR-2004.
PA (NEOS-) NEOSE TECHNOLOGIES INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 599
ID ADO28679 standard; protein; 562 AA.
DE Human tPA protein SEQ ID NO:108.
PN WO2004044178-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 600
ID ABM80983 standard; protein; 562 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO4, SEQ:2535.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 601
ID ADQ39248 standard; protein; 562 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 911.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 602
ID AAP70475 standard; protein; 564 AA.
DE Sequence of tissue plasminogen (TPA) analogue.
PN WO8703906-A.
PD 02-JUL-1987.
PA (UPJO) UPJOHN CO.
PA (MARO/) MAROTTI K R.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 603
ID AAR22664 standard; protein; 564 AA.
DE tPA analogue KK2A.

PN US5106741-A.
PD 21-APR-1992.
PA (UPJO) UPJOHN CO.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 604
ID ADI21256 standard; protein; 568 AA.
DE Novel human protein #231.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 605
ID AAR07477 standard; protein; 570 AA.
DE t-PA variant MB1023.
PN US4963357-A.
PD 16-OCT-1990.
PA (MONS) MONSANTO CO.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 606
ID AAP90169 standard; peptide; 571 AA.
DE Tissue plasminogen activator mutant 2G.
PN WO8907146-A.
PD 10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 607
ID AAP90168 standard; peptide; 580 AA.
DE Tissue plasminogen activator mutant 2F.
PN WO8907146-A.
PD 10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 608
ID AAP71741 standard; protein; 586 AA.
DE t-PA with extra finger domain.
PN EP241210-A.
PD 14-OCT-1987.
PA (BEEC) BEECHAM GROUP PLC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 609
ID AAP71744 standard; protein; 586 AA.
DE des(Cys51-Asp87)t-PA with extra finger- and growth factor-domains.
PN EP241210-A.
PD 14-OCT-1987.
PA (BEEC) BEECHAM GROUP PLC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 610
ID AAP90172 standard; peptide; 592 AA.
DE Tissue plasminogen activator mutant 1K1 2K2.
PN WO8907146-A.
PD 10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 611
ID AAP70059 standard; protein; 593 AA.
DE Hybrid plasminogen activator (PA) contg. urokinase kringle (UKK) 1-131 and tissue plasminogen activator (tPA) 92-527.
PN EP213794-A.
PD 11-MAR-1987.
PA (AMHP) AMERICAN HOME PROD CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 612
ID AAP71743 standard; protein; 594 AA.
DE Ile(277)t-PA with extra finger-domain.

PN EP241210-A.
PD 14-OCT-1987.
PA (BEEC) BEECHAM GROUP PLC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 613
ID AAR06239 standard; protein; 605 AA.
DE Novel mutant tissue plasminogen activator (tPA) encoded by plasmid plgn
DE delta GTPA.
PN EP379890-A.
PD 01-AUG-1990.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 614
ID AAM40056 standard; protein; 615 AA.
DE Human polypeptide SEQ ID NO 3201.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 615
ID ADA50545 standard; protein; 615 AA.
DE Human factor XII.
PN US2003073652-A1.
PD 17-APR-2003.
PA (POLL/) POLLARD H.
PA (POLL/) POLLARD B.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 616
ID ADN04180 standard; protein; 615 AA.
DE Antipsoxiatic protein sequence #285.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 617
ID ADM98382 standard; protein; 615 AA.
DE Human factor XII protein.
PN US2004077538-A1.
PD 22-APR-2004.
PA (POLL/) POLLARD H.
PA (POLL/) POLLARD B.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 618
ID ABM80709 standard; protein; 615 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO36372, SEQ:1829.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 619
ID AAU11271 standard; protein; 621 AA.
DE Human coagulation factor XII (F12) variant polypeptide.
PN WO200179228-A2.
PD 25-OCT-2001.
PA (GENA-) GENAISANCE PHARM INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 620
ID AAU11270 standard; protein; 621 AA.
DE Human coagulation factor XII (F12) polypeptide.
PN WO200179228-A2.
PD 25-OCT-2001.
PA (GENA-) GENAISANCE PHARM INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 621
ID AAP71742 standard; protein; 623 AA.
DE Ile(277)t-PA with extra finger- and extra growth factor-domains.
PN EP241210-A.
PD 14-OCT-1987.
PA (BEEC) BEECHAM GROUP PLC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 622
ID AAP71740 standard; protein; 623 AA.
DE t-PA with extra finger domain and extra growth factor domain.
PN EP241210-A.
PD 14-OCT-1987.
PA (BEEC) BEECHAM GROUP PLC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 623
ID AAP70060 standard; protein; 650 AA.
DE Hybrid plasminogen activator (PA) contg. tissue plasminogen activator
DE (tPA) 1-91, urokinase kringle (UKK) 50-131 and tPA 92-527.
PN EP213794-A.
PD 11-MAR-1987.
PA (AMHP) AMERICAN HOME PROD CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 624
ID AAP70084 standard; protein; 650 AA.
DE Hybrid plasminogen activator (PA) contg. tissue plasminogen activator
DE (tPA) 1-261, urokinase kringle (UKK) 50-131 and tPA 262-527.
PN EP213794-A.
PD 11-MAR-1987.
PA (AMHP) AMERICAN HOME PROD CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 625
ID ADE85979 standard; protein; 650 AA.
DE Human tissue urokinase plasminogen activator.
PN WO2003087393-A2.
PD 23-OCT-2003.
PA (GLOB-) GLOBAL BIOTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 626
ID AAE06934 standard; protein; 658 AA.
DE Human membrane-type serine protease (MTSP) 4-S splice variant.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 627
ID ADI10379 standard; protein; 658 AA.
DE Human cell surface protease #5.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 628
ID ADJ46903 standard; protein; 658 AA.
DE Human transmembrane serine protease (MTSP) polypeptide #5.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 629
ID AAP90173 standard; peptide; 680 AA.
DE Tissue plasminogen activator mutant 2K1 2K2.
PN WO8907146-A.
PD 10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0

RESULT 630
ID AAP90176 standard; peptide; 704 AA.
DE Tissue plasminogen activator mutant S+N.
PN WO8907146-A.
PD 10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 631
ID AAP90177 standard; peptide; 718 AA.
DE Tissue plasminogen activator mutant OMS.
PN WO8907146-A.
PD 10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 632
ID AAP90178 standard; peptide; 779 AA.
DE Tissue plasminogen activator mutant 2 Prot 1 CV.
PN WO8907146-A.
PD 10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 633
ID AAR06824 standard; protein; 780 AA.
DE Thrombomodulin analogue / t-PA fusion protein.
PN WO9010081-A.
PD 07-SEP-1990.
PA (CODO-) CODON.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 634
ID AAP90179 standard; peptide; 794 AA.
DE Tissue plasminogen activator mutant 2 Prot 2 CV.
PN WO8907146-A.
PD 10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 635
ID ABP43952 standard; protein; 795 AA.
DE Human PRO618.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 636
ID ADI16874 standard; protein; 799 AA.
DE Murine NOVX protein homologue SeqID 410.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 637
ID ADI16880 standard; protein; 799 AA.
DE Murine NOVX protein homologue SeqID 416.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 638
ID AAY41710 standard; protein; 802 AA.
DE Human PRO618 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH-) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 639
ID AAB44266 standard; protein; 802 AA.
DE Human PRO618 (UNQ354) protein sequence SEQ ID NO:169.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH-) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 640
ID AAB24052 standard; protein; 802 AA.
DE Human PRO618 protein sequence SEQ ID NO:24.
PN WO200053754-A1.
PD 14-SEP-2000.
PA (GETH-) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 641
ID AAE06933 standard; protein; 802 AA.
DE Human membrane-type serine protease (MTSP) 4-L splice variant.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 642
ID AAU82755 standard; protein; 802 AA.
DE Amino acid sequence of novel human protease #54.
PN WO200200860-A2.
PD 03-JAN-2002.
PA (SUGE-) SUGEN INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 643
ID ABO25212 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US200305039-A1.
PD 13-MAR-2003.
PA (GETH-) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 644
ID ABU72218 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH-) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 645
ID ABU84898 standard; protein; 802 AA.
DE Human secreted and transmembrane polypeptide PRO618.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH-) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 646
ID ABU61096 standard; protein; 802 AA.
DE Human PRO618 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH-) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 647
ID ABU80365 standard; protein; 802 AA.
DE Human secreted/transmembrane protein PRO618.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH-) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 648
ID ADA24708 standard; protein; 802 AA.

DE Novel human secreted and transmembrane protein PRO618.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 649
ID ABO19667 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 650
ID ADAL12369 standard; protein; 802 AA.
DE Human secreted/transmembrane polypeptide PRO618.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 651
ID ABO19558 standard; protein; 802 AA.
DE Novel human secreted and transmembrane polypeptide #26.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 652
ID ADB73675 standard; protein; 802 AA.
DE Human PRO polypeptide #26.
PN US2003045482-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 653
ID ADB76391 standard; protein; 802 AA.
DE Human PRO polypeptide #26.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 654
ID ADC3817 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 655
ID ADC61577 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 656
ID ADC63541 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 657
ID ADC66641 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003060406-A1.

PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 658
ID ADC68765 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 659
ID ADC62825 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 660
ID ADC67890 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 661
ID ADC41210 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 662
ID ADC67265 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 663
ID ADC62201 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 664
ID ADC41834 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 665
ID ADE49203 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 666
ID ADE35257 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203434-A1.
PD 30-OCT-2003.

PA (GETH) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0	
Query Match:	3.64%	Indels: 0	
RESULT 667			
ID ADE16371 standard; protein; 802 AA.			
DE Human secreted/transmembrane protein, PRO618.			
PN US2003203435-A1.			
PD 30-OCT-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0	
Query Match:	3.64%	Indels: 0	
RESULT 668			
ID ADD72986 standard; protein; 802 AA.			
DE Human secreted/transmembrane protein, PRO618.			
PN US2003203436-A1.			
PD 30-OCT-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0	
Query Match:	3.64%	Indels: 0	
RESULT 669			
ID ADD72344 standard; protein; 802 AA.			
DE Human secreted/transmembrane protein, PRO618.			
PN US2003194781-A1.			
PD 16-OCT-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0	
Query Match:	3.64%	Indels: 0	
RESULT 670			
ID ADE16995 standard; protein; 802 AA.			
DE Human secreted/transmembrane protein, PRO618.			
PN US2003203433-A1.			
PD 30-OCT-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0	
Query Match:	3.64%	Indels: 0	
RESULT 671			
ID ADP47009 standard; protein; 802 AA.			
DE Human secreted/transmembrane protein, PRO618.			
PN US2003195333-A1.			
PD 16-OCT-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0	
Query Match:	3.64%	Indels: 0	
RESULT 672			
ID ADG52766 standard; protein; 802 AA.			
DE Human secreted/transmembrane protein, PRO618.			
PN US2003216561-A1.			
PD 20-NOV-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0	
Query Match:	3.64%	Indels: 0	
RESULT 673			
ID ADG60086 standard; protein; 802 AA.			
DE Human secreted/transmembrane protein, PRO618.			
PN US2003206915-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0	
Query Match:	3.64%	Indels: 0	
RESULT 674			
ID ADI60846 standard; protein; 802 AA.			
DE Human secreted/transmembrane protein, PRO618.			
PN US2003077700-A1.			
PD 24-APR-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0	
Query Match:	3.64%	Indels: 0	
RESULT 675			
ID ADI10377 standard; protein; 802 AA.			
DE Human cell surface protease #4.			
PN WO200295007-A2.			
PD 28-NOV-2002.			
PA (CORV-) CORVAS INT INC.			

PA (GETH) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0	
Query Match:	3.64%	Indels: 0	
RESULT 676			
ID ADE48503 standard; protein; 802 AA.			
DE Human secreted/transmembrane protein, PRO618.			
PN US2003104536-A1.			
PD 05-JUN-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0	
Query Match:	3.64%	Indels: 0	
RESULT 677			
ID ADE89604 standard; protein; 802 AA.			
DE Human secreted/transmembrane protein, PRO618.			
PN US2003130181-A1.			
PD 10-JUL-2003.			
PA (ASHK/) ASHKENAZI A J.			
PA (BAKE/) BAKER K P.			
PA (BOTS/) BOTSTEIN D.			
PA (DESN/) DESNOYERS L.			
PA (EATO/) EATON D L.			
PA (FERR/) FERRARA N.			
PA (FILV/) FILVAROFF E.			
PA (FONG/) FONG S.			
PA (GAOW/) GAO W.			
PA (GERB/) GERBER H.			
PA (GERR/) GERRITSEN M E.			
PA (GODD/) GODDARD A.			
PA (GODO/) GODOWSKI P J.			
PA (GIRM/) GIRMALDI J C.			
PA (GUEN/) GUENEY A L.			
PA (HILL/) HILLMAN K J.			
PA (KLJA/) KLJAVIN I J.			
PA (KUOS/) KUO S S.			
PA (NAPI/) NAPIER M A.			
PA (PANJ/) PAN J.			
PA (PAON/) PAONI N F.			
PA (ROIM/) ROY M A.			
PA (SHEL/) SHELTON D L.			
PA (STEW/) STEWART T A.			
PA (TUNA/) TUNAS D.			
PA (WILL/) WILLIAMS P M.			
PA (WOOD/) WOOD W I.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match:	3.64%	Indels: 0	
RESULT 678			
ID ADP61244 standard; protein; 802 AA.			
DE Human secreted/transmembrane protein, PRO618.			
PN US2003195345-A1.			
PD 16-OCT-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0	
Query Match:	3.64%	Indels: 0	
RESULT 679			
ID ADP39936 standard; protein; 802 AA.			
DE Human secreted/transmembrane protein, PRO618.			
PN US2003198994-A1.			
PD 23-OCT-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0	
Query Match:	3.64%	Indels: 0	
RESULT 680			
ID ADF45732 standard; protein; 802 AA.			
DE Human secreted/transmembrane protein, PRO618.			
PN US2003195148-A1.			
PD 16-OCT-2003.			
PA (GETH) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0	
Query Match:	3.64%	Indels: 0	
RESULT 681			
ID ADF24128 standard; protein; 802 AA.			
DE Human secreted/transmembrane protein, PRO618.			
PN US2003204055-A1.			
PD 30-OCT-2003.			

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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 682
ID ADF40560 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 683
ID ADF23504 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 684
ID ADF33487 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 685
ID ADF26954 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 686
ID ADF27590 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 687
ID ADF41184 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 688
ID ADF32863 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 689
ID ADF25229 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 690
ID ADF26330 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 691
ID ADF34119 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 692
ID ADF46356 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 693
ID ADG50342 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 694
ID ADG49718 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 695
ID ADG51590 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 696
ID ADG49094 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 697
ID ADG48470 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 698
ID ADG50966 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 699
ID ADG58910 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 3.64% Indels: 0
RESULT 700
ID ADG2366 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 701
ID ADH25391 standard; protein; 802 AA.
DE Human neurotrophin homologue related protein sequence SEQ ID NO:169.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 702
ID ADJ46901 standard; protein; 802 AA.
DE Human transmembrane serine protease (WTSP) polypeptide #4.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 703
ID ADM17168 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 704
ID ADL07002 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 705
ID ADY91615 standard; protein; 802 AA.
DE Human PRO618 protein sequence.
PN AU2002317529-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 706
ID AAR20013 standard; protein; 807 AA.
DE PA mutant plg 1-541 [Arg298-299->Gln298-299] t-PA 262-527.
PN WO9118989-A.
PD 12-DEC-1991.
PA (BEEC ) BEECHAM GROUP PLC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 707
ID ABB98140 standard; protein; 863 AA.
DE Human PMM incyte ID 7484157CD1.
PN WO200246383-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 708
ID ABG24246 standard; protein; 913 AA.
DE Novel human diagnostic protein #24237.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 709
ID ABUI2066 standard; protein; 922 AA.
DE Human NOVI2b CG92293-02 protein SEQ ID 52.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 710
ID ADR43718 standard; protein; 932 AA.
DE Human protease PRTS-6, SEQ ID 6.
PN WO200220736-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 711
ID AAU82743 standard; protein; 970 AA.
DE Amino acid sequence of novel human protease #42.
PN WO200200860-A2.
PD 03-JAN-2002.
PA (SUGE-) SUGEN INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 712
ID ABUI2065 standard; protein; 986 AA.
DE Human NOVI2a CG92293-01 protein SEQ ID 50.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 713
ID ABP60993 standard; protein; 1031 AA.
DE Novel human protein. SEQ ID 80.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (GLAX ) GLAXO GROUP LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 714
ID AAP80692 standard; protein; 1039 AA.
DE Hybrid plasminogen/t-PA compound 2.
PN EP292326-A.
PD 23-NOV-1988.
PA (BEEC ) BEECHAM GROUP PLC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 715
ID AAP80691 standard; protein; 1087 AA.
DE Hybrid plasminogen/t-PA compound 1.
PN EP292326-A.
PD 23-NOV-1988.
PA (BEEC ) BEECHAM GROUP PLC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 716
ID ABG14588 standard; protein; 1576 AA.
DE Novel human diagnostic protein #14579.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 717
ID ABG07870 standard; protein; 1576 AA.
DE Novel human diagnostic protein #7861.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
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Query Match: 3.64% Indels: 0
RESULT 718
ID ABG1987 standard; protein; 1576 AA.
DE Novel human diagnostic protein #19878.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 719
ID ABG10218 standard; protein; 1576 AA.
DE Novel human diagnostic protein #10209.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 720
ID AAY72112 standard; peptide; 12 AA.
DE Peptide fragment #12 related to human serine protease.
PN WO20008247-A2.
PD 16-NOV-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 721
ID ABG31651 standard; peptide; 12 AA.
DE Human serine protease serine active site domain.
PN US2002119925-A1.
PD 29-AUG-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 722
ID AAE17932 standard; peptide; 12 AA.
DE Human gene 4 encoded serine protease fragment #1.
PN WO200198476-A1.
PD 27-DEC-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 723
ID ABB52232 standard; peptide; 18 AA.
DE Human API-180 tryptic digest peptide #4.
PN WO200175454-A2.
PD 11-OCT-2001.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA (PFIZ) PFIZER INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 724
ID ABB52105 standard; peptide; 18 AA.
DE Human API-26 tryptic digest peptide #3.
PN WO200175454-A2.
PD 11-OCT-2001.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA (PFIZ) PFIZER INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 725
ID ABR58948 standard; peptide; 18 AA.
DE Alzheimer's Disease-associated protein isoform, API-26, SEQ ID 68.
PN WO2003028543-A2.
PD 10-APR-2003.
PA (PFIZ) PFIZER PROD INC.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 726
ID ADN31742 standard; peptide; 18 AA.
DE Human Alzheimer's disease-API tryptic digest peptide - SEQ ID 68.
PN EPI408333-A2.
PD 14-APR-2004.
PA (PFIZ) PFIZER PROD INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 727
ID ADR72151 standard; peptide; 40 AA.
DE Human kallikrein 15 splice form 3 peptide.
PN US2004180380-A1.
PD 16-SEP-2004.
PA (ENGE-) ENGNEOS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 728
ID ABB63477 standard; protein; 141 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17223.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 729
ID AAU79393 standard; protein; 171 AA.
DE Novel human kallikrein KLK15, splice variant #3.
PN WO200214485-A2.
PD 21-FEB-2002.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 730
ID ADN10933 standard; protein; 171 AA.
DE Human kallikrein 15, marker of endocrine cancer.
PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 731
ID AAU82735 standard; protein; 222 AA.
DE Amino acid sequence of novel human protease #34.
PN WO200200860-A2.
PD 03-JAN-2002.
PA (SUGE-) SUGEN INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 732
ID AAB03862 standard; protein; 223 AA.
DE Human neurosin amino acid sequence.
PN WO20031284-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 733
ID AAR89430 standard; protein; 232 AA.
DE Trypsin-like enzyme.
PN AU9527248-A.
PD 08-FEB-1996.
PA (TEIJ) TEIJIN LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 734
ID AAY28591 standard; protein; 233 AA.
DE Pig Factor D.
PN WO9942133-A1.
PD 26-AUG-1999.
PA (TANO-) TANOX INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 735
ID AAB01942 standard; protein; 233 AA.
DE Human endotheliasin 1 protease domain.
PN WO200136604-A2.
PD 25-MAY-2001.
```

PA (CORV-) CORVAS INT INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 736
ID ADI10391 standard; protein; 233 AA.
DE Human cell surface protease #11.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 737
ID ADJ45915 standard; protein; 233 AA.
DE Human transmembrane serine protease (MTSP)-related polypeptide #1.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 738
ID AAB21310 standard; protein; 239 AA.
DE Human zyme.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 739
ID ADA50482 standard; protein; 241 AA.
DE Human protease SEQ ID NO:80.
PN WO2003040393-A2.
PD 15-MAY-2003.
PA (DECO-) DECODE GENETICS EHF. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 740
ID AAR44532 standard; protein; 244 AA.
DE Zyme APP-cleaving protease.
PN EP576152-A1.
PD 29-DEC-1993.
PA (ELIL) LILLY & CO ELI. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 741
ID AAW22985 standard; protein; 244 AA.
DE Human serine protease 59 (SP59).
PN JP09149790-A.
PD 10-JUN-1997.
PA (SUNR) SUNTORY LTD. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 742
ID AAW51006 standard; protein; 244 AA.
DE Protease M, a novel serine protease.
PN WO9811238-A2.
PD 19-MAR-1998.
PA (DAND) DANA FARRER CANCER INST INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 743
ID AAB21323 standard; protein; 244 AA.
DE Human zyme.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 744
ID ABG96357 standard; protein; 244 AA.
DE Human ovarian cancer marker OV33.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 745
ID AAE37572 standard; protein; 244 AA.
DE Human 2047 protein.
PN WO2003037258-A2.
PD 08-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 746
ID ADB0567 standard; protein; 244 AA.
DE Ovarian cancer-associated protein #66.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 747
ID ADN39212 standard; protein; 244 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:530.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 748
ID ADI39734 standard; protein; 244 AA.
DE Human protease M (prom) protein.
PN US6642013-B1.
PD 04-NOV-2003.
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 749
ID ADI37158 standard; protein; 244 AA.
DE Human protease m (Protm).
PN US2003199010-A1.
PD 23-OCT-2003.
PA (UYAR-) UNIV ARKANSAS. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 750
ID ADN04074 standard; protein; 244 AA.
DE Antipsoxiatic protein sequence #232.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 751
ID ADN29289 standard; protein; 244 AA.
DE Human kallikrein 6 associated protein.
PN US2004097452-A1.
PD 20-MAY-2004.
PA (ISIS-) ISIS PHARM INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 752
ID ADQ89076 standard; protein; 244 AA.
DE Human urological disorder related protein 2047 SEQ:28.
PN WO2004065576-A2.
PD 05-AUG-2004.
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 753
ID ADR72624 standard; protein; 244 AA.
DE Human renal cell carcinoma-related kallikrein 6 (hk6) protein.
PN WO2004077060-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL. Mismatches: 0
Best Local Similarity: 100.00%

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Query Match: 3.36% Indels: 0
RESULT 754
ID ADR72876 standard; protein; 244 AA.
DE Human ovarian cancer-related tumour marker kallikrein 6 (hk6) protein.
PN WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN ) MOUNT SINAI HOSPITAL.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 755
ID AAP90531 standard; protein; 256 AA.
DE Hypodermin B of ATCC # 67613.
PN EP326419-A.
PD 02-AUG-1989.
PA (USDA ) US SEC OF AGRIC.
PA (CODO-) CODON.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 756
ID ABB67198 standard; protein; 256 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28356.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 757
ID ABB71152 standard; protein; 256 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40248.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 758
ID ABB69404 standard; protein; 258 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35004.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 759
ID ABB61002 standard; protein; 260 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9798.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 760
ID AAO23287 standard; protein; 261 AA.
DE Culex pipiens pallens trypsin protein.
PN CN1354253-A.
PD 19-JUN-2002.
PA (UYNA-) UNIV NANJING MEDICAL.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 761
ID ABB64194 standard; protein; 262 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19374.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 762
ID ABB63475 standard; protein; 272 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17217.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
Query Match: 3.36% Indels: 0
RESULT 763
ID AD83072 standard; protein; 345 AA.
DE Human protein which is similar to DEBC protein - SEQ ID 63.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO) ) ALSOBOOK J P.
PA (TCHE) ) TCHERNEV V T.
PA (LIUX) ) LIU X.
PA (SPYT) ) SPYTEK K A.
PA (ZERH) ) ZERHUSEN B D.
PA (PATT) ) PATTURAJAN M.
PA (LEPL) ) LEPLEY D M.
PA (BURG) ) BURGESS C E.
PA (SHIM) ) SHIMKETS R A.
PA (GROS) ) GROSSE W M.
PA (SZEK) ) SEKERES E S.
PA (VERN) ) VERNET C A M.
PA (LILL) ) LI L.
PA (CASM) ) CASMAN S J.
PA (BOLD) ) BOLDOG F L.
PA (GORM) ) GORMAN L.
PA (GANG) ) GANGOLLI E A.
PA (FERN) ) FERNANDES E R.
PA (RIEG) ) RIEGER D K.
PA (EDIN) ) EDINGER S R.
PA (GUNT) ) GUNTHER E.
PA (MILL) ) MILLET I.
PA (SCIO) ) SCIORE P.
PA (ELLE) ) ELLERMAN K.
PA (MACD) ) MACDOUGALL J R.
PA (SMIT) ) SMITHSON G.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 764
ID AAO21900 standard; protein; 407 AA.
DE Homologous human protease protein.
PN WO200226947-A2.
PD 04-APR-2002.
PA (PEKE ) PE CORP NY.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 765
ID ADG31219 standard; protein; 416 AA.
DE Novel mouse protein #20.
PN WO2003089644-A1.
PD 30-OCT-2003.
PA (RIKE ) RIKEN KK.
PA (DNAP-) DNAFORM KK.
PA (MITU) ) MITSUBISHI CHEM CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 766
ID ABB77356 standard; protein; 417 AA.
DE Mouse AST SEQ ID NO 2.
PN JP2002065266-A.
PD 05-MAR-2002.
PA (TEIJ) ) TEIJIN LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 767
ID ABB06970 standard; protein; 417 AA.
DE Bovine AST protein sequence SEQ ID NO:33.
PN WO200218562-A1.
PD 07-MAR-2002.
PA (TEIJ) ) TEIJIN LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 768
ID ABB06965 standard; protein; 417 AA.
DE Mouse airway specific trypsin-like protease protein SEQ ID NO:2.
PN WO200218562-A1.
PD 07-MAR-2002.
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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 778			
ID AAE13769 standard; protein; 418 AA.			
DE Human lung tumour-specific protein L86S-46.			
FN WO200172295-A2.			
PD 04-OCT-2001.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 779			
ID AAE13778 standard; protein; 418 AA.			
DE Human lung tumour-specific protein L86S-36.			
FN WO200172295-A2.			
PD 04-OCT-2001.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 780			
ID AAE13779 standard; protein; 418 AA.			
DE Human lung tumour-specific protein L86S-46.			
FN WO200172295-A2.			
PD 04-OCT-2001.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 781			
ID ABB77355 standard; protein; 418 AA.			
DE Human AST SEQ ID NO 1.			
FN JP2002085266-A.			
PD 05-MAR-2002.			
PA (TEIJ) TEIJIN LTD.			
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 782			
ID AAU76372 standard; protein; 418 AA.			
DE Human airway trypsin protease protein sequence.			
FN WO200206455-A2.			
PD 24-JAN-2002.			
PA (FARB) BAYER AG.			
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 783			
ID ABB06964 standard; protein; 418 AA.			
DE Human airway specific trypsin-like protease protein SEQ ID NO:1.			
FN WO200218562-A1.			
PD 07-MAR-2002.			
PA (TEIJ) TEIJIN LTD.			
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 784			
ID ABB06968 standard; protein; 418 AA.			
DE Macaca fascicularis AST protein sequence SEQ ID NO:29.			
FN WO200218562-A1.			
PD 07-MAR-2002.			
PA (TEIJ) TEIJIN LTD.			
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 785			
ID ABB06971 standard; protein; 418 AA.			
DE Rabbit AST protein sequence SEQ ID NO:35.			
FN WO200218562-A1.			
PD 07-MAR-2002.			
PA (TEIJ) TEIJIN LTD.			
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 786			
ID ABB06972 standard; protein; 418 AA.			
DE Guinea pig AST protein sequence SEQ ID NO:37.			
FN WO200218562-A1.			
PD 07-MAR-2002.			
PA (TEIJ) TEIJIN LTD.			
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 787			
ID ABB06973 standard; protein; 418 AA.			
DE Human airway trypsin protease protein sequence SEQ ID NO:39.			
FN WO200218562-A1.			
PD 07-MAR-2002.			
PA (TEIJ) TEIJIN LTD.			
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.36%	Indels:	0

Query Match:	3.36%	Indels:	0
RESULT 787			
ID AD66390 standard; protein; 418 AA.			
DE Human lung tumour-specific related protein, SEQ ID No 82.			
PN WO200292001-A2.			
PD 21-NOV-2002.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match: 3.36%	Indels:	0	
RESULT 788			
ID AD66391 standard; protein; 418 AA.			
DE Human lung tumour-specific related protein, SEQ ID No 83.			
PN WO200292001-A2.			
PD 21-NOV-2002.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match: 3.36%	Indels:	0	
RESULT 789			
ID AD66370 standard; protein; 418 AA.			
DE Human lung tumour-specific related protein, SEQ ID No 62.			
PN WO200292001-A2.			
PD 21-NOV-2002.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match: 3.36%	Indels:	0	
RESULT 790			
ID ADE87644 standard; protein; 418 AA.			
DE Human lung tumour antigen polypeptide #31.			
PN US2003118599-A1.			
PD 26-JUN-2003.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match: 3.36%	Indels:	0	
RESULT 791			
ID ADE87645 standard; protein; 418 AA.			
DE Human lung tumour antigen polypeptide #32.			
PN US2003118599-A1.			
PD 26-JUN-2003.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match: 3.36%	Indels:	0	
RESULT 792			
ID ADE87624 standard; protein; 418 AA.			
DE Human lung tumour antigen polypeptide #22.			
PN US2003118599-A1.			
PD 26-JUN-2003.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match: 3.36%	Indels:	0	
RESULT 793			
ID ADI10402 standard; protein; 418 AA.			
DE Human cell surface protease #17.			
PN WO200295007-A2.			
PD 28-NOV-2002.			
PA (CORV-) CORVAS INT INC.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match: 3.36%	Indels:	0	
RESULT 794			
ID ADJ83071 standard; protein; 418 AA.			
DE Human airway trypsin-like protease protein - SEQ ID 62.			
PN US2003170630-A1.			
PD 11-SEP-2003.			
PA (ALSO/) ALSOBROOK J P.			
PA (TCHE/) TCHERNEV V T.			
PA (LIUX/) LIU X.			
PA (SPYT/) SPYTEK K A.			
PA (ZERH/) ZERHUSEN B D.			
PA (PATT/) PATTURAJAN M.			
PA (LEPL/) LEPLEY D M.			
PA (BURG/) BURGESS C E.			
PA (SHIM/) SHIMKETS R A.			
PA (GROS/) GROSE W M.			
PA (SZEK/) SZEKERES E S.			

PA (VERN/) VERNET C A M.			
PA (LILL/) LI L.			
PA (CASW/) CASMAN S J.			
PA (BOLD/) BOLDOG F L.			
PA (GORM/) GORMAN L.			
PA (GANG/) GANGOLLI E A.			
PA (PERN/) FERNANDES E R.			
PA (RIEG/) RIEGER D K.			
PA (EDIN/) EDINGER S R.			
PA (GUNT/) GUNTHER E.			
PA (MILL/) MILLET I.			
PA (SCIO/) SCIORE P.			
PA (ELLE/) ELLERMAN K.			
PA (MACD/) MACDOUGALL J R.			
PA (SMIT/) SMITHSON G.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match: 3.36%	Indels:	0	
RESULT 795			
ID ADJ46926 standard; protein; 418 AA.			
DE Human transmembrane serine protease (MTSP)-related polypeptide #7.			
PN US2004001801-A1.			
PD 01-JAN-2004.			
PA (CORV-) CORVAS INT INC.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match: 3.36%	Indels:	0	
RESULT 796			
ID ADN04299 standard; protein; 418 AA.			
DE Antiperoiatric protein sequence #344.			
PN WO2004028479-A2.			
PD 08-APR-2004.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match: 3.36%	Indels:	0	
RESULT 797			
ID ADQ30692 standard; protein; 418 AA.			
DE Human airway trypsin-like protease HAT.			
PN WO2004053496-A1.			
PD 24-JUN-2004.			
PA (HINZ/) HINZMANN B.			
PA (HEID/) HEIDEN E.			
PA (HERM/) HERMANN K.			
PA (ROSE/) ROSENTHAL A.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match: 3.36%	Indels:	0	
RESULT 798			
ID AAY94709 standard; protein; 422 AA.			
DE Human DESCI protein variant #2.			
PN WO200050061-A1.			
PD 31-AUG-2000.			
PA (OHIS) UNIV OHIO STATE RES FOUND.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match: 3.36%	Indels:	0	
RESULT 799			
ID AAY94708 standard; protein; 422 AA.			
DE Human DESCI protein variant #1.			
PN WO200050061-A1.			
PD 31-AUG-2000.			
PA (OHIS) UNIV OHIO STATE RES FOUND.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match: 3.36%	Indels:	0	
RESULT 800			
ID AAB01946 standard; protein; 422 AA.			
DE Human endotheliasin 1 protein.			
PN WO200136604-A2.			
PD 25-MAY-2001.			
PA (CORV-) CORVAS INT INC.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match: 3.36%	Indels:	0	
RESULT 801			
ID AAE18723 standard; protein; 422 AA.			
DE Human DESCI-like serine protease homologue.			
PN WO200206453-A2.			
PD 24-JAN-2002.			

PA (FARB) BAYER AG. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 802
ID ABUS6527 standard; protein; 422 AA.
DE Lung cancer-associated polypeptide #120.
PN WO20028443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 803
ID ADI10410 standard; protein; 422 AA.
DE Human cell surface protease #21.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 804
ID ADI10981 standard; protein; 422 AA.
DE Human cell surface protease #14.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 805
ID ADJ83073 standard; protein; 422 AA.
DE Human DESCI protein - SEQ ID 64.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPLY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 806
ID ADJ47505 standard; protein; 422 AA.
DE Human transmembrane serine protease (MTSP)-related polypeptide #4.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 807
ID ADJ46934 standard; protein; 422 AA.
DE Human transmembrane serine protease (MTSP)-related polypeptide #11.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (GETH) GENENTECH INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 808
ID AAY99414 standard; protein; 423 AA.
DE Human PRO1461 (UNQ742) amino acid sequence SEQ ID NO:269.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 809
ID AAB66163 standard; protein; 423 AA.
DE Protein of the invention #75.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 810
ID AAU01344 standard; protein; 423 AA.
DE Human TANGO 361 amino acid sequence.
PN WO200121631-A2.
PD 29-MAR-2001.
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 811
ID AAU01400 standard; protein; 423 AA.
DE Human TANGO 361, variant #2 amino acid sequence.
PN WO200121631-A2.
PD 29-MAR-2001.
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 812
ID AAU01401 standard; protein; 423 AA.
DE Human TANGO 361, variant #3 amino acid sequence.
PN WO200121631-A2.
PD 29-MAR-2001.
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 813
ID AAU01399 standard; protein; 423 AA.
DE Human TANGO 361, variant #1 amino acid sequence.
PN WO200121631-A2.
PD 29-MAR-2001.
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 814
ID AAU01402 standard; protein; 423 AA.
DE Human TANGO 361, variant #4 amino acid sequence.
PN WO200121631-A2.
PD 29-MAR-2001.
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 815
ID AAU29183 standard; protein; 423 AA.
DE Human PRO polypeptide sequence #160.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC. Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3.36%
RESULT 816
ID AAB87578 standard; protein; 423 AA.
DE Human PRO1461.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.


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ID ABU91818 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003027277-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 838
ID ABU9511 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003036141-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 839
ID ABU86352 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036146-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 840
ID ABU67565 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 841
ID ABU80593 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 842
ID ABU90928 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 843
ID ABO33987 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 844
ID ABR99511 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040063-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 845
ID ABR98901 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040064-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 846
ID ABO16424 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003027267-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 847
ID ABR2324 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003036160-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 848
ID ABO18965 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003044925-A1.
PD 06-MAR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 849
ID ABR78386 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 850
ID ABU72004 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 851
ID ABU85122 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003032114-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 852
ID ABO00261 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003032101-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 853
ID ABO11593 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036124-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 854
ID ABO22238 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003040054-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 855
ID ABU88812 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003036133-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 856
ID ABU83507 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036134-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
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RESULT 857
ID ABO06308 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003032117-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 858
ID ABR59344 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003027275-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 859
ID ABO09406 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003027324-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 860
ID ABO19270 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 861
ID ABO11288 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036123-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 862
ID ABR66906 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003036148-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 863
ID ABO16119 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003040060-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 864
ID ABO13825 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003044916-A1.
PD 06-MAR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 865
ID ABU71558 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 866
ID ABU65728 standard; protein; 423 AA.
DE Human secreted/transmembrane protein, SEQ ID 320.
PN US2003036156-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 867
ID ABR70122 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003032117-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 868
ID ABO03763 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036128-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 869
ID ABR67211 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003027266-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 870
ID ABO15814 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 871
ID ABU56095 standard; protein; 423 AA.
DE Human secreted/transmembrane protein, PRO1461.
PN US2003022298-A1.
PD 30-JAN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 872
ID ABU72339 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 873
ID ABU65423 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003032102-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 874
ID ABU95368 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003036117-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 875
ID ABU71271 standard; protein; 423 AA.
DE Human PRO1461 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 876
ID ABO07881 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003032130-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 877
ID ABR70122 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003032117-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0

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DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003022138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 878
ID ABR69455 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003036132-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 879
ID ABO01596 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 880
ID ABU81398 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003017542-A1.
PD 23-JAN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 881
ID ABR60195 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003032137-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 882
ID ABU91012 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 883
ID ABR67930 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003027269-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 884
ID ABR65318 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003027268-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 885
ID ABR68540 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003027274-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 886
ID ABR71952 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 887
ID ABO06661 standard; protein; 423 AA.

ID ABUS5432 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003022295-A1.
PD 30-JAN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 888
ID ABU99122 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003022297-A1.
PD 30-JAN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 889
ID ABUS3202 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003032105-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 890
ID ABUS9508 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003032123-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 891
ID ABUS0606 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003032108-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 892
ID ABUS4117 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003032111-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 893
ID ABUS9768 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 894
ID ABR65013 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003027263-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 895
ID ABO27333 standard; protein; 423 AA.
DE Human secreted/transmembrane polypeptide PRO1461.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 896
ID ABR68845 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003027271-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 897
ID ABO06661 standard; protein; 423 AA.

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DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036125-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 898
ID ABR99206 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040068-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 899
ID ABU57090 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003027280-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 900
ID ABU86042 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003022300-A1.
PD 30-JAN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 901
ID ABU82329 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003036136-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 902
ID ABU87340 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003036138-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 903
ID ABU83812 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003032109-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 904
ID ABO08186 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003040066-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 905
ID ABU92528 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003045694-A1.
PD 06-MAR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 906
ID ABU91897 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003032104-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 907
ID ABU66061 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003036157-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 908
ID ABU81198 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 909
ID ABR59890 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003032120-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 910
ID ABU94078 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003036155-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 911
ID ABU99931 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003022296-A1.
PD 30-JAN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 912
ID ABR66601 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 913
ID ABR91019 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040058-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 914
ID AB053312 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 915
ID ABU94446 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003017540-A1.
PD 23-JAN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 916
ID ABU79328 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003032106-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 917
ID ABU86657 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003032129-A1.
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PD 13-FEB-2003.
Query Match: Mismatches: 0
Indels: 0
RESULT 918
ID ABU86962 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003032131-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 919
ID ABU94751 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003032103-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 920
ID ABO04678 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003032107-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 921
ID ABR70427 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003032139-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 922
ID ABU98592 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US20030322301-A1.
PD 30-JAN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 923
ID ABR65991 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003036165-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 924
ID ABR64708 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003027262-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 925
ID ABU79633 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003032110-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 926
ID ABU93024 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036142-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 927
ID ABU95983 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003036145-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 928
ID ABU91203 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003036154-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 929
ID ABU90296 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003036153-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 930
ID ABO09711 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003044931-A1.
PD 06-MAR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 931
ID ABO10983 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036150-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 932
ID ABR71037 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040069-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 933
ID ABU98315 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 934
ID ABU87645 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003022293-A1.
PD 30-JAN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 935
ID ABU91513 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003032128-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 936
ID ABU89320 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 937
ID ABU84727 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003032116-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0

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RESULT 938
ID ABE69817 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003032122-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 939
ID ABU00194 standard; protein; 423 AA.
DE Human PRO protein #160.
PN US2003036139-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 940
ID ABU00194 standard; protein; 423 AA.
DE Human secreted and transmembrane protein PRO1461.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 941
ID ABU93463 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003017541-A1.
PD 23-JAN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 942
ID AB010016 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003017543-A1.
PD 23-JAN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 943
ID ABO09101 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036152-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 944
ID ABU96491 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 945
ID ABU10669 standard; protein; 423 AA.
DE Human secreted/transmembrane protein #160.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 946
ID ABU72161 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 947
ID ABU95678 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003032115-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 948
ID ABU96887 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003032140-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 949
ID ABR70732 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 950
ID ABO05083 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 951
ID ABO08491 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003044922-A1.
PD 06-MAR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 952
ID ABO05698 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003032118-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 953
ID ABR74087 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003036135-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 954
ID ABR95679 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 955
ID ABR80976 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 956
ID ABR81281 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 957
ID ABM00977 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049769-A1.
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PA 13-MAR-2003
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 958
ID ABR88579 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 959
ID ABR77400 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 960
ID ABO28884 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 961
ID ABO31629 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 962
ID ABO08046 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 963
ID ABO40526 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 964
ID ABO35951 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 965
ID ABO44090 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 966
ID ADA78072 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003073180-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 967
ID ABR24885 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 968
ID ABO03153 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 969
ID ABR90409 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 970
ID ABR17323 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 971
ID ABR95069 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 972
ID ABR95374 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 973
ID ADB17163 standard; protein; 423 AA.
DE Human transmembrane PRO polypeptide (SeqID 106).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 974
ID ABO21612 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 975
ID ABR97876 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 976
ID ABR87664 standard; protein; 423 AA.

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DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068705-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 977
ID ABM77705 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 978
ID ABM27935 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 979
ID ABM06216 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 980
ID ABM03722 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 981
ID ABM35173 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 982
ID ABM26410 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 983
ID ABO48192 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 984
ID ABR2934 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 985
ID ABO24695 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003065159-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 986
ID ABM11706 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 987
ID ABM02807 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 988
ID ABM16103 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 989
ID ABO27664 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 990
ID ABM29155 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 991
ID ABM07131 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068899-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 992
ID ABM21225 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 993
ID ABM09571 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 994
ID ABO41441 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068695-A1.
PD 10-APR-2003.
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PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 995			
ID ABO36256 standard; protein; 423 AA.			
DE Human PRO polypeptide #160.			
PN US2003088703-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 996			
ID ABO43785 standard; protein; 423 AA.			
DE Human PRO polypeptide #160.			
PN US2003068732-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 997			
ID ABO36256 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003082717-A1.			
PD 01-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 998			
ID ABO36256 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003104548-A1.			
PD 05-JUN-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 999			
ID ABO36256 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003104542-A1.			
PD 05-JUN-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1000			
ID ABO36256 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003104543-A1.			
PD 05-JUN-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1001			
ID ABO36256 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003036127-A1.			
PD 20-FEB-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1002			
ID ABO36256 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003040061-A1.			
PD 27-FEB-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1003			
ID ABO44291 standard; protein; 423 AA.			
DE Human secreted/transmembrane polypeptide PRO 1461.			
PN US2003018172-A1.			
PD 23-JAN-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1004			
ID ABR30714 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003073130-A1.			
PD 17-APR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1005			
ID ABR73782 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003054468-A1.			
PD 20-MAR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1006			
ID ABO17034 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003054470-A1.			
PD 20-MAR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1007			
ID ABR94459 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003044917-A1.			
PD 06-MAR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1008			
ID ABR75966 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003044929-A1.			
PD 06-MAR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1009			
ID ABR71342 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003059880-A1.			
PD 27-MAR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1010			
ID ABR93239 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003064455-A1.			
PD 03-APR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1011			
ID ABR93544 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003054478-A1.			
PD 20-MAR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1012			
ID ABR87969 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003068718-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1013			
ID ABO33656 standard; protein; 423 AA.			
DE Novel human secreted and transmembrane protein PRO1461.			
PN US2003073130-A1.			
PD 17-APR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		

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Query Match: 3.36% Indels: 0
RESULT 1014
ID ABO27969 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1015
ID ABO30104 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1016
ID ABO33313 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1017
ID ABO5001 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1018
ID ABO8961 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1019
ID ABO36561 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1020
ID ABO35646 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1021
ID ABO39611 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1022
ID ABO10486 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1023
ID ABO12011 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1024
ID ABO52157 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1025
ID ABO52462 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1026
ID ADA1968 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1027
ID ABO23780 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1028
ID ADB17351 standard; protein; 423 AA.
DE Human transmembrane PRO polypeptide (SeqID 106).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1029
ID ABR97286 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1030
ID ABR87054 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1031
ID ABO11096 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1032
ID ABO28240 standard; protein; 423 AA.
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DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1033
ID ABO32239 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1034
ID ABM15366 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1035
ID ABM06521 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1036
ID ABM04332 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1037
ID ABM22445 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1038
ID ABM07741 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1039
ID ABO40831 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1040
ID ABM35478 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1041
ID ABM33241 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.

PN US2003087374-A1.
PD 08-MAY-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1042
ID ABO52767 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1043
ID ABO50327 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1044
ID ABU99321 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003040055-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1045
ID ABO04373 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036164-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1046
ID ABO06003 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003040074-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1047
ID ABM18543 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1048
ID ABR97571 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1049
ID ABR80671 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1050
ID ABM01282 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0


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Query Match: 3.36% Indels: 0
RESULT 1070
ID ABM23360 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1071
ID ABM22140 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1072
ID ABM28545 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1073
ID ABM28850 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1074
ID ABM66494 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1075
ID ABM75876 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1076
ID ABM34156 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1077
ID ABM34461 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1078
ID ABO37781 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1079
ID ABO34219 standard; protein; 423 AA.
DE Human secreted/transmembrane polypeptide PRO 1461.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1080
ID ABR96656 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1081
ID ABR85834 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1082
ID ABR99816 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1083
ID ABM00367 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1084
ID ABM00672 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1085
ID ABO21307 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1086
ID ABO22222 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1087
ID ADA20140 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1088
ID ABR96656 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1089
ID ABR99816 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1090
ID ABM00367 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1091
ID ABM00672 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1092
ID ABO20392 standard; protein; 423 AA.
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Query Match:	3.36%	Indels:	0
RESULT 1089			
ID ABO29799 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003068700-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1090			
ID ABM23665 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003068736-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1091			
ID ABM29460 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003068679-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1092			
ID ABO38391 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003068767-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1093			
ID ABO45691 standard; protein; 423 AA.			
DE Human PRO polypeptide #160.			
PN US2003073182-A1.			
PD 17-APR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1094			
ID ABM20615 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003104557-A1.			
PD 05-JUN-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1095			
ID ADA81591 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003092121-A1.			
PD 15-MAY-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1096			
ID ABO16729 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003027276-A1.			
PD 06-FEB-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1097			
ID ABO18355 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003044920-A1.			
PD 06-MAR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1098			
ID ABO22782 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003064464-A1.			
PD 03-APR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1099			
ID ABO23087 standard; protein; 423 AA.			
DE Human PRO polypeptide #160.			
PN US2003054461-A1.			
PD 20-MAR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1100			
ID ABR92629 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003064446-A1.			
PD 03-APR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1101			
ID ABR81586 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003049744-A1.			
PD 13-MAR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1102			
ID ABM78010 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003049783-A1.			
PD 13-MAR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1103			
ID ABR9799 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003073171-A1.			
PD 17-APR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1104			
ID ABM26715 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003032121-A1.			
PD 13-FEB-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1105			
ID ABM13841 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003064458-A1.			
PD 03-APR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1106			
ID ABO28579 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003064460-A1.			
PD 03-APR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1107			
ID ABO30409 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003064464-A1.			
PD 03-APR-2003.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1108
ID ABO07436 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1109
ID ABO04027 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1110
ID ABO37171 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1111
ID ABO41746 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1112
ID ABO35341 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1113
ID ABO25190 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1114
ID ABO47582 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1115
ID ABO47887 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1116
ID ABO48497 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0

RESULT 1117
ID ABO51547 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1118
ID ABO51852 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1119
ID ABO50632 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1120
ID ABR79756 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1121
ID ABM17018 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1122
ID ABO18050 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1123
ID ABO21002 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1124
ID ABR96961 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1125
ID ABM12316 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1126
ID ABM16408 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064449-A1.

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PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1127
ID ABM24275 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064441-A1.
PD 03-APR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1128
ID ABM14756 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1129
ID ABM04637 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1130
ID ABM06826 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1131
ID ABM09266 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073174-A1.
PD 17-APR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1132
ID ABO39306 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1133
ID ABM75571 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1134
ID ABM25495 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104541-A1.
PD 05-JUN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1135
ID ABM20005 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1136
ID ABO46911 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1137
ID ABO47216 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1138
ID ADA83389 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1139
ID ABR71647 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003032133-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1140
ID ABR72257 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003032136-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1141
ID ABR98596 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003036129-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1142
ID ABO06966 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003040053-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1143
ID ABR4919 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040057-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1144
ID ABR73477 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1145
ID ABR76571 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003044932-A1.
PD 06-MAR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
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Query Match: 3.36% Indels: 0
RESULT 1146
ID ABR73172 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003027270-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1147
ID ABM18238 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1148
ID ABO20697 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003032126-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1149
ID ABO25440 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1150
ID ABO25745 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1151
ID ABR94154 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1152
ID ABR80061 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049738-A1.
PD 13-MAR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1153
ID ABM11401 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1154
ID ABO33008 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1155
ID ABO30714 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049754-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1156
ID ABO31019 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1157
ID ABM27325 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1158
ID ABM30070 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1159
ID ABM05606 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1160
ID ABM15671 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1161
ID ABM08656 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1162
ID ABO42356 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1163
ID ABO38086 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1164
ID ABO45996 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003049754-A1.
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PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1165
ID ABM66799 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1166
ID ADB20432 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1167
ID ABM19700 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1168
ID ABO49412 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1169
ID ABO49717 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1170
ID ADA78684 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1171
ID ABR88274 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1172
ID ADA00437 standard; protein; 423 AA.
DE Human secreted/transmembrane polypeptide PRO 1461.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1173
ID ABM27020 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1174
ID ABM03417 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1175
ID ABO39916 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1176
ID ABO50022 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1177
ID ABO50937 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1178
ID ABO5393 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1179
ID ABR74697 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US200304924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1180
ID ABO44509 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1181
ID ABR77176 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1182
ID ABM17933 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1183
ID ABR95984 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.

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PN US2003040073-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1184
ID ABO21917 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003054475-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1185
ID ABO20087 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1186
ID ABO24390 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1187
ID ABR86139 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1188
ID ABM10791 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1189
ID ABM76790 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1190
ID ABR89494 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1191
ID ABM12621 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1192
ID ABM05911 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1193
ID ABO35036 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1194
ID ABM03112 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1195
ID ABM19090 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1196
ID ABM19395 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1197
ID ABO46606 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1198
ID ABO49107 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1199
ID ABR69150 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1200
ID ABR89189 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1201
ID ABR72562 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1202
ID ABR74392 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
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PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1203
ID ABO18660 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1204
ID ABR80366 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1205
ID ABO1587 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1206
ID ABO2197 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1207
ID ABR87359 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068887-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1208
ID ABO12926 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1209
ID ABO3680 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1210
ID ABO24580 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1211
ID ABO29494 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1212
ID ABO31324 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1213
ID ABO14451 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1214
ID ABO09876 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1215
ID ABO39001 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1216
ID ABO34766 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1217
ID ABO51242 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1218
ID ABO04068 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1219
ID ABO10538 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1220
ID ABR77781 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1221
ID ABR78991 standard; protein; 423 AA.
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DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054456-A1.
PD 20-MAR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1222
ID ABO24085 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1223
ID ABR93849 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1224
ID ABO1892 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1225
ID ABM78315 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1226
ID ABO33533 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1227
ID ABR90104 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1228
ID ABM27630 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1229
ID ABM13231 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1230
ID ABO31934 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068731-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1231
ID ABM14146 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068683-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1232
ID ABM08351 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1233
ID ABO40221 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068681-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1234
ID ABM74656 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1235
ID ABM33851 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1236
ID ABM20310 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1237
ID ABO48802 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1238
ID ABR72867 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003036122-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1239
ID ABO15509 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0

RESULT 1240
ID ABR85224 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040065-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1241
ID ABO15204 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003044919-A1.
PD 06-MAR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1242
ID ABO17339 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003040077-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1243
ID ABO17628 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003044928-A1.
PD 06-MAR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1244
ID ABR85529 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049746-A1.
PD 13-MAR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1245
ID ABO17095 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054484-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1246
ID ABO28274 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1247
ID ABO23055 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1248
ID ABO30375 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1249
ID ABO21835 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068741-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1250
ID ABO21530 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1251
ID ABO15061 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1252
ID ABO41136 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1253
ID ABO36866 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1254
ID ABO37476 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1255
ID ABO75266 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1256
ID ABO33546 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1257
ID ABO46301 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1258
ID ADA82755 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1259
ID ADB85679 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1260
ID ABM31900 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1261
ID ABM31290 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1262
ID ADB86063 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1263
ID ABM32205 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1264
ID ABM32510 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1265
ID ADB68358 standard; protein; 423 AA.
DE Human PRO1461 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1266
ID ADB68165 standard; protein; 423 AA.
DE Human PRO1461 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1267
ID ABM31595 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0

RESULT 1268
ID ABM30985 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1269
ID ADB90982 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1270
ID ADC07062 standard; protein; 423 AA.
DE Human PRO1461 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1271
ID ADC18138 standard; protein; 423 AA.
DE Human PRO polypeptide #75.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1272
ID ADC17241 standard; protein; 423 AA.
DE Mammalian PRO polypeptide (SeqID 106).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1273
ID ADC14939 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1274
ID ADC52434 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1275
ID ADD05793 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1276
ID ADD70784 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1277

ID ADD39861 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1278
ID ADD70307 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1279
ID ADD36110 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1280
ID ADD38428 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1281
ID ADD39384 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1282
ID ADD38907 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1283
ID ADD40338 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1284
ID ADE50559 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1285
ID ADE20171 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1286
ID ADE50082 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1287
ID ADE21640 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003083628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1288
ID ADF30065 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1289
ID ADF5958 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1290
ID ADG01111 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1291
ID ADG08664 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1292
ID ADG02788 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1293
ID ADG01495 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1294
ID ADF95670 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1295
ID ADF95285 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.

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PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1296
ID ADG12485 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1297
ID ADH24138 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1298
ID ADH34164 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1299
ID ADH23997 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1300
ID ADH09145 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1301
ID ADH09145 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1302
ID ADG85372 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1303
ID ADH24648 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1304
ID ADH37504 standard; protein; 423 AA.
DE Human secreted and transmembrane protein PRO1461.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1305
ID ADH02093 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1306
ID ADH37674 standard; protein; 423 AA.
DE Human secreted and transmembrane protein PRO1461.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1307
ID ADG85712 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1308
ID ADH24308 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1309
ID ADH38602 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1310
ID ADG83723 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1311
ID ADH29531 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1312
ID ADH27647 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1313
ID ADH37844 standard; protein; 423 AA.
DE Human secreted and transmembrane protein PRO1461.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1314
ID ADH38021 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1315
ID ADH57441 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1316
ID ADH53583 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1317
ID ADH3753 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1318
ID ADH52089 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1319
ID ADH49944 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1320
ID ADI25454 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1321
ID ADH90247 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1322
ID ADI25624 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1323
ID ADH97798 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1324
ID ADH99462 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1325
ID ADI03646 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1326
ID ADI12003 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1327
ID ADH90077 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1328
ID ADH98478 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1329
ID ADI11153 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1330
ID ADI11663 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1331
ID ADH98308 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
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RESULT 1332
ID ADH98648 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1333
ID ADH98138 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1334
ID ADI05126 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1335
ID ADI03476 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1336
ID ADI04871 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1337
ID ADH78325 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1338
ID ADI19669 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1339
ID ADH90417 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1340
ID ADI03136 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1341
ID ADH79542 standard; protein; 423 AA.

ID ADH77985 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1342
ID ADH97968 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1343
ID ADI01353 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003190689-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1344
ID ADI02048 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1345
ID ADI03306 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1346
ID ADI11493 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1347
ID ADI02395 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1348
ID ADI11833 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1349
ID ADI05470 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1350
ID ADH79542 standard; protein; 423 AA.

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DE Novel human secreted and transmembrane protein PRO1461.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1351
ID AD119499 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1352
ID AD105300 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1353
ID ADH79712 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1354
ID AD101538 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1355
ID AD101708 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1356
ID AD101878 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1357
ID ADH79882 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1358
ID AD104700 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1359
ID AD102836 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003040013-A1.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1360
ID ADH78155 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1361
ID AD125794 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1362
ID AD125964 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1363
ID ADK65476 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1364
ID ADH98818 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1365
ID ADH80059 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1366
ID ADL32926 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US200307396-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1367
ID ADM30460 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1368
ID ADL93789 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003040013-A1.
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PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1369
ID ADC52244 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1370
ID ADE74457 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003211572-A1.
PD 13-NOV-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1371
ID ADE75069 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003211574-A1.
PD 13-NOV-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1372
ID ADE96642 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1373
ID ADF25953 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1374
ID ADF24852 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1375
ID ADF29588 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1376
ID ADE97119 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1377
ID ADF96282 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003215909-A1.
PD 20-NOV-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0

RESULT 1378
ID ADG04553 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1379
ID ADG00713 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1380
ID ADH06676 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1381
ID ADH06506 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1382
ID ADG68927 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1383
ID ADH27817 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1384
ID ADH25158 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1385
ID ADH33790 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1386
ID ADG82969 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1387

ID ADH03157 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1388
ID ADH02433 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1389
ID ADH08040 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1390
ID ADG69437 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1391
ID ADH39257 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1392
ID ADH04111 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1393
ID ADH03634 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1394
ID ADH26250 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1395
ID ADG83998 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1396
ID ADG85542 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1397
ID ADH06336 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1398
ID ADH30166 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1399
ID ADH24478 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1400
ID ADH33219 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1401
ID ADG69607 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1402
ID ADH07870 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1403
ID ADG85882 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1404
ID ADH39428 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1405
ID ADH33620 standard; protein; 423 AA.
DE Human PRO polypeptide #53.

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PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1406
ID ADH33960 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1407
ID ADH01170 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1408
ID ADG69777 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1409
ID ADH02263 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1410
ID ADG69267 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1411
ID ADG86052 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1412
ID ADH24988 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1413
ID ADH39605 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1414
ID ADH02603 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1415
ID ADG69097 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1416
ID ADH07700 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1417
ID ADG86222 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1418
ID ADH24818 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1419
ID ADH25866 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1420
ID ADH38432 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1421
ID ADH57271 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1422
ID ADH52258 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1423
ID ADH04588 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2004005626-A1.
PD 08-JAN-2004.
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1424
ID ADH49624 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1425
ID ADH90587 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1426
ID ADH90587 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1427
ID ADH98988 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1428
ID ADI02218 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1429
ID ADH61589 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1430
ID ADH90757 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1431
ID ADJ54958 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1432
ID ADJ98632 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1433
ID ADJ98902 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1434
ID ADH78961 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1435
ID ADJ99195 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1436
ID ADJ99365 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1437
ID ADJ98983 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1438
ID ADH79130 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1439
ID ADK00991 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1440
ID ADK14512 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1441
ID ADJ64729 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
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Query Match: 3.36% Indels: 0
RESULT 1442
ID ADM31625 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1443
ID ADM36672 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1444
ID ADM40477 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1445
ID ADM80961 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1446
ID ADL94788 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1447
ID ADN38085 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1448
ID ADQ89174 standard; protein; 423 AA.
DE Human urological disorder related protein 32409 SEQ:126.
PN WO2004065576-A2.
PD 05-AUG-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1449
ID AAR06459 standard; protein; 431 AA.
DE v-PA beta.
PN EP383417-A.
PD 22-AUG-1990.
PA (SCHD) SCHERING AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1450
ID AAR14930 standard; protein; 13 AA.
DE OT-2 antibody binding peptide (3).
PN WO9117258-A.
PD 14-NOV-1991.
PA (CETU) CETUS CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0

RESULT 1451
ID AAE17240 standard; peptide; 14 AA.
DE Human transmembrane serine protease-related type I fibronectin domain #1.
PN WO200196538-A2.
PD 20-DEC-2001.
PA (FARB) BAYER AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1452
ID AAE18999 standard; peptide; 14 AA.
DE Human matritase-like serine protease related fibronectin domain #1.
PN WO200208392-A2.
PD 31-JAN-2002.
PA (FARB) BAYER AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1453
ID AAR67942 standard; protein; 22 AA.
DE (1-3)-beta-D-glucan sensitive factor peptide fragment 10.
PN WO9501432-A1.
PD 12-JAN-1995.
PA (SEK) SEIKAGAKU KOGYO CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1454
ID AAE17246 standard; peptide; 24 AA.
DE Serine protease peptide #2 of the trypsin family.
PN WO200196538-A2.
PD 20-DEC-2001.
PA (FARB) BAYER AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1455
ID AAE19007 standard; peptide; 24 AA.
DE Human matritase-like serine protease related peptide #3.
PN WO200208392-A2.
PD 31-JAN-2002.
PA (FARB) BAYER AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1456
ID AAE17239 standard; peptide; 35 AA.
DE Human transmembrane serine protease-related apple domain #1.
PN WO200196538-A2.
PD 20-DEC-2001.
PA (FARB) BAYER AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1457
ID AAE19008 standard; peptide; 35 AA.
DE Human matritase-like serine protease related apple domain #2.
PN WO200208392-A2.
PD 31-JAN-2002.
PA (FARB) BAYER AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1458
ID AAM50210 standard; protein; 97 AA.
DE Human plasminogen-like AMF4 C-terminal polypeptide.
PN WO200174897-A2.
PD 11-OCT-2001.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1459
ID ADA05696 standard; protein; 102 AA.
DE Human NOV11e protein SEQ ID NO:56.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1460

ID ADN62860 standard; protein; 102 AA.
DE Human NOV11d.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTI/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWV/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1461
ID AAR3961 standard; protein; 105 AA.
DE Hepatocyte growth factor converting protease fragment.
PN EP596524-A2.
PD 11-MAY-1994.
PA (MITU/) MITSUBISHI KASEI CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1462
ID AAB71662 standard; protein; 118 AA.
DE Human colon associated protein #10.
PN WO200112781-A1.
PD 22-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1463
ID ADA05694 standard; protein; 119 AA.
DE Human NOV11d protein SEQ ID NO:54.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1464
ID ADA05700 standard; protein; 119 AA.
DE Human NOV11g protein SEQ ID NO:60.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1465

ID ADN62858 standard; protein; 119 AA.
DE Human NOV11d.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTI/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWV/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1466
ID ADG75740 standard; protein; 141 AA.
DE Human protein modification and maintenance molecule polypeptide SeqID64.
PN WO2003083084-A2.
PD 09-OCT-2003.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1467
ID ADA05688 standard; protein; 142 AA.
DE Human NOV11a protein SEQ ID NO:48.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1468
ID ADN62852 standard; protein; 142 AA.
DE Human NOV11a.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.

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PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGE E M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1469
ID ADN62856 standard; protein; 147 AA.
DE Human NOV11c.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYN/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATI/) PATURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGE E M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1470
ID ADA05692 standard; protein; 148 AA.
DE Human NOV11c protein SEQ ID NO:52.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1471
ID AAU68926 standard; protein; 149 AA.
DE Human protease domain of protease M.
PN US6294663-B1.
PD 25-SEP-2001.
PA (UYAR-) UNIV ARKANSAS.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1472
ID ADE13246 standard; protein; 149 AA.
DE Protease domain from human protease M.
PN US2003170707-A1.
PD 11-SEP-2003.
PA (OBRI/) O'BRIEN T J.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1473
ID ADH78455 standard; protein; 149 AA.
DE Human protease M protease domain.
PN US2003207316-A1.
PD 06-NOV-2003.
PA (UYAR-) UNIV ARKANSAS.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1474
ID ABR41514 standard; protein; 156 AA.
DE Human DITHP protein modification/maintenance protein.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1475
ID AAU68929 standard; protein; 157 AA.
DE Human protease domain of TADG-12.
PN US6294663-B1.
PD 25-SEP-2001.
PA (UYAR-) UNIV ARKANSAS.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1476
ID ADE13374 standard; protein; 157 AA.
DE Protease domain from human TADG-12 #2.
PN US2003170707-A1.
PD 11-SEP-2003.
PA (OBRI/) O'BRIEN T J.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1477
ID ADH78458 standard; protein; 157 AA.
DE Human TADG-12 protease domain.
PN US2003207316-A1.
PD 06-NOV-2003.
PA (UYAR-) UNIV ARKANSAS.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1478
ID ADP43664 standard; protein; 162 AA.
DE Human PMW-21 protein SEQ ID NO:21.
PN WO2004053068-A2.
PD 24-JUN-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1479
ID ABM84664 standard; protein; 165 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4913.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1480
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ID AAU75082 standard; protein; 178 AA.
DE Human prostatic-like serine protease protein.
PN WO2001198467-A2.
PD 27-DEC-2001.
PA (FARB) BAYER AG.
Query Match: Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
RESULT 1481
ID AD116332 standard; protein; 181 AA.
DE Human protein modification and maintenance molecule (PMM4) protein #17.
PN WO2003100016-A2.
PD 04-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match: Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
RESULT 1482
ID ABG75787 standard; protein; 191 AA.
DE Serine protease zymogen domain consensus sequence, PD000000046, #1.
PN US2002165152-A1.
PD 07-NOV-2002.
PA (KAP-) KAPILLER-LIBERMANN R.
Query Match: Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
RESULT 1483
ID AAG73966 standard; protein; 193 AA.
DE Human colon cancer antigen protein SEQ ID NO:4730.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match: Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
RESULT 1484
ID ADM79155 standard; protein; 194 AA.
DE Human delta trypsin variant protein.
PN WO2004033494-A1.
PD 22-APR-2004.
PA (UNIX) UNISEARCH LTD.
Query Match: Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
RESULT 1485
ID ADG42737 standard; protein; 199 AA.
DE Human beta trypsin precursor protein #3.
PN US2003202971-A1.
PD 30-OCT-2003.
PA (MAJU) MAJUMDER K.
Query Match: Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
RESULT 1486
ID ADJ5806 standard; peptide; 199 AA.
DE Peptide homologous to a fragment of a human NOV12 protein SeqID 98.
PN US2003199455-A1.
PD 23-OCT-2003.
PA (MALY) MALYANKAR U M.
PA (TCHE) TCHERNEV V T.
PA (PADI) PADIGARU M.
PA (TAUP) TAPIER R J.
PA (SPYT) SPYTEK K A.
PA (GUOX) GUO X.
PA (SPAD) SPADERNA S K.
PA (BOLD) BOLDOG F L.
PA (GERL) GERLACH V.
PA (ELLE) ELLERMAN K.
PA (MACD) MACDOUGALL J R.
PA (SMIT) SMITHSON G.
Query Match: Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
RESULT 1487
ID ADM76644 standard; protein; 199 AA.
DE Human NOV12 protein-related protein fragment SeqID98.
PN WO2004009634-A2.
PD 29-JAN-2004.
PA (CURA-) CURAGEN CORP.
Query Match: Mismatches: 0
Best Local Similarity: 100.00% Indels: 0

Query Match: 3.08% Indels: 0
RESULT 1488
ID AAY28641 standard; protein; 207 AA.
DE Human secreted protein from cDNA clone HKAE741.
PN WO9940183-A1.
PD 12-AUG-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match: Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
RESULT 1489
ID ABR48479 standard; protein; 207 AA.
DE Human Plasminogen.
PN WO200294864-A2.
PD 28-NOV-2002.
PA (GEST) GENSET.
Query Match: Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
RESULT 1490
ID ADQ67690 standard; protein; 211 AA.
DE Novel human protein sequence #2356.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match: Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
RESULT 1491
ID AD117075 standard; protein; 225 AA.
DE Murine NOVX protein homologue SeqID 611.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match: Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
RESULT 1492
ID ADM79152 standard; protein; 226 AA.
DE Human delta trypsin variant protein SEQ ID NO:3.
PN WO2004033494-A1.
PD 22-APR-2004.
PA (UNIX) UNISEARCH LTD.
Query Match: Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
RESULT 1493
ID AAB21312 standard; protein; 228 AA.
DE Human TLSP.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match: Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
RESULT 1494
ID AD110641 standard; protein; 228 AA.
DE Cell surface protease.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match: Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
RESULT 1495
ID ADG5348 standard; protein; 228 AA.
DE Alternative PDI from Human MTSPI2.
PN WO2003104394-A2.
PD 18-DEC-2003.
PA (DEND-) DENDREON SAN DIEGO LLC.
Query Match: Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
RESULT 1496
ID ADJ47165 standard; protein; 228 AA.
DE Human transmembrane serine protease (WTSP) polypeptide #16.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match: Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
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RESULT 1497
ID AAR56474 standard; protein; 230 AA.
DE Mutant plasmin protease domain.
PN WO9403614-A1.
PD 17-FEB-1994.
PA (BRBI-) BRITISH BIO-TECHNOLOGY LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1498
ID AAR56475 standard; protein; 230 AA.
DE Mutant plasmin protease domain.
PN WO9403614-A1.
PD 17-FEB-1994.
PA (BRBI-) BRITISH BIO-TECHNOLOGY LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1499
ID AAR56476 standard; protein; 230 AA.
DE Mutant plasmin protease domain.
PN WO9403614-A1.
PD 17-FEB-1994.
PA (BRBI-) BRITISH BIO-TECHNOLOGY LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
RESULT 1500
ID AAR56471 standard; protein; 230 AA.
DE Mutant plasmin protease domain.
PN WO9403614-A1.
PD 17-FEB-1994.
PA (BRBI-) BRITISH BIO-TECHNOLOGY LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
```


[illegible]

Db 21 LysIlePheAsnGlyThrGluCysGlyArgAsnSerGlnProTrrpGlnValGlyLeuPhe 40
QY 241 GAGGACACAGCTGGCTGGGGGTGCTCTATTGACACAGAGTGGTCTCACAGC 300
Db 41 GluGlyThrSerLeuArgCysGlyGlyValLeuIleAspHisArgTrrpValLeuThrAla 60
QY 301 GCTCACTGAGCGGACAGAGTACTGGGTGGCCCTGGGGGAACACAGCTCAGCCAGTCC 360
Db 61 AlaHisCysSerGlySerArgTrrpValArgLeuGlyGluHisSerLeuSerGlnLeu 80
QY 361 GACTGACGAGACAGATCCGACAGCGGCTTCTGTGACCCATCCCGGCTACTCTGGGA 420
Db 81 AspTrrpThrGluIleArgHisSerGlyPheSerValThrHisProGlyTrrpLeuGly 100
QY 421 GCCTGACGAGCAGACAGCACTCCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 480
Db 101 AlaSerThrSerHisGluHisAspLeuArgLeuLeuArgLeuProValArgVal 120
QY 481 ACCAGCAGCGTTCAACCCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGC 540
Db 121 ThrSerSerValGlnProLeuProLeuProAsnAspCysAlaThrAlaGlyThrGluCys 140
QY 541 CACGCTCAGCTGGGACATCCACACACACAGCAACCCATTCGCGATCTGCTCCAG 600
Db 141 HisValSerGlyTrrpGlyIleThrAsnHisProArgAsnProPheProAspLeuGln 160
QY 601 TGCCTCACTCTCCATCTCTCCATGCTCCATGCTCCATGCTCCATGCTCCATGCTCC 660
Db 161 CysLeuAsnLeuSerIleValSerHisAlaThrCysHisGlyValTrrpProGlyArgIle 180
QY 661 ACAGCAACATCGTGTGTGTCAGCGCGCTGCCCGGCGAGGATGCTGCCAGGCTGATTCT 720
Db 181 ThrSerAsnMetValCysAlaGlyValProGlyGlnAspAlaCysGlnGlyAspSer 200
QY 721 GGGGCGCCCTCGTGTGTGGGAGTCTTCAAGTCTGGTCTCTGGGGTCTGTGGGG 780
Db 201 GlyGlyProLeuValCysGlyGlyValLeuGlnGlyLeuValSerTrrpGlySerValGly 220
QY 781 CCCTGTGGACAGATGGCATCCCTGGAGTCTACACCTATATTTC 825
Db 221 ProCysGlyGlnAspGlyIleProGlyValTrrpThrTyrlleCys 235

RESULT 2

US-09-949-016-8151
; Sequence 8151, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8151
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8151

Alignment Scores:
Pred. No.: 1,14e-195 Length: 249
Score: 222.00 Matches: 249
Percent Similarity: 98.81% Conservative: 0
Best Local Similarity: 98.81% Mismatches: 0
Query Match: 62.18% Indels: 3

DB: 4 Gaps: 0
US-10-015-385A-193 (1-1091) x US-09-949-016-8151 (1-249)
QY 115 CCCACATGGGGCTCAGCATCTTTTGTCTCTGTGTGTCTTGGCTCAGCCAGCAGCC 174
Db 1 ProThrMetGlyLeuSerIlePheLeuLeuLeuCysValLeuGlyLeuSerGlnAlaAla 20
QY 175 ACACCGAAGATTTTCAATGGCAGTCTAGTGGGCTAACTCACAGCCCTGGCAGGTGGG 234
Db 21 ThrProLysIlePheAsnGlyThrGluCysGlyArgAsnSerGlnProTrrpGlnValGly 40
QY 235 CTGTTTGGAGGACACAGCTCGCTGGCGGGGTGCTTATTGACACAGTGGGTCTCTC 294
Db 41 LeuPheGluGlyThrSerLeuArgCysGlyGlyValLeuIleAspHisArgTrrpValLeu 60
QY 295 ACAGCGGCTCACTGAGCGGCGAGAGTACTGGGTGGCGCTGGGGGAACACAGCCTCAGC 354
Db 61 ThrAlaAlaHisCysSerGly---ArgTrrpValArgLeuGlyGluHisSerLeuSer 79
QY 355 CAGCTCCGACTGACCGACAGATCCGACAGCGGCTTCTCTGTGACCCATCCCGGCTAC 414
Db 80 GlnLeuAspTrrpThrGluGlnIleArgHisSerGlyPheSerValThrHisProGlyTrrp 99
QY 415 CTGGAGGCTCGACAGACAGACAGACAGCACTCCCGCTGTGGCGCTGGCGCTGGCGCTC 474
Db 100 LeuGlyAlaSerThrSerHisGluHisAspLeuArgLeuLeuArgLeuProVal 119
QY 475 CGCTTAACACAGAGGTTCAACCCCTGCCCTGCCCAATGACTGTGCAACCGCTGCGCACC 534
Db 120 ArgValThrSerSerValGlnProLeuProLeuProAsnAspCysAlaThrAlaGlyThr 139
QY 535 CAGTCCCACTGCTCAGGCTGGGCGATCACCAACACACCGAACCCTATTCGCGGATCTG 594
Db 140 GluCysHisValSerGlyTrrpGlyIleThrAsnHisProArgAsnProPheProAspLeu 159
QY 595 TCCAGTGCCTCAACCTTCCATCTCCATGCTCCCATGCTCCATGCTCCATGCTCCATGCT 654
Db 160 LeuGlnCysLeuAsnLeuSerIleValSerHisAlaThrCysHisGlyValTrrpProGly 179
QY 655 AGAATCAGACGACACATGCTGTGTGTCAGCGCGCTGCCGGGCGAGATGCTCTGGGGTCT 714
Db 180 ArgIleThrSerAsnMetValCysAlaGlyGlyValProGlyGlnAspAlaCysGlnGly 199
QY 715 GATTCCTGGGGCGCCCTGCTGTGTGGGGAGTCTCTTCAAGTCTGCTCTGGGGTCT 774
Db 200 AspSerGlyGlyProLeuValCysGlyGlyValLeuGlnGlyLeuValSerTrrpGlySer 219
QY 775 GFGGGGCTGTGGACAGATGGCATCCCTGGAGTCTACACCTATATTTCGAGTATGTG 834
Db 220 ValGlyProCysGlyGlnAspGlyIleProGlyValTrrpThrTyrlleCysLysTrrpVal 239
QY 835 GACTCGATCCGATCATGATGAGGAACAAC 864
Db 240 AspTrrpIleArgMetIleMetArgAsnAsn 249
RESULT 3
US-09-244-111-6
; Sequence 6, Application US/09244111
; Patent No. 6566498
; GENERAL INFORMATION:
; APPLICANT: NI, et al.
; TITLE OF INVENTION: Human Serine Protease and Serpin Polypeptides
; FILE REFERENCE: PF391
; CURRENT APPLICATION NUMBER: US/09/244,111
; CURRENT FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 60/073,961
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 162
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-244-111-6

Alignment Scores:
Pred. No.: 5,36e-77 Length: 162
Score: 93.00 Matches: 93
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.05% Indels: 0
DB: 4 Gaps: 0

US-10-015-385A-193 (1-1091) x US-09-244-111-6 (1-162)

QY 586 CCGATCTGCTCCAGTCCCTCAACCTCTCCATGCTCCCATGCCACCTGCCATGTGTG 645
Db 70 ProAspLeuLeuGlnCysLeuAsnLeuSerIleValSerHisAlaThrCysHisGlyVal 89
QY 646 TATCCCGGAGATCAGCACATGCTGTGTCAGCGGCGCTCCCGGGCAGGATGCC 705
Db 90 TyrProGlyArgIleThrSerAsnMetValCysAlaGlyValProGlyGlnAspAla 109
QY 706 TGCAGGGTGATCTGGGGGCCCCCTGGTGTGTGGGGAGTCTTCAAGTCTGGGTGCC 765
Db 110 CysGlnGlyAspSerGlyProLeuValCysGlyGlyValLeuGlnGlyValSer 129
QY 766 TGGGGTCTGTGGGGCCCCCTGTGGACAAGATGGCATCCCTGGAGCTTACACCTATTATTC 825
Db 130 TripGlySerValGlyProCysGlyGlnAspGlyIleProGlyValTyrThrTyrIleCys 149
QY 826 AGTATGTGGACTGGATCCGGATGATCATCATGAGGAACAAC 864
Db 150 LysTyrValAspTrpIleArgMetIleMetArgAsnAsn 162

RESULT 4
5200340-4
; Patent No. 5200340
; APPLICANT: POSTER, DONALD C.; MULVIHILL, EILEEN R.; O'HARA,
; PATRICK J.; PINGEL, KURT; YOSHITAKE, SHINJI
; TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
; ACTIVATORS
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/53,412
; FILING DATE: 22-MAY-1987
; SEQ ID NO:4:
; LENGTH: 138
5200340-4

Alignment Scores:
Pred. No.: 0.00209 Length: 138
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 6 Gaps: 0

US-10-015-385A-193 (1-1091) x 5200340-4 (1-138)

QY 700 GATGCTCCAGGATGATTCGGGGCCCCCTGGTGTGTGT 738
Db 83 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 95

RESULT 5
5200340-4
; Patent No. 5200340
; APPLICANT: POSTER, DONALD C.; MULVIHILL, EILEEN R.; O'HARA,
; PATRICK J.; PINGEL, KURT; YOSHITAKE, SHINJI
; TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
; ACTIVATORS
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/53,412
; FILING DATE: 22-MAY-1987

; SEQ ID NO:4:
; LENGTH: 138
5200340-4

Alignment Scores:
Pred. No.: 0.00209 Length: 138
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 6 Gaps: 0

US-10-015-385A-193 (1-1091) x 5200340-4 (1-138)

QY 700 GATGCTCCAGGATGATTCGGGGCCCCCTGGTGTGTGT 738
Db 83 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 95

RESULT 6
5223425-6
; Patent No. 5223425
; APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,
; BARRY M.; WHITE, TYLER R.
; TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
; D ACTIVITY
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/277,963
; FILING DATE: 30-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 34,203
; FILING DATE: 02-APR-1987
; SEQ ID NO:6:
; LENGTH: 222
5223425-6

Alignment Scores:
Pred. No.: 0.00197 Length: 222
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 6 Gaps: 0

US-10-015-385A-193 (1-1091) x 5223425-6 (1-222)

QY 712 GGTGATTCGGGGCCCCCTGGTGTGTGGGAGTCCTT 750
Db 176 GlyAspSerGlyGlyProLeuValCysGlyGlyValLeu 188

RESULT 7
5223425-6
; Patent No. 5223425
; APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,
; BARRY M.; WHITE, TYLER R.
; TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
; D ACTIVITY
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/277,963
; FILING DATE: 30-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 34,203
; FILING DATE: 02-APR-1987
; SEQ ID NO:6:
; LENGTH: 222
5223425-6

Alignment Scores:
Pred. No.: 0.00197 Length: 222
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.64% Indels: 0
DB: 6 Gaps: 0

US-10-015-385A-193 (1-1091) x 5223425-6 (1-222)

QY 712 GGTGATTCTGGGGCCCCCTGTGTGTGGGGAGTCCTT 750
DB 176 GlyAspSerGlyGlyProLeuValCysGlyGlyValLeu 188

RESULT 8

US-08-944-483-44
; Sequence 44, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; TITLE OF INVENTION: OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-3623
; TELEX:

; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e

US-08-944-483-44

Alignment Scores:
Pred. No.: 0.00197 Length: 228
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 3 Gaps: 0

US-10-015-385A-193 (1-1091) x US-08-944-483-44 (1-228)

QY 712 GGTGATTCTGGGGCCCCCTGTGTGTGGGGAGTCCTT 750

DB 181 GlyAspSerGlyGlyProLeuValCysGlyGlyValLeu 193

RESULT 9

5223425-5
; Patent No. 5223425
; APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,
; BARRY M.; WHITE, TYLER R.
; TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
; D ACTIVITY

; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/277,963
; FILING DATE: 30-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 34,203
; FILING DATE: 02-APR-1987
; SEQ ID NO: 5:
; LENGTH: 238
5223425-5

Alignment Scores:
Pred. No.: 0.00196 Length: 238
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 6 Gaps: 0

US-10-015-385A-193 (1-1091) x 5223425-5 (1-238)

QY 712 GGTGATTCTGGGGCCCCCTGTGTGTGGGGAGTCCTT 750
DB 191 GlyAspSerGlyGlyProLeuValCysGlyGlyValLeu 203

RESULT 10

5223425-5
; Patent No. 5223425
; APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,
; BARRY M.; WHITE, TYLER R.
; TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
; D ACTIVITY

; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/277,963
; FILING DATE: 30-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 34,203
; FILING DATE: 02-APR-1987
; SEQ ID NO: 5:
; LENGTH: 238
5223425-5

Alignment Scores:
Pred. No.: 0.00196 Length: 238
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 6 Gaps: 0

US-10-015-385A-193 (1-1091) x 5223425-5 (1-238)

QY 712 GGTGATTCTGGGGCCCCCTGTGTGTGGGGAGTCCTT 750
DB 191 GlyAspSerGlyGlyProLeuValCysGlyGlyValLeu 203

RESULT 11

US-08-944-483-70
; Sequence 70, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE

APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6232456e
US-08-944-483-70

Alignment Scores:
Pred. No.: 0.00195 Length: 243
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 3 Gaps: 0

US-10-015-385A-193 (1-1091) x US-08-944-483-70 (1-243)

QY 700 GATGCTGCAGGTGATCTGGGGCCCCCTGGTGT 738
Db 185 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 197

RESULT 12
5223425-4
Patent No. 5223425
APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,
BARRY M.; WHITE, TYLER R.
TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
D ACTIVITY
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/277,963
FILING DATE: 30-NOV-1988
PRIOR APPLICATION DATA:

APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6232456e
US-08-944-483-70

Alignment Scores:
Pred. No.: 0.00195 Length: 243
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 3 Gaps: 0

US-10-015-385A-193 (1-1091) x 5223425-4 (1-250)

QY 712 GGTGATTCTGGGGCCCCCTGGTGTGGGGAGTCCTT 750
Db 203 GlyAspSerGlyGlyProLeuValCysGlyGlyValLeu 215

RESULT 13
5223425-4
Patent No. 5223425
APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,
BARRY M.; WHITE, TYLER R.
TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
D ACTIVITY
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/277,963
FILING DATE: 30-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 34,203
FILING DATE: 02-APR-1987
SEQ ID NO: 4:
LENGTH: 250
5223425-4

Alignment Scores:
Pred. No.: 0.00195 Length: 250
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 6 Gaps: 0

US-10-015-385A-193 (1-1091) x 5223425-4 (1-250)

QY 712 GGTGATTCTGGGGCCCCCTGGTGTGGGGAGTCCTT 750
Db 203 GlyAspSerGlyGlyProLeuValCysGlyGlyValLeu 215

RESULT 14
US-08-944-483-72
Sequence 72, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park

STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6232456e
US-08-944-483-72

Alignment Scores:
Pred. No.: 0.00195 Length: 252
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 3 Gaps: 0

US-10-015-385A-193 (1-1091) x US-08-944-483-72 (1-252)

QY 700 GATGCTGCCAGGTGATTCTGGGGCCCCCTGGTGTGT 738
Db 197 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 209

RESULT 15

US-09-027-337-8
Sequence 8, Application US/09027337B
Patent No. 5972616
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotschi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 8
LENGTH: 253
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Serine protease catalytic domain of tissue plasminogen
activator (Tpa) homologous to similar domain in TADG-15
US-09-027-337-8

Alignment Scores:
Pred. No.: 0.00194 Length: 253
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.64% Indels: 0
DB: 2 Gaps: 0
US-10-015-385A-193 (1-1091) x US-09-027-337-8 (1-253)
QY 700 GATGCTGCCAGGTGATTCTGGGGCCCCCTGGTGTGT 738
Db 198 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 210
Search completed: March 5, 2005, 23:47:13
Job time : 50.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 5, 2005, 23:34:20 ; Search time 49 Seconds
(without alignments)
4284.591 Million cell updates/sec

Title: US-10-015-385A-193

Perfect score: 357

Sequence: 1 caagcaggtcatccctctgg.....aggggcaaaaaaaaaa 1091

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Word size: 1

Total number of hits satisfying chosen parameters: 565918

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DRV=xlp
-Q/cgn2 1/USPTO_spool_p/US10015385/runat_05032005_173710_18168/app_query.fasta_1.1287
-DB=PIR79 -Qfmt=fastan -SUFFIX=olin2p.rpr -MINMATCH=0.1 -LOOPCL=0 -ICOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1500
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptp
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10015385 @CGN 1.1 63 @runat_05032005_173710_18168 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -HEADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	3.6	246	1 DBHU	complement factor
2	13	3.6	394	2 JS0600	t-plasminogen acti
3	13	3.6	431	2 JS0599	t-plasminogen acti
4	13	3.6	477	1 A34369	t-plasminogen acti
5	13	3.6	477	2 JS0597	t-plasminogen acti
6	13	3.6	477	2 JS0598	t-plasminogen acti
7	13	3.6	559	1 A29941	t-plasminogen acti
8	13	3.6	559	1 A35029	t-plasminogen acti
9	13	3.6	562	1 UKHUT	t-plasminogen acti
10	13	3.6	593	2 S45281	coagulation factor
11	13	3.6	603	2 S28941	coagulation factor
12	13	3.6	615	1 KFHU12	coagulation factor
13	13	3.6	1524	2 T30337	polyprotein - Afri
14	12	3.4	191	2 S54115	complement factor

15	12	3.4	254	2 S65465	trypsin-like prote
16	12	3.4	256	1 TRFF	trypsin-like prote
17	12	3.4	264	2 S32794	trypsin-like prote
18	12	3.4	267	2 S40006	serine proteinase
19	12	3.4	271	2 S41308	trypsin (EC 3.4.21
20	12	3.4	274	2 S35339	trypsin (EC 3.4.21
21	12	3.4	275	2 S40007	trypsin (EC 3.4.21
22	12	3.4	275	2 S40005	trypsin (EC 3.4.21
23	12	3.4	277	2 S35340	trypsin (EC 3.4.21
24	12	3.4	285	2 T35195	probable serine pr
25	11	3.1	126	2 A23473	chymotrypsin-like
26	11	3.1	225	2 S45356	probable serine pr
27	11	3.1	237	2 S55378	serine proteinase
28	11	3.1	237	2 S68702	trypsin (EC 3.4.2
29	11	3.1	260	2 I56559	neuropain - mouse
30	11	3.1	264	2 I38136	chymotrypsin-like
31	11	3.1	266	2 JC4850	trypsin-like prote
32	11	3.1	270	2 S56160	mast cell tryptase
33	11	3.1	273	2 A47246	tryptase (EC 3.4.2
34	11	3.1	274	2 JC4171	tryptase (EC 3.4.2
35	11	3.1	275	2 C35863	tryptase (EC 3.4.2
36	11	3.1	275	2 B35863	tryptase (EC 3.4.2
37	11	3.1	275	2 A35863	tryptase (EC 3.4.2
38	11	3.1	275	2 A32410	tryptase (EC 3.4.2
39	11	3.1	276	2 A38654	mast cell proteina
40	11	3.1	309	2 B49878	coagulation factor
41	11	3.1	343	1 A57014	prostatin (EC 3.4.
42	11	3.1	400	1 A48050	coagulation factor
43	11	3.1	431	1 UKHU	u-plasminogen acti
44	11	3.1	433	1 JN0560	u-plasminogen acti
45	11	3.1	433	1 UKBAY	u-plasminogen acti
46	11	3.1	442	1 UKPG	u-plasminogen acti
47	11	3.1	455	2 A61545	plasmin (EC 3.4.21
48	11	3.1	460	2 B61545	plasmin (EC 3.4.21
49	11	3.1	555	1 A45688	hepatocyte growth
50	11	3.1	790	1 PLFG	plasmin (EC 3.4.21
51	11	3.1	810	1 PLHU	plasmin (EC 3.4.21
52	11	3.1	810	2 I46260	plasmin (EC 3.4.21
53	11	3.1	810	2 B30848	plasmin (EC 3.4.21
54	11	3.1	812	1 PLBO	plasmin (EC 3.4.21
55	11	3.1	812	1 PLMS	plasmin (EC 3.4.21
56	11	3.1	1004	2 T30338	oviductin (EC 3.4.
57	11	3.1	2616	2 A57096	nudel protein prec
58	11	3.1	4548	1 S00657	apoptin(a) (EC
59	10	2.8	30	2 C32946	serine proteinase
60	10	2.8	43	2 A61168	cocoanase (EC 3.4.
61	10	2.8	61	2 PS0049	serine proteinase
62	10	2.8	161	2 I62744	coagulation factor
63	10	2.8	161	2 I48158	coagulation factor
64	10	2.8	238	1 TRWV5Y	chymase (EC 3.4.21
65	10	2.8	244	2 A46721	trypsin-like prote
66	10	2.8	244	2 A34910	mast cell proteina
67	10	2.8	248	2 A43520	natural killer cel
68	10	2.8	248	2 S33755	granzyme-like prot
69	10	2.8	249	2 A55634	granzyme M (EC 3.4
70	10	2.8	254	1 TRWV3Y	trypsin-like prote
71	10	2.8	254	2 S35585	chymotrypsin-like
72	10	2.8	258	2 A45161	serine proteinase
73	10	2.8	263	1 I55608	complement factor
74	10	2.8	303	2 T13598	trypsin homolog -
75	10	2.8	375	1 A23689	limulus clotting e
76	10	2.8	417	1 S00845	hepsin (EC 3.4.21
77	10	2.8	475	1 EXCH	coagulation factor
78	10	2.8	482	1 EXRT	coagulation factor
79	10	2.8	488	1 EXHU	coagulation factor
80	10	2.8	492	1 EXBO	coagulation factor
81	10	2.8	705	1 C1HURB	complement subcomp
82	9	2.5	73	2 S44462	elastase (EC 3.4.2
83	9	2.5	195	2 T03245	G-box binding prote
84	9	2.5	213	2 S17537	fibrinolytic prote
85	9	2.5	214	2 S17680	fibrinolytic prote
86	9	2.5	226	2 S69370	duodenase - bovine
87	9	2.5	226	2 JE0151	myonase (EC 3.4.-

1402 2 448 2 S33926 wilms' tumor prote
1403 2 449 2 A38080 Wilms tumor suscep
1404 2 449 2 A39692 Wilms' tumor prote
1405 2 449 2 S07682 OmpA family protei
1406 2 450 2 S07051 cysteine proteinas
1407 2 450 2 S12099 cysteine proteinas
1408 2 451 2 A36646 probable tartrate
1409 2 452 2 H96710 hypothetical prote
1410 2 454 2 A68803 probable mitotic c
1411 2 455 1 TVCRGG phosphoglycerate k
1412 2 455 2 A10599 probable ATP-depen
1413 2 455 2 T05081 hypothetical prote
1414 2 455 2 B86427 hypothetical prote
1415 2 456 2 A40492 early growth respo
1416 2 456 2 S55661 hypothetical prote
1417 2 457 2 E88456 protein W03A5.3 [i
1418 2 457 2 E88456 aminotransferase,
1419 2 457 2 AF2975 probable aminotran
1420 2 457 2 E98307 dihydrolipoamide a
1421 2 458 2 A30775 hypothetical prote
1422 2 458 2 T02804 peptidase, M23/M37
1423 2 458 2 H87624 homeotic protein N
1424 2 458 2 A49690 homeotic protein N
1425 2 459 2 F71257 hypothetical prote
1426 2 460 2 D84396 signal recognition
1427 2 460 2 T21626 hypothetical prote
1428 2 460 2 G70803 hypothetical prote
1429 2 461 1 A46077 steroid hormone re
1430 2 461 2 D64701 thiophene and fura
1431 2 461 2 G71818 probable thiophene
1432 2 461 2 F82819 D-lactate dehydrog
1433 2 461 2 S45568 nuclear factor I-A
1434 2 462 1 A56120 steroid hormone re
1435 2 462 2 A40716 steroid hormone re
1436 2 463 2 A48375 cellulase (EC 3.2.
1437 2 463 2 T45565 hypothetical prote
1438 2 463 2 T36810 probable integral
1439 2 464 2 JC7143 endoglucohydrolase I -
1440 2 464 2 A56600 intermediate filam
1441 2 464 2 A87675 carboxyl-terminal
1442 2 464 2 T21628 hypothetical prote
1443 2 464 2 T50955 hypothetical prote
1444 2 464 2 S75831 hypothetical prote
1445 2 464 2 S22697 extensin - Volvox
1446 2 465 1 W01820 glycine-rich cell
1447 2 465 1 Z2BEB4 5L.3K capsid prote
1448 2 465 2 A42128 embryonal long ter
1449 2 465 2 G02738 FREAC-4 - human
1450 2 465 2 G02738 FREAC-4 - human
1451 2 466 1 CYDKD1 delta-1-crystallin
1452 2 466 2 JN0486 argininosuccinate
1453 2 466 2 S29247 argininosuccinate
1454 2 466 2 T45585 hypothetical prote
1455 2 467 2 I50476 keratin type I - 9
1456 2 467 2 A41318 hypothetical prote
1457 2 467 2 C87349 efflux system prot
1458 2 467 2 T18744 hypothetical prote
1459 2 467 2 S35782 serine/threonine p
1460 2 468 1 CYDKD2 delta-2-crystallin
1461 2 469 2 T02325 probable selenium-
1462 2 470 2 T31602 hypothetical prote
1463 2 470 2 A30136 developmental cont
1464 2 471 2 S09110 hypothetical prote
1465 2 472 1 WMADF6 early B1B 52K prot
1466 2 474 2 A35732 protective protein
1467 2 474 2 F83550 serine proteinase
1468 2 474 2 A43312 hypothetical ATP-b
1469 2 474 2 S57239 gene forked protei
1470 2 474 2 T10271 capsid-associated
1471 2 474 2 I38240 transcription fact
1472 2 475 2 C84384 hypothetical prote
1473 2 475 2 A43915 homeotic protein e
1474 2 476 2 S60927 hypothetical prote

1475 7 1.9 476 2 H87352 hypothetical prote
1476 7 2.0 477 2 J38409 adenylyl cyclase-a
1477 7 2.0 477 2 J34386 adenylyl cyclase-a
1478 7 1.9 477 2 T45722 hypothetical prote
1479 7 2.0 478 2 J4940 synapsin I1b - hum
1480 7 1.9 478 2 J26558 hypothetical prote
1481 7 1.9 479 1 A31753 transcription fact
1482 7 1.9 479 1 S22542 transcription fact
1483 7 1.9 479 2 S75693 hypothetical prote
1484 7 1.9 479 2 H70847 probable oxidoredu
1485 7 1.9 480 2 A83487 probable MFS trans
1486 7 1.9 481 2 A35628 lorixin - mouse
1487 7 1.9 481 2 A25483 bindin precursor -
1488 7 2.0 482 2 J97583 basic helix-loop-h
1489 7 2.0 482 2 E97748 virB10 protein [im
1490 7 1.9 482 2 T48337 hypothetical prote
1491 7 1.9 483 1 TVRTKA protein kinase (EC
1492 7 2.0 483 2 D87752 protein C18E3.6 li
1493 7 2.0 483 2 T15180 hypothetical prote
1494 7 2.0 483 2 F71684 virB10 protein (vi
1495 7 2.0 483 2 T25992 hypothetical prote
1496 7 1.9 484 2 A40988 54K arginine-rich
1497 7 1.9 485 1 S22543 transcription fact
1498 7 2.0 485 2 A33647 sulfated surface g
1499 7 2.0 485 2 T27147 hypothetical prote
1500 7 2.0 485 2 PC4427 Nck, Ash and phosp

ALIGNMENTS

RESULT 1

DBHU

Complement factor D (EC 3.4.21.46) precursor [validated] - human (fragment)

N:Alternate names: adipsin; C3 convertase activator

C:Species: Homo sapiens (man)

C>Date: 28-Aug-1985 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004

C:Accession: A40197; A60936; A60571; S86645

R:White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, J.S.;

J. Biol. Chem. 267, 9210-9213, 1992

A:Title: Human adipsin is identical to complement factor D and is expressed at high level

A:Reference number: A40197; MUID:92250520; PMID:1374388

A:Accession: A40197

A:Molecule type: mRNA

A:Residues: 1-246 <WHI>

R:Niemann, M.A.; Brown, A.S.; Bennett, J.C.; Volanakis, J.E.

Biochemistry 23, 2482-2486, 1984

A:Title: Amino acid sequence of human D of the alternative complement pathway.

A:Reference number: A00936; MUID:85000441; PMID:6383466

A:Accession: A00936

A:Molecule type: protein

A:Residues: 19-44,'G',46-51,'Q',53-75,'TH',78,'P',80-83,'XXXITTE',90-172,86-91,185-235,'J

A:Note: a few residues were assigned from the previously published sequence of Reid et al

R:Miyata, T.; Oda, O.; Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.; Yan

Mol. Immunol. 27, 637-644, 1990

A:Title: Molecular and functional identification and purification of complement component

A:Reference number: A60571; MUID:90370044; PMID:2395435

A:Accession: A60571

A:Molecule type: protein

A:Residues: 19-20,'XX',23-27,'XX',30-31,'XX',34,'X',36-40 <MIY>

R:Balk, N.; Holtkamp, U.; Hoerl, W.H.; Tschesche, H.

FEBS Lett. 371, 300-302, 1995

A:Title: Inhibition of degranulation of human polymorphonuclear leukocytes by complement

A:Reference number: S66645; MUID:96013156; PMID:7556615

A:Accession: S66645

A>Status: preliminary

A:Molecule type: protein

A:Residues: 19-44,'C',46-48 <BAL>

C:Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, activ

C:Genetics:

A:Gene: GDB:DF

A:Cross-references: GDB:132645; OMIM:134350

A:Map position: Xpter-Xqter

C:Superfamily: trypsin; trypsin homology
C:Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-246/Product: complement factor D (fragment) #status experimental <MAT>
F:19-241/Domain: trypsin homology <TRY>
F:44-60,141-207,172-188,197-222/Disulfide bonds: #status predicted
F:59,105,201/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.: 0.00139 Length: 246
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 1 Gaps: 0

US-10-015-385A-193 (1-1091) x DKHU (1-246)

QY 712 GGTGATCTGGGGCCCTGGTGTTGGGGAGTCTT 750
|||||
Db 199 GlyAppSerGlyGlyProLeuValCysGlyGlyValLeu 211
|||||

RESULT 2
JS0600
t-plasminogen activator (EC 3.4.21.68) gamma precursor - common vampire bat
N/Alternate names: tissue plasminogen activator
C:Species: Desmodus rotundus (common vampire bat)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JS0600
R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don
Gene 105, 229-237, 1991
A:Title: The plasminogen activator family from the salivary gland of the vampire bat Des
A:Reference number: JS0597; MUID:92039036; PMID:1937019
A:Accession: JS0600
A:Molecule type: mRNA
A:Residues: 1-394 <KRA>
A:Cross-references: UNIPROT:P49150; GB:M63990; NID:gl66078; PIDN:AAA31595.1; PID:gl66079
A:Note: the authors translated the codon ATC for residue 75 as Thr
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-36/Domain: propeptide #status predicted <PRO>
F:37-394/Product: plasminogen activator gamma #status predicted <PLA>
F:45-126/Domain: kringle homology <KRK>
F:143-388/Domain: trypsin homology <TRY>
F:45-126,66-108,97-121,131-262,174-190,182-251,276-351,308-324,341-369/Disulfide bonds:
F:142-143/Cleavage site: His-Ser (plasmin) #status predicted
F:189,238,345/Active site: His, Asp, Ser #status predicted
F:315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.: 0.00125 Length: 394
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x JS0600 (1-394)

QY 700 GATGCTCCAGGTGATTCGGGGCCCTGGTGTT 738
|||||
Db 339 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 351
|||||

RESULT 3
JS0599
t-plasminogen activator (EC 3.4.21.68) beta precursor - common vampire bat
N/Alternate names: tissue plasminogen activator
C:Species: Desmodus rotundus (common vampire bat)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JS0599
R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don
Gene 105, 229-237, 1991

A:Title: The plasminogen activator family from the salivary gland of the vampire bat Des
A:Reference number: JS0597; MUID:92039036; PMID:1937019
A:Accession: JS0599
A:Molecule type: mRNA
A:Residues: 1-431 <KRA>
A:Cross-references: UNIPROT:P98121; GB:M63989; NID:gl66076; PIDN:AAA31594.1; PID:gl66077
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-36/Domain: propeptide #status predicted <PRO>
F:37-431/Product: plasminogen activator beta #status predicted <PLA>
F:41-74/Domain: kringle homology <KRG>
F:82-163/Domain: trypsin homology <TRY>
F:180-425/Domain: trypsin homology <TRY>
F:41-52,46-63,65-74,82-163,103-145,134-158,168-299,211-227,219-288,313-388/Disulfide bonds:
F:139,352/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:179-180/Cleavage site: His-Ser (plasmin) #status predicted
F:226,275,382/Active site: His, Asp, Ser #status predicted
F:345-361,378-406/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 0.00122 Length: 431
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x JS0599 (1-431)

QY 700 GATGCTCCAGGTGATTCGGGGCCCTGGTGTT 738
|||||
Db 376 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 388
|||||

RESULT 4
A34369
t-plasminogen activator (EC 3.4.21.68) precursor - false vampire bat (Megaderma lyra)
C:Species: Megaderma lyra
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A34369
R:Gardelli, S.J.; Duong, L.T.; Diehl, R.E.; York, J.D.; Hare, T.R.; Register, R.B.; Jacob
J. Biol. Chem. 264, 17947-17952, 1989
A:Title: Isolation, characterization, and cDNA cloning of a vampire bat salivary plasmin
A:Reference number: A34369; MUID:90036867; PMID:2509450
A:Accession: A34369
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-477 <GAR>
A:Cross-references: UNIPROT:P15638; GB:J05082; NID:gl66080; PIDN:AAA31596.1; PID:gl66081
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-36/Domain: propeptide #status predicted <PRO>
F:37-477/Product: plasminogen activator #status predicted <PLA>
F:42-79/Domain: fibronectin type I repeat homology <1FA>
F:87-120/Domain: EGF homology <EGF>
F:128-209/Domain: kringle homology <KRG>
F:226-471/Domain: trypsin homology <TRY>
F:42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4
F:272,321,428/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.: 0.0012 Length: 477
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 1 Gaps: 0

US-10-015-385A-193 (1-1091) x A34369 (1-477)

QY 700 GATGCTCCAGGTGATTCGGGGCCCTGGTGTT 738
|||||

Db 422 AspAlaCySGlnGlyAspSerGlyGlyProLeuValCys 434

RESULT 5

JS0597
t-plasminogen activator (EC 3.4.21.68) alpha-1 precursor - common vampire bat
N/Alternate names: tissue plasminogen activator
C/Species: Desmodus rotundus (common vampire bat)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: JS0597
R/Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don
Gene 105, 229-237, 1991
A/Title: The plasminogen activator family from the salivary gland of the vampire bat Des
A/Reference number: JS0597; MUID:92039036; PMID:1937019
A/Accession: JS0597
A/Molecule type: mRNA
A/Residues: 1-477 <KRA>
A/Cross-references: UNIPROT:P98119; GB:M63987; NID:G166070; PIDN:AAA31593.1; PID:G166071
C/Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C/Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F/1-21/Domain: signal sequence #status predicted <SIG>
F/22-36/Domain: propeptide #status predicted <PRO>
F/37-477/Product: plasminogen activator alpha-1 #status predicted <PLA>
F/42-79/Domain: fibronectin type I repeat homology <IFA>
F/87-120/Domain: EGF homology <EGF>
F/128-209/Domain: kringle homology <KRG>
F/226-471/Domain: trypsin homology <TRY>
F/42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4
F/153,398/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/225-226/Cleavage site: His-Ser (plasma) #status predicted
F/272,321,428/Active site: His, Asp, Ser #status predicted

Alignment Scores:

Pred. No.:	0.0012	Length:	477
Score:	13.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.64%	Indels:	0
DB:	2	Gaps:	0

US-10-015-385A-193 (1-1091) x JS0597 (1-477)

QY 700 GATGCTGCACGGTGATTCCTGGGGCCCCCTGGTGTTGT 738

Db 422 AspAlaCySGlnGlyAspSerGlyGlyProLeuValCys 434

RESULT 6

JS0598
t-plasminogen activator (EC 3.4.21.68) alpha-2 precursor - common vampire bat
N/Alternate names: tissue plasminogen activator
C/Species: Desmodus rotundus (common vampire bat)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: JS0598
R/Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don
Gene 105, 229-237, 1991
A/Title: The plasminogen activator family from the salivary gland of the vampire bat Des
A/Reference number: JS0597; MUID:92039036; PMID:1937019
A/Accession: JS0598
A/Molecule type: mRNA
A/Residues: 1-477 <KRA>
A/Cross-references: UNIPROT:P15638; GB:M63988; NID:G166074; PIDN:AAA31593.1; PID:G166075
C/Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C/Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F/1-21/Domain: signal sequence #status predicted <SIG>
F/22-36/Domain: propeptide #status predicted <PRO>
F/37-477/Product: plasminogen activator alpha-2 #status predicted <PLA>
F/42-79/Domain: fibronectin type I repeat homology <IFA>
F/87-120/Domain: EGF homology <EGF>
F/128-209/Domain: kringle homology <KRG>
F/226-471/Domain: trypsin homology <TRY>
F/42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4
F/185,398/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/225-226/Cleavage site: His-Ser (plasma) #status predicted
F/272,321,428/Active site: His, Asp, Ser #status predicted

Alignment Scores:

Pred. No.:	0.0012	Length:	477
Score:	13.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.64%	Indels:	0
DB:	2	Gaps:	0

US-10-015-385A-193 (1-1091) x JS0598 (1-477)

QY 700 GATGCTGCACGGTGATTCCTGGGGCCCCCTGGTGTTGT 738

Db 422 AspAlaCySGlnGlyAspSerGlyGlyProLeuValCys 434

RESULT 7

AZ9941
t-plasminogen activator (EC 3.4.21.68) precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: AZ9941; S48205; S48207; S48206
R/Rickles, R.J.; Darrow, A.L.; Strickland, S.
J. Biol. Chem. 263, 1563-1569, 1988
A/Title: Molecular cloning of complementary DNA to mouse tissue plasminogen activator mRN
A/Reference number: AZ9941; MUID:88087303; PMID:2826484
A/Accession: AZ9941
A/Molecule type: mRNA
A/Residues: 1-559 <RIC>
A/Cross-references: UNIPROT:P11214; GB:J03520; NID:G202109; PIDN:AAA40470.1; PID:G202110
R/Rijnhen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 863-871, 1994
A/Title: Characterization of the murine plasma fibrinolytic system.
A/Reference number: S48202; MUID:95010076; PMID:7523120

A/Accession: S48205

A/Molecule type: protein

A/Residues: 33-37, X', 39-40 <LIJ>

A/Accession: S48207

A/Molecule type: protein

A/Residues: 309-316 <LI2>

A/Accession: S48206

A/Molecule type: protein

A/Residues: 33-37, X', 39-40 <LIW>

C/Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom

C/Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase

F/1-17/Domain: signal sequence #status predicted <SIG>

F/18-29/Domain: propeptide #status predicted <PRO>

F/30-559/Product: t-plasminogen activator #status predicted <MAT>

F/30-308/Product: t-plasminogen activator chain A #status predicted <ACH>

F/38-75/Domain: fibronectin type I repeat homology <IF1>

F/83-116/Domain: EGF homology <EGF>

F/124-205/Domain: kringle homology <KR1>

F/213-294/Domain: kringle homology <KR2>

F/309-559/Product: t-plasminogen activator chain B #status predicted <BCH>

F/309-553/Domain: trypsin homology <TRY>

F/38-68,66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265-289,297-4

F/149,481/Binding site: carbohydrate (Asn) (covalent) #status predicted

F/308-309/Cleavage site: Arg-Ile (plasma, trypsin) #status predicted

F/355,404,510/Active site: His, Asp, Ser #status predicted

Alignment Scores:

Pred. No.:	0.00115	Length:	559
Score:	13.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.64%	Indels:	0
DB:	1	Gaps:	0

US-10-015-385A-193 (1-1091) x AZ9941 (1-559)

QY 700 GATGCTGCACGGTGATTCCTGGGGCCCCCTGGTGTTGT 738

Db 504 AspAlaCySGlnGlyAspSerGlyGlyProLeuValCys 516

RESULT 8

A35029
t-plasminogen activator (BC 3.4.21.68) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A35029; A31597
R:Feng, P.; Ohlsson, M.; Ny, T.
J. Biol. Chem. 265, 2022-2027, 1990
A:Title: The structure of the TATA-less rat tissue-type plasminogen activator gene. Spec
A:Reference number: A35029; MUID:90130448; PMID:2105315
A:Accession: A35029
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-559 <FEN>
A:Cross-references: UNIPROT:P19637; GB:M31197; NID:G207429; PIDN:AAA42261.1; PID:G207431
R:Ny, T.; Leonardsson, G.; Hsueh, A.J.W.
DNA 7, 671-677, 1988
A:Title: Cloning and characterization of a cDNA for rat tissue-type plasminogen activator
A:Reference number: A31597; MUID:89170114; PMID:3148445
A:Accession: A31597
A:Molecule type: mRNA
A:Residues: 1-379, 'K', 381-559 <NVT>
A:Cross-references: GB:M23697; NID:G530159; PIDN:AAA41812.1; PID:G530160
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-29/Domain: propeptide #status predicted <PRO>
F:30-559/Product: t-plasminogen activator #status predicted <WAT>
F:30-308/Product: t-plasminogen activator chain A #status predicted <ACH>
F:38-75/Domain: fibronectin type I repeat homology <IF1>
F:83-116/Domain: EGF homology <EGF>
F:124-205/Domain: kringle homology <KR1>
F:213-294/Domain: kringle homology <KR2>
F:309-559/Product: t-plasminogen activator chain B #status predicted <BCH>
F:309-553/Domain: trypsin homology <TRY>
F:38-68, 66-75, 83-94, 88-105, 107-116, 124-205, 145-187, 176-200, 213-294, 234-276, 265-289, 297-4
F:149, 481/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:308-309/Cleavage site: Arg-Ile (plasmin, trypsin) #status predicted
F:355, 404, 510/Active site: His, Asp, Ser #status predicted

Alignment Scores:

Pred. No.:	Length:	Score:
0.00115	559	13.00
Percent Similarity:	Matches:	13
100.00%	Conservative:	0
Best Local Similarity:	Mismatches:	0
100.00%	Indels:	0
Query Match:	Gaps:	0
3.64%		
1		
DB:		

US-10-015-385A-193 (1-1091) x A35029 (1-559)

QY 700 GATGCTGCACGGTGATTCGGGGCCGCCCTGGTGTTGT 738
|||||
DB 504 AspAlaCyGlnGlyAspSerGlyGlyProLeuValCys 516
|||||

RESULT 9

UKHUT
t-plasminogen activator (BC 3.4.21.68) precursor [validated] - human
N:Alternate names: t-PA; tissue plasminogen activator
C:Species: Homo sapiens (man)
C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
C:Accession: A94004; A23529; J70562; A93293; S02125; A91343; A93951; A91322; A54645; 160
R:Ny, T.; Elgh, F.; Lund, B.
Proc. Natl. Acad. Sci. U.S.A. 81, 5355-5359, 1984
A:Title: The structure of the human tissue-type plasminogen activator gene: correlation
A:Reference number: A94004; MUID:84298137; PMID:6089198
A:Accession: A94004
A:Molecule type: DNA
A:Residues: 1-562 <NYT>
A:Cross-references: UNIPROT:P00750; GB:L00141
A:Note: the codon given for residue 93 (ACC) is inconsistent with the authors' translati
R:Friessner Degen, S.J.; Rajput, B.; Reich, E.
J. Biol. Chem. 261, 6972-6985, 1986
A:Title: The human tissue plasminogen activator gene.

A:Reference number: A23529; MUID:86196143; PMID:3009482
A:Accession: A23529
A:Molecule type: DNA
A:Residues: 1-562 <DEG>
A:Cross-references: GB:K03021; NID:G339817; PIDN:AAA98809.1; PID:G339818
R:Itagaki, Y.; Yasuda, H.; Morinaga, T.; Mitsuoka, S.; Higashio, K.
Agric. Biol. Chem. 55, 1225-1232, 1991
A:Title: Purification and characterization of tissue plasminogen activator secreted by h
A:Reference number: J70562; MUID:91291340; PMID:1368681
A:Accession: J70562
A:Molecule type: mRNA
A:Residues: 31-562 <ITA>
A:Cross-references: DDBJ:D01096; NID:G220128; PIDN:BAA00881.1; PID:G441174
A:Experimental source: embryonic lung fibroblast IMR-90 cells
A:Note: part of this sequence, including the amino end of the mature protein, was confir
R:Pennica, D.; Holmes, W.E.; Kohr, W.J.; Harkins, R.N.; Vohar, G.A.; Ward, C.A.; Bennett,
Nature 301, 214-221, 1983
A:Title: Cloning and expression of human tissue-type plasminogen activator cDNA in Escher
A:Reference number: A93293; MUID:83115262; PMID:6337343
A:Accession: A93293
A:Molecule type: mRNA
A:Residues: 1-562 <PEN>
A:Cross-references: GB:L00141
A:Experimental source: melanoma cells
R:Sasaki, H.; Saito, Y.; Hayashi, M.; Otsuka, K.; Niwa, M.
Nucleic Acids Res. 16, 5695, 1988
A:Title: Nucleotide sequence of the tissue-type plasminogen activator cDNA from human fet
A:Reference number: S02125; MUID:88262579; PMID:3133640
A:Accession: S02125
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-562 <SAS>
A:Cross-references: EMBL:X07393; NID:G37243; PIDN:CAA30302.1; PID:G37244
A:Experimental source: fetal lung cells
R:Kagitani, H.; Tagawa, M.; Hatanaka, K.; Ikari, T.; Saito, A.; Bando, H.; Okada, K.; Mat
FEBS Lett. 189, 145-149, 1985
A:Title: Expression in Escherichia coli of finger-domain lacking tissue-type plasminogen
A:Reference number: A91343; MUID:85285620; PMID:3896853
A:Accession: A91343
A:Molecule type: mRNA
A:Residues: 1-38, 'G', 86-433, 'E', 435-562 <KAG>
A:Experimental source: Detroit 562 cells; ATCC 138
R:Edlund, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, E.; Josephson, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 349-352, 1983
A:Title: Isolation of cDNA sequences coding for a part of human tissue plasminogen activa
A:Reference number: A93951; MUID:83169656; PMID:6572897
A:Accession: A93951
A:Molecule type: mRNA
A:Residues: 251-358 <BDL>
A:Experimental source: melanoma cells
R:Pohl, G.; Kallstrom, M.; Bergsdorf, N.; Wallen, P.; Jornvall, H.
Biochemistry 23, 3701-3707, 1984
A:Title: Tissue plasminogen activator: peptide analyses confirm an indirectly derived am
differences.
A:Reference number: A90488; MUID:85000468; PMID:6433976
A:Contents: annotation; melanoma cells, partial sequence of residues 36-562, active and i
R:Pohl, G.; Kaplan, L.; Einarsson, M.; Wallen, P.; Jornvall, H.
FEBS Lett. 168, 29-32, 1984
A:Title: Differences between uterine and melanoma forms of tissue plasminogen activator.
A:Reference number: A91322; MUID:84158956; PMID:6538514
A:Accession: A91322
A:Molecule type: protein
A:Residues: 33-45; 311-320 <POH>
A:Experimental source: uterus
A:Note: in the uterus, cleavage of the activation peptide may also occur after 38-Gln
R:van Zonneveld, A.J.; Veerman, H.; Pannekoek, H.
J. Biol. Chem. 261, 14214-14218, 1986
A:Reference number: A37567; MUID:87033611; PMID:3021732
R:Verheijen, J.H.; Caspers, M.P.M.; Chang, G.T.G.; de Munk, G.A.W.; Pouwels, P.H.; Enger-
EMBO J. 5, 3525-3530, 1986
A:Title: Involvement of finger domain and kringle 2 domain of tissue-type plasminogen act
A:Reference number: A37568; MUID:87161761; PMID:3030730

A:Contents: annotation; fibrin binding site
R:Dodd, I.; Nunn, B.; Robinson, J.H.
Thromb. Haemost. 59, 523-528, 1988
A:Title: Isolation, identification and pharmacokinetic properties of human tissue-type plasminogen activator; PMID:3142086
A:Reference number: A60902; MUID:89044681; PMID:3142086
A:Contents: annotation; novel forms of expressed recombinant t-PA
R:Haris, T.J.R.; Patel, T.; Marston, F.A.O.; Little, S.; Emtage, J.S.; Opdenakker, G.; Mol. Biol. Med. 3, 279-292, 1986
A:Title: Cloning of cDNA coding for human tissue-type plasminogen activator and its expression; PMID:3090401
A:Reference number: A54645; MUID:86284200; PMID:3090401
A:Accession: A54645
A:Molecule type: mRNA
A:Residues: 1-562 <HAR>
A:CROSS-references: GB:M15518; NID:G190031; PIDN:AAA60111.1; PID:G190032
A:Note: parts of this sequence were confirmed by peptide sequencing
R:Reddy, V.B.; Garramone, A.J.; Sasak, H.; Wei, C.
DNA 6, 461-472, 1987
A:Title: Expression of human uterine tissue-type plasminogen activator in mouse cells using a cDNA expression vector; PMID:2824147
A:Reference number: I60110; MUID:188054470; PMID:2824147
A:Accession: I60110
A:Molecule type: mRNA
A:Status: translated from GB/EMBL/DBJ
A:Residues: 1-562 <RES>
A:CROSS-references: GB:M18182; NID:G340176; PIDN:AAA36800.1; PID:G340177
R:Fisher, R.; Waller, E.K.; Grossi, G.; Thompson, D.; Tizard, R.; Schleuning, W.D.
J. Biol. Chem. 260, 11223-11230, 1985
A:Title: Isolation and characterization of the human tissue-type plasminogen activator cDNA; PMID:3161893
A:Reference number: I55232; MUID:85289338; PMID:3161893
A:Accession: I55232
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-36 <RE2>
A:CROSS-references: GB:M11890; NID:G339837; PIDN:AAA61213.1; PID:G339839
A:Comment: Cleavage by plasmin or trypsin produces two chains held together by a single disulfide bond.
C:Comment: t-PA converts plasminogen to plasmin by hydrolyzing a single Arg-Val bond. It is a single chain protein.
C:Comment: t-PA binds chain A of fibrin by kringle 2 and the fibronectin type I repeat.
C:Genetics:
A:Gene: GDB:PLAT
A:CROSS-references: GDB:119496; OMIM:173370
A:Map position: 8p12-8p12
A:Introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3; 510/1
A:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat homology
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-32/Domain: propeptide #status predicted <PRO>
F:33-562/Product: t-plasminogen activator #status experimental <MAT>
F:33-310/Product: t-plasminogen activator chain A #status experimental <ACH>
F:41-78/Domain: fibronectin type I repeat homology <FI1>
F:86-119/Domain: EGF homology <EGF>
F:127-208/Domain: kringle homology <KR1>
F:215-296/Domain: kringle homology <KR2>
F:311-562/Product: t-plasminogen activator chain B #status experimental <BCH>
F:311-556/Domain: trypsin homology <TRY>
F:41-71, 69-78, 86-97, 91-108, 119-127, 208, 148-190, 179-203, 215-296, 236-278, 267-291, 299-421, 483/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:152,483/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:219/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:310-311/Cleavage site: Arg-Ile (plasmin, trypsin) #status experimental
F:357,406/Active site: His, Asp #status predicted
F:513/Active site: Ser #status experimental

Alignment Scores:
Pred. No.: Length: 562
Score: 0.00115 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 1 Gaps: 0

US-10-015-385A-193 (1-1091) x UKHUT (1-562)

QY 700 GATGCTGCAGGTGATTCGGGGCCCCCTGGTGTGT 738
|||||
DB 507 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 519
|||||

RESULT 10

S45281
coagulation factor XIIa (EC 3.4.21.38) precursor - bovine (fragment)
N:Alternate names: Hageman factor (activated)
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Apr-1995 #sequence_revision 22-Apr-1995 #text_change 09-Jul-2004
C:Accession: S45281; A61329
R:Shibuya, Y.; Samba, U.; Okabe, H.; Kambara, T.; Yamamoto, T.
Biochim. Biophys. Acta 1206, 63-70, 1994
A:Title: Primary structure of bovine Hageman factor (blood coagulation factor XII): comparison with human factor XII; PMID:81866251
A:Reference number: S45281; MUID:94242782; PMID:81866251
A:Accession: S45281
A:Molecule type: mRNA
A:Residues: 1-593 <SHI>
A:CROSS-references: UNIPROT:P98140; GB:S70164
A:Note: the authors translated the codon GAG for residue 23 as Val, GAG for residue 70 as Pro, CTC for residue 203 as Phe, GTG for residue 247 as Leu, CCG for residue 286 as Glu, and ATC for residue 505 as Leu
R:Fujikawa, K.; Walsh, K.A.; Davie, E.W.
Biochemistry 16, 2270-2278, 1977
A:Title: Isolation and characterization of bovine factor XII (Hageman factor).
A:Reference number: A61329; MUID:77182112; PMID:861210
A:Accession: A61329
A:Molecule type: protein
A:Residues: 10-16, 'X', 18-19; 525-550 <FUJ>
C:Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
C:Keywords: blood coagulation; fibrinolysis; glycoprotein; hydrolase; monomer; plasma; serine proteinase
F:37-78/Domain: fibronectin type II repeat homology <1F2>
F:88-120/Domain: EGF homology <EGF>
F:125-160/Domain: fibronectin type I repeat homology <FB1>
F:207-287/Domain: kringle homology <KRG>
F:350-587/Domain: trypsin homology <TRY>
F:541/Active site: Ser #status predicted

Alignment Scores:
Pred. No.: Length: 593
Score: 0.00114 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x S45281 (1-593)

QY 700 GATGCTGCAGGTGATTCGGGGCCCCCTGGTGTGT 738
|||||

DB 535 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 547
|||||

RESULT 11

S28941
coagulation factor XIIa (EC 3.4.21.38) - guinea pig (fragment)
N:Alternate names: Hageman factor
C:Species: Cavia porcellus (guinea pig)
C:Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: S28941
R:Samba, U.; Yamamoto, T.; Kunitada, T.; Shibuya, Y.; Tanase, S.; Kambara, T.; Okabe, H.
Biochim. Biophys. Acta 1159, 113-121, 1992
A:Title: Primary structure of guinea-pig Hageman factor: sequence around the cleavage site
A:Reference number: S28941; MUID:93003367; PMID:1390917
A:Accession: S28941
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-603 <SEM>
A:CROSS-references: UNIPROT:Q04962; EMBL:X68615; NID:G49578; PIDN:CAA48600.1; PID:G49578
C:Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
C:Keywords: hydrolase; serine proteinase
F:46-87/Domain: fibronectin type II repeat homology <1F2>
F:134-169/Domain: fibronectin type I repeat homology <FB1>
F:177-208/Domain: EGF homology <EGF>
F:216-294/Domain: kringle homology <KRG>
F:359-597/Domain: trypsin homology <TRY>

Alignment Scores:
Pred. No.: Length: 562
Score: 0.00115 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 1 Gaps: 0

US-10-015-385A-193 (1-1091) x UKHUT (1-562)

QY 700 GATGCTGCAGGTGATTCGGGGCCCCCTGGTGTGT 738
|||||

DB 507 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 519
|||||

Alignment Scores:

Pred. No.: 0.00113 Length: 603
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x S28941 (1-603)

QY 700 GATGCTCCAGGCTGATTCGGGGCCCTCGGTGTGT 738
|||||
Db 545 AspAlaCysGlnGlyAspSerGlyProLeuValCys 557
|||||

RESULT 12

KFHU12

coagulation factor XIIa (EC 3.4.21.38) precursor [validated] - human

N/Alternate names: Hageman factor (activated)

C/Species: Homo sapiens (man)

C/Date: 27-Nov-1985 #sequence revision 30-Jun-1991 #text change 09-Jul-2004

C/Accession: A26814; A00930; A25191; A22248; A21037

R/Cool, D.E.; MacGillivray, R.T.A.

J. Biol. Chem. 262, 13662-13673, 1987

A/Title: Characterization of the human blood coagulation factor XII gene. Intron/exon ge

A/Reference number: A29411; MUID:88007593; PMID:2888762

A/Accession: A29411

A/Molecule type: DNA

A/Residues: 1-615 <COO>

A/Cross-references: UNIPROT:P00748; GB:M17466; GB:J02807; NID:g180355; PIDN:AA859490.1;

R/Tripodi, M.; Citarella, F.; Guida, S.; Galeffi, P.; Fantoni, A.; Cortese, R.

Nucleic Acids Res. 14, 3146, 1986

A/Title: cDNA sequence coding for human coagulation factor XII (Hageman).

A/Reference number: A26814; MUID:86176794; PMID:3754331

A/Accession: A26814

A/Molecule type: mRNA

A/Residues: 4-615 <TRI>

A/Cross-references: GB:M31315; NID:g182291; PIDN:AAA70225.1; PID:g182292

R/Cool, D.E.; Edgell, C.J.S.; Louie, G.V.; Zoller, M.J.; Brayer, G.D.; MacGillivray, R.T.

J. Biol. Chem. 260, 13666-13676, 1985

A/Title: Characterization of human blood coagulation factor XII cDNA. Prediction of the

A/Reference number: A00930; MUID:86033830; PMID:3877053

A/Accession: A00930

A/Molecule type: mRNA

A/Residues: 14-332, 'S', 334-615 <CO2>

A/Cross-references: GB:M11723; NID:g180358; PIDN:AAA51986.1; PID:g180359

R/Que, B.G.; Davie, E.W.

Biochemistry 25, 1525-1528, 1986

A/Title: Characterization of a cDNA coding for human factor XII (Hageman factor).

A/Reference number: A25191; MUID:86216049; PMID:3011063

A/Accession: A25191

A/Molecule type: mRNA

A/Residues: 146-378, 'G', 380-615 <QUE>

A/Cross-references: GB:M13147; NID:g180360; PIDN:AAA70224.1; PID:g180361

R/McMullen, B.A.; Fujikawa, K.

J. Biol. Chem. 260, 5328-5341, 1985

A/Title: Amino acid sequence of the heavy chain of human alpha-factor XIIa (activated Ha

A/Reference number: A22248; MUID:85182674; PMID:3886654

A/Accession: A22248

A/Molecule type: protein

A/Residues: 20-379 <MCW>

R/Fujikawa, K.; McMullen, B.A.

J. Biol. Chem. 258, 10924-10933, 1983

A/Title: Amino acid sequence of human beta-factor XIIa.

A/Reference number: A21037; MUID:83291041; PMID:6604055

A/Accession: A21037

A/Molecule type: protein

A/Residues: 354-362/373-615 <FUJ>

R/Harris, R.J.; Ling, V.T.; Spellman, M.W.

J. Biol. Chem. 267, 5102-5107, 1992

A/Title: O-linked fucose is present in the first epidermal growth factor domain of facto

A/Reference number: A44606; MUID:92184750; PMID:1544894

A/Contents: annotation; carbohydrate binding site

C/Genetics:

A/Gene: GDB:F12

A/Cross-references: GDB:119892; OMIM:234000

A/Map position: 5q34-5qter

A/Introns: 19/3; 39/1; 72/2; 96/1; 133/1; 177/1; 212/1; 267/2; 340/1; 417/2; 463/1; 511/1

C/Complex: factor XII, prekallikrein, and HMW kininogen form a complex bound to anionic f

C/Function:

A/Description: factor XIIa catalyzes the proteolytic activation of plasminogen, plasma pr

ikrein

A/Pathway: blood coagulation; fibrinolysis

C/Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;

C/Keywords: blood coagulation; fibrinolysis; glycoprotein; hydrolase; kringle; plasma; s

F1-19/Domain: signal sequence #status predicted <SIG>

F120-372,373-615/Product: coagulation factor XIIa, alpha form #status experimental <A12>

F147-88/Domain: fibronectin type II repeat homology <FB2>

F198-130/Domain: EGF homology <EG1>

F1135-170/Domain: fibronectin type I repeat homology <IF1>

F178-209/Domain: EGF homology <EG2>

F217-295/Domain: kringle homology <KR>

F298-356/Region: proline-rich

F354-362,373-615/Product: coagulation factor XIIa, beta form #status experimental <B12>

F373-609/Domain: trypsin homology <TRY>

F198-110,104-119,121-130,135-163,161-170,178-189,183-198,200-209,217-295,238-277,266-290,

F109/Binding site: carbohydrate (Thr) (covalent) #status experimental

F1249,305,328,329,337/Binding site: carbohydrate (Asn) (covalent) #status experimental

F1299,305,328,329,337/Binding site: carbohydrate (Thr) (covalent) #status predicted

F1308/Binding site: carbohydrate (Ser) (covalent) #status predicted

F1412,461,563/Active site: His, Asp, Ser #status predicted

Alignment Scores:

Pred. No.: 0.00113 Length: 615
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 1 Gaps: 0

US-10-015-385A-193 (1-1091) x KFHu12 (1-615)

QY 700 GATGCTCCAGGCTGATTCGGGGCCCTCGGTGTGT 738
|||||

Db 557 AspAlaCysGlnGlyAspSerGlyProLeuValCys 569
|||||

RESULT 13

T30337

polyprotein - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C/Accession: T30337

R/fang, J.C.; Lindsey, L.L.; Hedrick, J.L.

submitted to the EMBL Data Library, March 1998

A/Description: cDNA cloning of ovocytinase, a chymotrypsin-like protease released from Xer

A/Reference number: Z20829

A/Accession: T30337

A/Status: preliminary; translated from GB/EMBL/DBBJ

A/Molecule type: mRNA

A/Residues: 1-1524 <YAN>

A/Cross-references: UNIPROT:Q91674; EMBL:U81290; NID:g2981640; PID:g2981641; PIDN:AAAC2471;

C/Superfamily: trypsin related polyprotein; trypsin homology

Alignment Scores:

Pred. No.: 0.000923 Length: 1524
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x T30337 (1-1524)

QY 700 GATGCTCCAGGCTGATTCGGGGCCCTCGGTGTGT 738
|||||

Db 762 AspAlaCysGlnGlyAspSerGlyProLeuValCys 774
|||||

Search completed: March 5, 2005, 23:49:08
Job time : 70 secs

RESULT 14

S54115
complement factor D (EC 3.4.21.46) - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S54115

R:Nicolas, N.

submitted to the EMBL Data Library, April 1995

A:Reference number: S54115

A:Accession: S54115

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-191 <NIC>

A:Cross-references: UNIPROT:P51779; EMBL:Z49058; NID:g773264; PIDN:CAA88844.1; PID:g7732

C:Superfamily: trypsin; trypsin homology

C:Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase

F:1-181/Domain: trypsin homology (fragment) <TRY>

Alignment Scores:

Pred. No.:	0.013	Length:	191
Score:	12.00	Matches:	12
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.36%	Indels:	0
DB:	2	Gaps:	0

US-10-015-385A-193 (1-1091) x S54115 (1-191)

QY 712 GGTGATTCGGGGCCCCCTGTGTGGGGAGTC 747

DB 139 GlyAspSerGlyGlyProLeuValCysGlyGlyVal 150

RESULT 15

S65465

trypsin-like proteinase (EC 3.4.21.-) precursor - flesh fly (Sarcophaga bullata)

C:Species: Sarcophaga bullata

C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S65465; S65403

R:Botovskiy, D.; Janssen, I.; Vanden Broeck, J.; Huybrechts, R.; Verhaert, P.; de Bondt,

Eur. J. Biochem. 237, 279-287, 1996

A:Title: Molecular sequencing and modeling of Neobellieria bullata trypsin. Evidence for

A:Reference number: S65403; MUID:96203936; PMID:8620885

A:Accession: S65465

A:Molecule type: mRNA

A:Residues: 1-254 <BOR>

A:Cross-references: UNIPROT:P51588; EMBL:X94691; NID:g1177315; PIDN:CAA64354.1; PID:g117

A:Accession: S65403

A:Molecule type: protein

A:Residues: 27-36 <BOW>

A>Note: 27-Leu, 35-Leu were also found

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; serine proteinase

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-26/Domain: propeptide #status predicted <PRO>

F:27-254/Product: trypsin #status experimental <MAT>

F:27-247/Domain: trypsin homology <TRY>

F:53-69,154-158,195-238,204-228/Disulfide bonds: #status predicted

F:68,113,208/Active site: His, Asp, Ser #status predicted

Alignment Scores:

Pred. No.:	0.0122	Length:	254
Score:	12.00	Matches:	12
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.36%	Indels:	0
DB:	2	Gaps:	0

US-10-015-385A-193 (1-1091) x S65465 (1-254)

QY 700 GATGCTGCAGGGTATTCGGGGCCCCCTGGTG 735

DB 202 AspAlaCysGlnGlyAspSerGlyGlyProLeuVal 213

cl404	8	2.2	205	2	Q75QN9	Q75qn9 triticum ae
cl405	8	2.2	205	2	Q7XC68	Q7xc68 oryza sativ
1406	8	2.2	205	2	Q7XSA7	Q7xsa7 oryza sativ
1407	8	2.2	206	2	Q961W8	Q961w8 drosophila
cl408	8	2.2	207	1	EGG2 SCHJA	P19469 schistosoma
1409	8	2.2	207	1	SCX MOUSE	Q64124 mus musculus
cl410	8	2.2	207	2	Q03797	Q03797 schistosoma
cl411	8	2.2	207	2	Q8S765	Q8s765 oryza sativ
cl412	8	2.2	207	2	Q6YW94	Q6yw94 oryza sativ
cl413	8	2.2	207	2	Q92220	Q92220 rhizobium m
1414	8	2.2	207	2	Q6P6L3	Q6p6l3 mus musculus
1415	8	2.2	208	2	Q9H718	Q9h718 homo sapien
cl416	8	2.2	208	2	Q6F3C6	Q6f3c6 oryza sativ
1417	8	2.2	208	2	Q6Z1Y5	Q6z1y5 oryza sativ
1418	8	2.2	209	2	Q8N1J9	Q8n1j9 homo sapien
1419	8	2.2	209	2	Q7VVU4	Q7vvu4 bordetella
1420	8	2.2	209	2	Q7W9D4	Q7w9d4 bordetella
1421	8	2.2	209	2	Q7W9C9	Q7whc9 bordetella
1422	8	2.2	210	2	Q9NHB9	Q9nxb9 homo sapien
cl423	8	2.2	211	2	Q6H016	Q6h016 fremyella d
cl424	8	2.2	212	1	EGG1 SCHJA	P19470 schistosoma
cl425	8	2.2	212	2	Q9FSN7	Q9fsn7 oryza sativ
1426	8	2.2	212	2	Q6WJ4	Q6wj4 bdellovibri
cl427	8	2.2	213	2	Q8FNV1	Q8fnv1 corynebacte
cl428	8	2.2	214	1	GRF2 NICSY	P27484 nicotiana s
cl429	8	2.2	214	2	Q49280	Q49280 arabidopsis
1430	8	2.2	214	2	Q73GW8	Q73gw8 wolbachia p
1431	8	2.2	215	2	Q8MPJ2	Q8mpj2 plasmodium
cl432	8	2.2	215	2	Q67UN2	Q67un2 oryza sativ
1433	8	2.2	215	2	Q89UY6	Q89uy6 bradyrhizob
1434	8	2.2	216	1	CTR2_VESOR	P00768 vespa orien
1435	8	2.2	216	1	VSPB_LACMU	P84036 lachesis mu
1436	8	2.2	216	2	Q8MPJ3	Q8mpj3 plasmodium
1437	8	2.2	216	2	Q8MPJ4	Q8mpj4 plasmodium
1438	8	2.2	216	2	Q8MPJ6	Q8mpj6 plasmodium
1439	8	2.2	216	2	Q8MPJ7	Q8mpj7 plasmodium
cl440	8	2.2	216	2	Q8L524	Q8l524 oryza sativ
1441	8	2.2	216	2	Q94DV0	Q94dv0 oryza sativ
cl442	8	2.2	216	2	Q75KH8	Q75kh8 oryza sativ
cl443	8	2.2	216	2	Q7XU81	Q7xu81 oryza sativ
1444	8	2.2	216	2	Q7O6M4	Q7o6m4 pseudomonas
cl445	8	2.2	217	1	NOA1 HUMAN	Q9ny12 homo sapien
1446	8	2.2	218	1	CTR2_VESCR	P00769 vespa crabr
cl447	8	2.2	218	2	Q6ZS46	Q6zs46 homo sapien
1448	8	2.2	218	2	Q8MP17	Q8mp17 plasmodium
cl449	8	2.2	218	2	Q6Z114	Q6z114 oryza sativ
1450	8	2.2	219	2	Q8MPJ8	Q8mpj8 plasmodium
1451	8	2.2	219	2	Q7FJ75	Q7fj75 anopheles g
cl452	8	2.2	219	2	Q75LD8	Q75ld8 oryza sativ
1453	8	2.2	219	2	Q9M3G8	Q9m3g8 arabidopsis
cl454	8	2.2	219	2	Q66A81	Q66a81 yersinia ps
cl455	8	2.2	219	2	Q8ZE52	Q8ze52 yersinia pe
1456	8	2.2	219	2	Q91036	Q91036 gadus morhu
cl457	8	2.2	220	2	Q7FJ13	Q7fj13 anopheles g
1458	8	2.2	220	2	Q8RZV1	Q8rzv1 oryza sativ
1459	8	2.2	220	2	Q43631	Q43631 phaseolus v
1460	8	2.2	220	2	Q75LR6	Q75lr6 oryza sativ
cl461	8	2.2	221	2	Q65514	Q65514 arabidopsis
cl462	8	2.2	222	1	OS28 PLAGA	Q05439 plasmodium
1463	8	2.2	222	2	Q7S1G2	Q7s1g2 solenopsis
1464	8	2.2	222	2	Q8AV11	Q8av11 oncorhynch
cl465	8	2.2	223	2	Q7RY56	Q7ey56 oryza sativ
cl466	8	2.2	224	2	Q8W0N9	Q8w0n9 oryza sativ
cl467	8	2.2	224	2	Q9ZS09	Q9zs09 arabidopsis
cl468	8	2.2	225	2	Q8L7T1	Q8l7t1 arabidopsis
1469	8	2.2	225	2	Q6DL00	Q6dl00 oryza sativ
cl470	8	2.2	225	2	Q75HQ2	Q75hq2 oryza sativ
1471	8	2.2	225	2	Q9LTJ1	Q9ltj1 arabidopsis
cl472	8	2.2	226	2	Q948H7	Q948h7 oryza sativ
cl473	8	2.2	226	2	Q7XEU0	Q7xeu0 oryza sativ
cl474	8	2.2	226	2	Q6AYAI	Q6ayal rattus norv
1475	8	2.2	227	1	TRYP_SACER	P24664 saccharopol
1476	8	2.2	227	2	Q81X14	Q81x14 homo sapien

ALIGNMENTS

RESULT 1

KLKC_HUMAN

ID KLKC_HUMAN STANDARD; PRT; 248 AA.

AC Q9UKR0; Q9UKR1;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein 5)
 DE (KLK-L5) (UNQ669/PRO1303).
 GN Homo sapiens (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 SEQUENCE FROM N.A. (ISOFORM 1).
 RP MEDLINE=20118156; PubMed=10652563;
 RX Yousef G.M., Luo L.-Y., Diamandis E.P.;
 RT "Identification of novel human kallikrein-like genes on chromosome
 RT 19q13.3-q13.4.";
 RL Anticancer Res. 19:2843-2852(1999).
 RN [2]
 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RP Yousef G.M., Magklara A., Scorilas A., Diamandis E.P.;
 RT "Cloning of new alternatively spliced forms of the kallikrein-like
 RT gene 5 (KLK-L5).";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 SEQUENCE FROM N.A. (ISOFORM 1).
 RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
 RA Moss P., Paepker B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene
 RT cluster located in chromosome 19q13 region.";
 RL Gene 257:119-130(2000).
 RN [4]
 SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klinkowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,

Q6xi22 drosophila
 Q84zcl oryza sativ
 Q06556 mycobacteri
 Q7u014 mycobacteri
 Q9xy49 ctenocephal
 P00764 squalus aca
 Q7pkj8 anopheles g
 Q7qtx3 anopheles g
 Q8lpa7 triticum ae
 Q6aun6 oryza sativ
 Q6avv7 oryza sativ
 Q641w0 xenopus lae
 Q9fls1 arabidopsis
 Q6nxd4 rhodococcus
 Q6nlp8 rhodopseudo
 Q9cy66 mus musculu
 P35032 salmo salar
 P00761 sus scrofa
 Q75qn8 triticum ae
 Q8h555 oryza sativ
 P81824 bothriops ja
 P81661 bothriops ja
 Q94508 dermatophag
 Q9xy45 ctenocephal


```
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS02440; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON TER 1
SQ SEQUENCE 234 AA; 25888 MW; 6D81E609EDD39110 CRC64;

Alignment Scores:
Pred. No.: 1,496-20 Length: 234
Score: 31.00 Matches: 31
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.68% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q9CV76 (1-234)

QY 700 GATGCTGCGAGGTGATTCTGGGGCCCTGGTGTGTGGGGAGTCTTCAAGGTCTG 759
Db 180 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCysGlyGlyValLeuGlnGlyLeu 199
QY 760 GTGTCTCTGGGGGTCTGTGGGGCCCTGTGGACAA 792
Db 200 ValSerTyrGlySerValGlyProCysGlyGln 210

RESULT 4
Q7ZT70 PRELIMINARY; PRT; 681 AA.
AC Q7ZT70;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mannose-binding lectin associated serine protease-1.
GN Name=MASP-1;
OS Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lethenteron.
OX NCBI_TaxID=94989;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22593355; PubMed=12707349;
RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Matsusita A., Takahashi M.,
RA Matsushita M., Fujita T.;
RT "Origin of mannose-binding lectin-associated serine protease (MASP)-1
RT and MASP-3 involved in the lectin complement pathway traced back to
RT the invertebrate, amphioxus."
RL J. Immunol. 170:4701-4707(2003).
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AB08265; BAC75884.1; -.
DR HSSP; Q9JJS8; INTO.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006956; P:complement activation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Peptidase_S1.
```

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DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR011361; Pept_S1_Comp_Act.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF07645; EGF_CA; 1.
DR Pfam; PF00084; Sushi; 2.
DR Pfam; PF00089; Trypsin; 1.
DR PIRSF; PIRSF001155; Clk_C1s_MASP; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00034; CCP; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS0923; SUSHI; 2.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Lectin; Protease; Serine protease.
SQ SEQUENCE 681 AA; 75277 MW; 27386FA117C1D437 CRC64;

Alignment Scores:
Pred. No.: 0,000434 Length: 681
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.92% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q7ZT70 (1-681)

QY 694 GGGCAGGATGCTGCCAGGTGATTCTGGGGCCCTGGTG 735
Db 622 GlyGlnAspAlaCysGlnGlyAspSerGlyGlyProLeuVal 635

RESULT 5
Q824U6 PRELIMINARY; PRT; 200 AA.
AC Q824U6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serine protease-like 1.
GN Name=1700036D21Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Matsui H., Takahashi T.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AB047758; BAB63919.1; -.
DR HSSP; P00750; 1RTF.
DR MEROPS; S01.106; -.
DR MGD; MGI:1920586; 1700036D21Rik.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 200 AA; 22135 MW; 972959E4686EF603 CRC64;
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Alignment Scores:
Pred. No.: 0.00463 Length: 200
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q924U6 (1-200)

QY 700 GATGCTGCCAGGCTGATTCGGGGCCCCCTGGTGCTGT 738
Db 128 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 140

RESULT 6

QFIDH Q6FWH3 PRELIMINARY; PRT; 228 AA.
AC Q6FWH3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE DF protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; CR536575; CAG38812.1; -;
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 228 AA; 24423 MW; B1B9EA3B73E802C5 CRC64;

Alignment Scores:
Pred. No.: 0.00457 Length: 228
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q6FWH3 (1-228)

QY 712 GGTGATTCGGGGCCCCCTGGTGTCGGGGAGTCCTT 750
Db 181 GlyAspSerGlyGlyProLeuValCysGlyGlyValLeu 193

RESULT 7

Q8N4E0 Q8N4E0 PRELIMINARY; PRT; 235 AA.
ID Q8N4E0;
AC Q8N4E0;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE DF protein (Fragment).
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smaluk D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.

RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; BC034529; AAH34529.1; -;
DR HSP; P00746; 1BIO.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease.
FT NON TER 1
SQ SEQUENCE 235 AA; 25110 MW; 9DEF67A48D5913F6 CRC64;

Alignment Scores:
Pred. No.: 0.00455 Length: 235
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q8N4E0 (1-235)

QY 712 GGTGATTCGGGGCCCCCTGGTGTCGGGGAGTCCTT 750
Db 188 GlyAspSerGlyGlyProLeuValCysGlyGlyValLeu 200

RESULT 8

Q80VS4 Q80VS4 PRELIMINARY; PRT; 242 AA.
ID Q80VS4;
AC Q80VS4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

Klk14 protein (Fragment).
DE Name=Klk14;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP
RQ
RS
RT
RU
RV
RW
RX
RY
RZ
SA
SB
SC
SD
SE
SF
SG
SH
SI
SJ
SK
SL
SM
SN
SO
SP
SQ
SEQUENCE FROM N.A.
STRAIN=NNRI; TISSUE=Mammary tumor;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wegner L., Shenmen C.W., Schuler G.D.,
Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T.T., Max S.J., Wang J., Heieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uedlin T.B., Toshlyuk S., Carrinci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smalish D.E., Schnurch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
STRAIN=NNRI; TISSUE=Mammary tumor;
Srausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to peptidase family S1.
DR ENBL; BC044756; AAH44756.1; -.
DR HSSP; P00760; LEZX.
DR MEROPS; S01.029; -.
DR MGD; MG1.2447564; Klk14.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidease_S1.
DR InterPro; IPR001314; Peptidease_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYSPIN_DOM; 1.
DR PROSITE; PS50240; TRYP SIN DOM; 1.
DR PROSITE; PS00134; TRYP SIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYP SIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 242 AA; 26059 MW; A3F8A624DE481D36 CRC64;

Alignment Scores:
Pred. No.: 0.00454 Length: 242
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q80VS4 (1-242)

Qy 706 TGCGAGGGTATTCTGTGGGCCCCCTGTGTGTGGGGA 744
|||||
Db 191 CysGlnGlyASerGlyCysGlyProLeuValCysGlyGly 203
|||

RESULT 10	ID	088301	PRELIMINARY;	PRT;	246 AA.
AC	AT	088301;			
DC	DT	01-NOV-1998	(TrEMBLrel. 08, Created)		
DT	DT	01-NOV-1998	(TrEMBLrel. 08, Last sequence update)		
DT	DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)		
DE	DT	Brain serine protease (BSP)	(BSSP).		
GN	GS	Names:Prsrl8; Synonyms:BSP, mbSP;			
OS	GN	Mus musculus (Mouse).			
OC	OC	Eukaryota; Eukarya; Chordata; Craniata; Vertebrata;			
OC	OC	Mammalia; Metheria; Rodentia; Sciurognathi; Muridae;			
OX	OX	NCBI_TaxID=10090;			
RN	RP	[1]			
RP	RP	SEQUENCE FROM N.A.			
RC	RC	STRAIN=C57BL; TISSUE=Brain;			
RC	RC	MEDLINE=20219148; PubMed=10753908; DOI=10.1074/jbc.2.2			
RC	RC	Matsui H., Kimura A., Yamashiki N., Moriyama A., Kay,			
RA	RA	Takeda N., Takahashi T.;			
RA	RA	"Molecular and biochemical characterization of a ser			
RT	RT	predominantly expressed in the medulla oblongata and			
RT	RT	matter of mouse brain."			
RT	RT	J. Biol. Chem. 275:11050-11057(2000).			
RN	RN	[2]			
RC	RC	SEQUENCE FROM N.A.			
RC	RC	STRAIN=Balb/c; TISSUE=Skin;			
RC	RC	MEDLINE=99262106; PubMed=1029394; DOI=10.1006/bbrc.			
RC	RC	Meier N., Dear T.N., Boehm T.;			
RA	RA	"A novel serine protease overexpressed in the hair f			
RA	RA	micse."			
RT	RT	Biochem. Biophys. Res. Commun. 258:374-378(1999).			
RT	RT	-1- SIMILARITY: Belongs to peptidase family S1.			
CC	CC	EMBL; AB015206; BAA28895.1; -;			
DR	DR	EMBL; Y18723; CAAT7269.1; -;			
DR	DR	EMBL; AB032402; BAA84544.1; -;			
DR	DR	HSP; P00746; 1FDP.			
DR	DR	MEROPS; S01.236; -;			
DR	DR	MGD; MGI:1343166; Prsrl8.			
DR	DR	GO; GO:0005737; C:cytoplasm; ISS.			
DR	DR	GO; GO:0005615; C:extracellular space; TAS.			
DR	DR	GO; GO:0005515; F:protein binding; ISS.			
DR	DR	GO; GO:0042982; F:amyloid precursor protein metaboli			
DR	DR	GO; GO:0007417; P:central nervous system development			
DR	DR	GO; GO:0030574; P:collagen catabolism; ISS.			
DR	DR	GO; GO:0042445; P:hormone metabolism; ISS.			
DR	DR	GO; GO:0023552; P:myelination; ISS.			
DR	DR	GO; GO:0016540; P:protein autoprocessing; ISS.			
DR	DR	InterPro; IPR001254; Peptidase S1.			
DR	DR	InterPro; IPR001314; Peptidase_S1A.			
DR	DR	InterPro; IPR009003; Pept_Ser_Cys.			
DR	DR	Fram; PF00089; Trypsin; 1.			
DR	DR	PRINTS; PR00722; CHYMOTRYPSIN.			
DR	DR	SMART; SM00020; Tryp_SPC; 1.			
DR	DR	PROSITE; PS00240; TRYPSIN_DOM; 1.			
DR	DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.			
DR	DR	PROSITE; PS00135; TRYPSIN_SER; 1.			
KW	KW	Hydrolase; Protease; Serine protease.			
SQ	SQ	SEQUENCE 246 AA; 27496 MW; E20C080087139B63 CRC6			
Alignment Scores:					
Pred. No.:		0.00453	Length:	246	
Score:		13.00	Matches:	13	
Percent Similarity:		100.00%	Conservative:	0	
Best Local Similarity:		100.00%	Mismatches:	0	
Query Match:		3.64%	Indels:	0	
DB:		2	Gaps:	0	
US-10-015-385A-193 (1-1091) x 088301 (1-246)					
Qy	706	TGCCAGGTGATTCTGGGGCCCCCTGGTGTGGGGGA	7444		
Db	193	CysGlnGlyAspSerGlyGlyProLeuValCysGlyGly	2051		

DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 247 AA; 26948 MW; DC4B647179DD972 CRC64;

Alignment Scores:
Pred. No.: 0.00453 Length: 247
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q9W7Q5 (1-247)

QY 700 GATGCTGCAGGGTGATTCCTGGGGCCCCCTGGTGTTGT 738
|||||
Db 194 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 206
|||||

RESULT 13
Q6QX59
ID Q6QX59 PRELIMINARY; PRT; 249 AA.
AC Q6QX59;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Intestinal trypsin 5 precursor (EC 3.4.21.4).
OS Lepeophtheirus salmonis (salmon louse).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Maxillopoda; Copepoda;
OC Siphonostomatoida; Caligidae; Lepeophtheirus.
OX NCBI_TaxID=72036;
RN [1]
RP SEQUENCE FROM N.A.
RA Kvanne B.O., Skern R., Frost P., Nilsen F.;
RT "Molecular characterization of five trypsin-like peptidase transcripts
from the salmon louse (Lepeophtheirus salmonis) intestine.";
RL Int. J. Parasitol. 0.0-0(2004).
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AY522441; AAS91796.1; -.
DR HSSP; P00761; 1AKS.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease; Signal.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 23 activation peptide.
SQ SEQUENCE 249 AA; 26915 MW; 58C604D819043096 CRC64;

Alignment Scores:
Pred. No.: 0.00452 Length: 249
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.64% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q6QX59 (1-249)

QY 700 GATGCTGCAGGGTGATTCCTGGGGCCCCCTGGTGTTGT 738
|||||
Db 199 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 211
|||||

RESULT 14
Q8CGR5
ID Q8CGR5 PRELIMINARY; PRT; 250 AA.
AC Q8CGR5;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Glandular kallikrein KLK14.
GN Name=KLK14;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22325484; PubMed=12437987; DOI=10.1016/S0006-291X(02)02629-3;
RA Olsson A.Y., Lundwall A.;
RT "Organization and evolution of the glandular kallikrein locus in Mus
musculus";
RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M., Mural R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AY152433; AAN78421.1; -.
DR HSSP; P00760; IEZX.
DR MEROPS; S01.029; -.
DR MGD; MGI:2447564; Klk14.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 250 AA; 27016 MW; F62FEBF2290FEBE8 CRC64;

Alignment Scores:
Pred. No.: 0.00452 Length: 250
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q8CGR5 (1-250)

QY 706 TCCACAGGTGATTCCTGGGGCCCCCTGGTGTTGGGGGA 744
|||||
Db 199 CysGlnGlyAspSerGlyGlyProLeuValCysGlyGly 211
|||||

RESULT 15
O54854
ID O54854 PRELIMINARY; PRT; 251 AA.
AC O54854;
DT 01-JUN-1998 (TRENBLrel. 06, Created)

01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Myelencephalon specific protease.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;
 RX MEDLINE=97477435; PubMed=9334391;
 RA Scarisbrick I.A.; Towne M.D.; Isackson P.J.;
 RT "Nervous system-specific expression of a novel serine protease:
 regulation in the adult rat spinal cord by excitotoxic injury.";
 RL J. Neurosci. 17:8156-8168(1997).
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 DR EMBL; AF016269; AAC02300.1; --
 DR HSSP; P00760; IEZX.
 DR MEROPS; S01.236; --
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 251 AA; 28014 MW; E21967BF06CEBBF9 CRC64;

Alignment Scores:
 Pred. No.: 0.00452 Length: 251
 Score: 13.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.64% Indels: 0
 DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x 054854 (1-251)

QY 706 TGCACGGTGCATTCTGGGGCCCCCTGTGTGGGGGA 744
 DB 200 CysGlnGlyAspSerGlyGlyProLeuValCysGlyGly 212

Search completed: March 5, 2005, 23:56:35
 Job time : 240.5 secs

OM protein - protein search, using sw model
Run on: March 5, 2005, 20:42:45 ; Search time 167 Seconds
(without alignments)
574.351 Million cell updates/sec

Title: US-10-015-385A-194
Perfect score: 1374
Sequence: 1 MGLSFLLCVLGLSQATP.....GVYTYICKYVDWIRIMRNN 248
Scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%

Database :
Listing first 100 summaries
Maximum Match 100%
1: A_Geneseq_16Dec04:*
2: Geneseqp1980s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003Bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAB21304	standard; protein; 248 AA.				
DE	Human KLU-L5 protein #4.					
PN	WO200053776-A2.					
PD	14-SEP-2000.					
PA	(MOUN) MOUNT SINAI HOSPITAL.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 2						
ID	AAB24428	standard; protein; 248 AA.				
DE	Human PRO1303 protein sequence SEQ ID NO:203.					
PN	WO200032221-A2.					
PD	08-JUN-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 3						
ID	AAB24032	standard; protein; 248 AA.				
DE	Human PRO1303 protein sequence SEQ ID NO:33.					
PN	WO200053750-A1.					
PD	14-SEP-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 4						
ID	AAY93933	standard; protein; 248 AA.				
DE	Human PRO1303 (UNQ669) amino acid sequence SEQ ID NO:194.					
PN	WO200012708-A2.					
PD	09-MAR-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 5						
ID	AA23994	standard; protein; 248 AA.				
DE	Human EST encoded protein SEQ ID NO: 1519.					
PN	WO200154477-A2.					
PD	02-AUG-2001.					
PA	(HYSE-) HYSEQ INC.					
Query Match	100.0%;	Score 1374;	DB 4;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 6						
ID	AAB66142	standard; protein; 248 AA.				

DE Protein of the invention #54.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 4; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 7
ID ABO33635 standard; protein; 248 AA.
DE Novel human secreted and transmembrane protein PRO1303.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 6; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 8
ID ABO44488 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 9
ID ABO33512 standard; protein; 248 AA.
DE Novel human secreted and transmembrane protein PRO1303.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 10
ID ADC18063 standard; protein; 248 AA.
DE Human PRO polypeptide #54.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 11
ID ADD70709 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 12
ID ADD39786 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 13
ID ADD70232 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 14
ID ADD38353 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 15
ID ADD39309 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.

PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 16
ID ADD38832 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 17
ID ADD40263 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 18
ID ADE50484 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 19
ID ADE20096 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 20
ID ADE50007 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 21
ID ADE21565 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 22
ID ADF29990 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 23
ID ADF5883 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 24
ID ADH99387 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003065142-A1.
PD 08-JAN-2004.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 25
ID ADE96567 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 26
ID ADF25878 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 27
ID ADF24777 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 28
ID ADF29513 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 29
ID ADE97044 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 30
ID ADH03082 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 31
ID ADH04036 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 32
ID ADH03559 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 33
ID ADH04513 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2004005626-A1.
PD 08-JAN-2004.

PA (GETH) GENENTECH INC.
Query Match 94.7%; Score 1301; DB 8; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.2e-92;
RESULT 34
ID ADH61514 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 35
ID ADN10927 standard; protein; 248 AA.
DE Human kallikrein 12, marker of endocrine cancer.
PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 36
ID ADL94713 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 37
ID ADT94373 standard; protein; 248 AA.
DE Human PRO1303 protein.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 38
ID AAO29516 standard; protein; 248 AA.
DE Human kallikrein-like protein 5 (19817).
PN WO2003039475-A2.
PD 15-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 99.5%; Score 1367; DB 6; Length 248;
Best Local Similarity 99.6%; Pred. No. 1.7e-97;
RESULT 39
ID AAB21303 standard; protein; 254 AA.
DE Human KLK-L5 protein #3.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 94.7%; Score 1301; DB 3; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.2e-92;
RESULT 40
ID ABG66676 standard; protein; 254 AA.
DE Human novel polypeptide #11.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 94.7%; Score 1301; DB 5; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.2e-92;
RESULT 41
ID ADN10926 standard; protein; 254 AA.
DE Human kallikrein 12, marker of endocrine cancer.
PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 94.7%; Score 1301; DB 8; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.2e-92;
RESULT 42
ID ADP56174 standard; protein; 254 AA.
DE Human PRO protein sequence SEQ ID NO:2150.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.

Query Match 94.7%; Score 1301; DB 8; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.2e-92;
RESULT 43
ID AAB21301 standard; protein; 184 AA.
DE Human KLK-L5 protein #1.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 74.2%; Score 1019; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 8.5e-71;
RESULT 44
ID AAY28642 standard; protein; 162 AA.
DE Human secreted protein from cDNA clone HKAFV61.
PN WO9940183-A1.
PD 12-AUG-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 59.0%; Score 811; DB 2; Length 162;
Best Local Similarity 64.1%; Pred. No. 8.1e-55;
RESULT 45
ID AAY32852 standard; protein; 260 AA.
DE Human serine protease protein sequence.
PN JP11225765-A.
PD 24-AUG-1999.
PA (SUNR) SUNTORY LTD.
Query Match 45.9%; Score 630.5; DB 2; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 46
ID AAY41744 standard; protein; 260 AA.
DE Human PRO322 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 2; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 47
ID AAY03220 standard; protein; 260 AA.
DE Amino acid sequence of human tumour antigen derived gene-14 protein.
PN WO9909138-A1.
PD 25-FEB-1999.
PA (UYAR-) UNIV ARKANSAS.
Query Match 45.9%; Score 630.5; DB 2; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 48
ID AAB21322 standard; protein; 260 AA.
DE Human neuropsin.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 45.9%; Score 630.5; DB 3; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 49
ID AAB44300 standard; protein; 260 AA.
DE Human PRO322 (UNQ283) protein sequence SEQ ID NO:395.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 3; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 50
ID AAY51131 standard; protein; 260 AA.
DE Human neuropsin protein.
PN JP11318461-A.
PD 24-NOV-1999.
PA (SHIO/) SHIOZAKA S.
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
Query Match 45.9%; Score 630.5; DB 3; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 51
ID AAU12369 standard; protein; 260 AA.
DE Human PRO322 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.

Query Match 45.9%; Score 630.5; DB 4; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 52
ID AAB53087 standard; protein; 260 AA.
DE Human angiogenesis-associated protein PRO322, SEQ ID NO:127.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 4; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 53
ID ABG23373 standard; protein; 260 AA.
DE Novel human diagnostic protein #23364.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 45.9%; Score 630.5; DB 4; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 54
ID ABB84852 standard; protein; 260 AA.
DE Human PRO322 protein sequence SEQ ID NO:72.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 5; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 55
ID AAU61959 standard; protein; 260 AA.
DE Human PRO322.
PN WO200109327-A2.
PD 08-FEB-2001.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 5; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 56
ID ABB95438 standard; protein; 260 AA.
DE Human angiogenesis related protein PRO322 SEQ ID NO: 72.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 5; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 57
ID ADI17076 standard; protein; 260 AA.
DE Human NOVX protein homologue SeqID 612.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.9%; Score 630.5; DB 5; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 58
ID ABO17813 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 59
ID ABO25246 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 60
ID ABU81067 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 61
ID ABU72252 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 62
ID ADA05702 standard; protein; 260 AA.
DE Human NOV11h protein SEQ ID NO:62.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 63
ID ABU66767 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 64
ID ABU84932 standard; protein; 260 AA.
DE Human secreted and transmembrane PRO polypeptide #8.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 65
ID ABU59848 standard; protein; 260 AA.
DE Novel secreted and transmembrane protein PRO322.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 66
ID ABU61130 standard; protein; 260 AA.
DE Human PRO322 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 67
ID ABO25038 standard; protein; 260 AA.
DE Human secreted/transmembrane protein (PRO) #198.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 68

ID ABU80399 standard; protein; 260 AA.
DE Human secreted/transmembrane protein PRO322.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 69
ID ABU67043 standard; protein; 260 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 396.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 70
ID ADA45915 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 71
ID ADA76346 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 72
ID ADA18996 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 73
ID ADA61619 standard; protein; 260 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 74
ID ADB19404 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 75
ID ADB27945 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 76
ID ADA96424 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 77
ID ADB15988 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.

DE Human PRO polypeptide #198.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 78
ID ADA47774 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 79
ID ADA67569 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 80
ID ADB30576 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 81
ID ADA85872 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 82
ID ADA97084 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 83
ID ADA79388 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 84
ID ADA87527 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 85
ID ADB16729 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 86
ID ADA91821 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.

PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 87
ID ADB14884 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 88
ID ADA24934 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 89
ID ADB18845 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 90
ID ADA94060 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US200307722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 91
ID ADB19956 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 92
ID ADB13268 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 93
ID ABO43346 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 94
ID ABO19701 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 95
ID ADA12595 standard; protein; 260 AA.
DE Human secreted/transmembrane polypeptide PRO322.
PN US2003055216-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 96
ID ADA74522 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 97
ID ADB24755 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 98
ID ADA82279 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 99
ID ADA75242 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 100
ID ADA85320 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 101
ID ADA84768 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 102
ID ADB30024 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 103
ID ADA80552 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 104
ID ADA75794 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082703-A1.
PD 01-MAY-2003.

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PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 105
ID ADA47019 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 106
ID ADB25315 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 107
ID ADA93491 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 108
ID ADB26841 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 109
ID ADB31128 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US200309386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 110
ID ADA61056 standard; protein; 260 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 111
ID ADB24203 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 112
ID ADA96532 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 113
ID ADA81104 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 114
ID ADA95980 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 115
ID ADB26289 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 116
ID ADB21774 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 117
ID ABO19592 standard; protein; 260 AA.
DE Novel human secreted and transmembrane polypeptide #60.
PN US2003049633-A1.
PD 13-MAR-2003.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 118
ID ADA77553 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 119
ID ADB18293 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 120
ID ADA86976 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 121
ID ADA88079 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 122
ID ADA46467 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
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RESULT 123
ID ADB28497 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 124
ID ADB29049 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 125
ID ADA77001 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 126
ID ADA88631 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 127
ID ADA97636 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 128
ID ADB27393 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 129
ID ADB22326 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 130
ID ADA67017 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 131
ID ADB22878 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 132
ID ADB3651 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003082764-A1.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 133
ID ADA92373 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 134
ID ADB15436 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 135
ID ADB38688 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 136
ID ADB38136 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 137
ID ADB66608 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 138
ID ADB89688 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 139
ID ADB90420 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 140
ID ADB80561 standard; protein; 260 AA.
DE Ovarian cancer-associated protein #63.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (ECSB-) EOS BIOTECHNOLOGY INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 141
ID ADB39521 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082764-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 142
ID ADB73901 standard; protein; 260 AA.
DE Human PRO polypeptide #60.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 143
ID ADB47144 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 144
ID ADB86751 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 145
ID ADB76617 standard; protein; 260 AA.
DE Human PRO polypeptide #60.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 146
ID ADB77356 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 147
ID ADB34513 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 148
ID ADB35617 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 149
ID ADB33961 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 150
ID ADB35065 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077718-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 151
ID ADB36169 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 152
ID ADB46564 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 153
ID ADC44043 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 154
ID ADC61803 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 155
ID ADC63767 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 156
ID ADC66867 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 157
ID ADC68991 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 158
ID ADC63051 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 159
ID ADC68116 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

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Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 160
ID ADC41436 standard; protein; 260 AA.
DE Novel human secreted/transmembrane protein, PRO322.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 161
ID ADC67491 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 162
ID ADC62427 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 163
ID ADC42060 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 164
ID ADC50437 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 165
ID ADC71984 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 166
ID ADC59963 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 167
ID ADC52970 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein Seq ID396.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 168
ID ADC57324 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein Seq ID396.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 169
ID ADC60515 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 170
ID ADC50990 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 171
ID ADC65517 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 172
ID ADC54615 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein Seq ID396.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 173
ID ADC53576 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein Seq ID396.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 174
ID ADC59099 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein Seq ID396.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 175
ID ADC55977 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein Seq ID396.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 176
ID ADC58547 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein Seq ID396.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
RESULT 177
ID ADD03221 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
                    50.2%; Pred. No. 1.1e-40;
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RESULT 178
ID ADC90213 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 179
ID ADC69632 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 180
ID ADC48521 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 181
ID ADD10050 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 182
ID ADD04625 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 183
ID ADC80581 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 184
ID ADD09100 standard; protein; 260 AA.
DE Human kalikrein 8 protein SEQ ID NO:2.
PN WO2003085404-A1.
PD 16-OCT-2003.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 185
ID ADD11088 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 186
ID ADD10361 standard; protein; 260 AA.
DE Human secreted/transmembrane PRO polypeptide #36.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 187
ID ABW00074 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 188
ID ADC47969 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 189
ID ADC80029 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 190
ID ADD11321 standard; protein; 260 AA.
DE Human secreted/transmembrane PRO polypeptide #36.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 191
ID ADD41211 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 192
ID ADD52350 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 193
ID ADD53090 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 194
ID ADD53642 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 195
ID ADD37114 standard; protein; 260 AA.
DE Human secreted/transmembrane PRO polypeptide #36.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 196
ID ABW00074 standard; protein; 260 AA.

DE Human tumour antigen derived gene-14 (TADG-14) protein.
PN US2002037591-A1.
PD 28-MAR-2002.
PA (UABR-) UAB RES FOUND.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 197
ID ADD51798 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 198
ID ADD02597 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 199
ID ADD02031 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 200
ID ADD54213 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 201
ID ADE49429 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 202
ID ADD2530 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 203
ID ADD31426 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 204
ID ADE04040 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 205
ID ADE32337 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194767-A1.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 206
ID ADE22269 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 207
ID ADD79493 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 208
ID ADE35483 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 209
ID ADE16597 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 210
ID ADD73212 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 211
ID ADE42029 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 212
ID ADE17846 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 213
ID ADD91978 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 214
ID ADE33441 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194767-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 215
ID ADE33993 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 216
ID ADD80045 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 217
ID ADD93082 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 218
ID ADD72570 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 219
ID ADE19502 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 220
ID ADE18950 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 221
ID ADE43146 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 222
ID ADD95935 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 223
ID ADE22821 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199064-A1.
PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 224
ID ADD78939 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 225
ID ADE32889 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 226
ID ADE42581 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 227
ID ADE17221 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 228
ID ADD80597 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 229
ID ADD89625 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 230
ID ADE40909 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 231
ID ADE04708 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 232
ID ADE92837 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 233
ID ADP47235 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 234
ID ADG21546 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 235
ID ADG23187 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 236
ID ADF97522 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 237
ID ADG80586 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 238
ID ADG52992 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 239
ID ADG50312 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 240
ID ADG80034 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 241
ID ADH55326 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;

Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 242
ID ADH55878 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 243
ID ADI61072 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 244
ID ADI64097 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 245
ID ADH81959 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 246
ID ADH81407 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 247
ID ADM82576 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 248
ID ADNI5975 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 249
ID ADNI6604 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 250
ID ADN39182 standard; protein; 260 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:500.
PN W02003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

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RESULT 251
ID ADN15423 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 252
ID ADN14871 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 253
ID ADI65046 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 254
ID ADI63545 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 255
ID ADC81133 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 256
ID ADD76581 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 257
ID ADD87945 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 258
ID ADD86349 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 259
ID ADE75797 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 260
ID ADE89830 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 261
ID ADE41322 standard; protein; 260 AA.
DE Human secreted/transmembrane PRO polypeptide #36.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 262
ID ADE23373 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 263
ID ADE23925 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 264
ID ADE24568 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 265
ID ADD87393 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 266
ID ADE89259 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 267
ID ADE18398 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 268
ID ADE88707 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 269
ID ADE89830 standard; protein; 260 AA.
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DE Human secreted/transmembrane protein, PRO322.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERE/) GERBER H.
PA (GERG/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 270
ID ADF61470 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 271
ID ADF40162 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 272
ID ADF45958 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 273
ID ADE94727 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 274
ID ADE91138 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 275
ID ADE92285 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 276
ID ADE91389 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 277
ID ADF24354 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 278
ID ADF40786 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 279
ID ADF23730 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 280
ID ADF33713 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 281
ID ADF34970 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 282
ID ADF27180 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 283
ID ADF27816 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 284
ID ADE92285 standard; protein; 260 AA.

DE Novel human secreted and transmembrane protein PRO322.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 285
ID ADE90586 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 286
ID ADF41410 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 287
ID ADF33089 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 288
ID ADF25455 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 289
ID ADF26556 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 290
ID ADF34345 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 291
ID ADF46582 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 292
ID ADE91733 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 293
ID ADG02312 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 294
ID ADG22098 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 295
ID ADG20168 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 296
ID ADF98074 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 297
ID ADG24291 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 298
ID ADF98645 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 299
ID ADG03476 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 300
ID ADF99197 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 301
ID ADG16782 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 302
ID ADG05241 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207375-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 303
ID ADG19508 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 304
ID ADG13345 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 305
ID ADG08402 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 306
ID ADG15572 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 307
ID ADF96970 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 308
ID ADG06155 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 309
ID ADG23739 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 310
ID ADG04028 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 311
ID ADG24929 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 312
ID ADG07226 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 313
ID ADG07778 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 314
ID ADG55273 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 315
ID ADG60937 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 316
ID ADG62041 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 317
ID ADG82242 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 318
ID ADG57481 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 319
ID ADG56929 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 320
ID ADG55825 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 321
ID ADG585 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 322
ID ADG70951 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 323
ID ADG58033 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 324
ID ADG53617 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 325
ID ADG71503 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 326
ID ADG50568 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 327
ID ADG81690 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 328
ID ADH30652 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US200307723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 329
ID ADH12019 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

RESULT 330
ID ADG49944 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 331
ID ADG51816 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 332
ID ADG52441 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 333
ID ADG54169 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 334
ID ADG49320 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 335
ID ADG81138 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 336
ID ADG56377 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 337
ID ADH12643 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 338
ID ADG48696 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 339
ID ADG48696 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

ID ADG61489 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 340
ID ADH28576 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 341
ID ADG54721 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 342
ID ADG59761 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 343
ID ADG51192 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 344
ID ADH43505 standard; protein; 260 AA.
DE Human PRO polypeptide #36.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 345
ID ADG59136 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 346
ID ADG62592 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 347
ID ADI81185 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 348
ID ADI39730 standard; protein; 260 AA.

DE Human TADG-14 protein.
PN US6642013-B1.
PD 04-NOV-2003.
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 349
ID ADH25617 standard; protein; 260 AA.
DE Human neurotrophin homologue related protein sequence SEQ ID NO:395.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 350
ID ADG09928 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 351
ID ADI15399 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 352
ID ADG09276 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 353
ID ADI14731 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 354
ID ADI18326 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 355
ID ADI37154 standard; protein; 260 AA.
DE Human TADG-14 protein.
PN US2003199010-A1.
PD 23-OCT-2003.
PA (UYAR-) UNIV ARKANSAS.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 356
ID ADJ63607 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 357
ID ADJ77502 standard; protein; 260 AA.
DE Human PRO polypeptide #198.

PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 358
ID ADK82850 standard; protein; 260 AA.
DE Human PRO polypeptide #36.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 359
ID ADJ65624 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 360
ID ADM27760 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 361
ID ADM17394 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 362
ID ADL07228 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 363
ID ADM42484 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 364
ID ADN62866 standard; protein; 260 AA.
DE Human NOV11h.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT) SMITHSON G.
PA (MILL) MILLET I.
PA (PEYM) PEYMAN J A.
PA (KEK) KEKUDA R.
PA (JULJ) JU J.
PA (LILL) LI L.
PA (GUOX) GUO X.
PA (PATT) PATTURAJAN M.
PA (SPYT) SPYTEK K A.
PA (EDIN) EDINGER S R.
PA (ELLE) ELLERMAN K.
PA (MALY) MALYANKAR U M.
PA (ORTT) ORT T.
PA (GORM) GORMAN L.
PA (ZERR) ZERRHUSEN B D.

PA (ANDE) ANDERSON D W.
PA (ZHON) ZHONG M.
PA (CATT) CATTERTON E.
PA (JIWW) JI W.
PA (MILL) MILLER C E.
PA (RAST) RASTELLI L.
PA (STON) STONE D J.
PA (PENA) PENA C E A.
PA (SHEN) SHENOY S G.
PA (SHIM) SHIMKETS R A.
PA (ROTH) ROTHENBERG M E.
PA (LEAC) LEACH M D.
PA (AGEE) AGE E M L.
PA (BERG) BERGHS C.
PA (DIFI) DIPIPO V A.
PA (EISE) EISEN A.
PA (GANG) GANGOLLI E A.
PA (RIEG) RIEGER D K.
PA (SPAD) SPADERNA S K.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 365
ID ADN04214 standard; protein; 260 AA.
DE Antipsoziatic protein sequence #302.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 366
ID ADM28346 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 367
ID ADI95828 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 368
ID ADI96380 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 369
ID ADR72883 standard; protein; 260 AA.
DE Human ovarian cancer-related tumour marker kallikrein 8 (HK8) protein.
PN WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 370
ID AAY32853 standard; protein; 305 AA.
DE Human serine protease protein sequence.
PN JP1225765-A.
PD 24-AUG-1999.
PA (SUNR) SUNTORY LTD.
Query Match 45.6%; Score 627; DB 2; Length 305;
Best Local Similarity 50.9%; Pred. No. 2.4e-40;
RESULT 371
ID AAB37985 standard; protein; 306 AA.
DE Human secreted protein encoded by gene 2 clone HWJAE49.
PN WO200055371-A1.

PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 45.6%; Score 627; DB 3; Length 306;
Best Local Similarity 50.9%; Pred. No. 2.4e-40;
RESULT 372
ID ABP41332 standard; protein; 315 AA.
DE Human ovarian antigen HCOQP78, SEQ ID NO:2464.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 45.6%; Score 627; DB 5; Length 315;
Best Local Similarity 50.9%; Pred. No. 2.4e-40;
RESULT 373
ID AAW87703 standard; protein; 260 AA.
DE A human serine protease designated HGBAB90.
PN EP887414-A2.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 45.6%; Score 627; DB 5; Length 315;
Best Local Similarity 50.9%; Pred. No. 2.4e-40;
RESULT 374
ID AAB21311 standard; protein; 275 AA.
DE Human neuropsin.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 45.6%; Score 626.5; DB 3; Length 275;
Best Local Similarity 50.4%; Pred. No. 2.3e-40;
RESULT 375
ID AAW10694 standard; protein; 260 AA.
DE Human recombinant neuropsin, used for antibody production.
PN JP09245700-A.
PD 24-SEP-1996.
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
Query Match 45.3%; Score 622.5; DB 2; Length 260;
Best Local Similarity 49.0%; Pred. No. 4.5e-40;
RESULT 376
ID AAW12393 standard; protein; 260 AA.
DE Mouse neuropsin protein.
PN JP08311099-A.
PD 26-NOV-1996.
PA (SHIO/) SHIOZAKA S.
Query Match 45.3%; Score 622.5; DB 2; Length 260;
Best Local Similarity 49.0%; Pred. No. 4.5e-40;
RESULT 377
ID AAY06438 standard; protein; 260 AA.
DE Human protease HUPW-7.
PN WO9936550-A2.
PD 22-JUL-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 45.3%; Score 622.5; DB 2; Length 260;
Best Local Similarity 49.8%; Pred. No. 4.5e-40;
RESULT 378
ID ABB57219 standard; protein; 260 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:533.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 45.3%; Score 622.5; DB 5; Length 260;
Best Local Similarity 49.0%; Pred. No. 4.5e-40;
RESULT 379
ID ADI17073 standard; protein; 260 AA.
DE Murine NOVX protein homologue SeqID 609.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.3%; Score 622.5; DB 5; Length 260;
Best Local Similarity 49.0%; Pred. No. 4.5e-40;
RESULT 380
ID ADI39731 standard; protein; 260 AA.
DE Mouse neuropsin protein.
PN US6642013-B1.
PD 04-NOV-2003.

PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.
Query Match 45.3%; Score 622.5; DB 8; Length 260;
Best Local Similarity 49.0%; Pred. No. 4.5e-40;
RESULT 381
ID ADI37155 standard; protein; 260 AA.
DE Mouse neuropsin.
PN US2003199010-A1.
PD 23-OCT-2003.
PA (UYAR-) UNIV ARKANSAS.
Query Match 45.3%; Score 622.5; DB 8; Length 260;
Best Local Similarity 49.0%; Pred. No. 4.5e-40;
RESULT 382
ID ADI17074 standard; protein; 260 AA.
DE Rat NOVX protein homologue SeqID 610.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.2%; Score 621.5; DB 5; Length 260;
Best Local Similarity 48.6%; Pred. No. 5.3e-40;
RESULT 383
ID AAB21325 standard; protein; 250 AA.
DE Human TLSP.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 45.0%; Score 618.5; DB 3; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 384
ID AAY99390 standard; protein; 250 AA.
DE Human PRO1279 (UNQ649) amino acid sequence SEQ ID NO:170.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 3; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 385
ID AAB66139 standard; protein; 250 AA.
DE Protein of the invention #51.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 4; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 386
ID AAU12424 standard; protein; 250 AA.
DE Human PRO1279 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 4; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 387
ID ABB50479 standard; protein; 250 AA.
DE Human secreted protein encoded by gene 179 SEQ ID NO:427.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 45.0%; Score 618.5; DB 4; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 388
ID AAU83684 standard; protein; 250 AA.
DE Human PRO protein, Seq ID No 186.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 5; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 389
ID ABG61816 standard; protein; 250 AA.
DE Prostate cancer-associated protein #17.
PN WO200230268-A2.
PD 18-APR-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match 45.0%; Score 618.5; DB 5; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 390
ID ABB84920 standard; protein; 250 AA.
DE Human PRO1279 protein sequence SEQ ID NO:208.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 5; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 391
ID ABB95526 standard; protein; 250 AA.
DE Human angiogenesis related protein PRO1279 SEQ ID NO: 208.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 45.0%; Score 618.5; DB 5; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 392
ID ABO17868 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US20030321156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 393
ID ABUS0831 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 394
ID ABO33797 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 395
ID ABUS1122 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 396
ID ABUS6739 standard; protein; 250 AA.
DE Lung cancer-associated polypeptide #332.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

RESULT 397
ID ABUS6822 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 398
ID ABUS9903 standard; protein; 250 AA.
DE Novel secreted and transmembrane protein PRO1279.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 399
ID ABO25093 standard; protein; 250 AA.
DE Human secreted/transmembrane protein (PRO) #253.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 400
ID ABUS2140 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 401
ID ABUS7098 standard; protein; 250 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 506.
PN US20030321155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 402
ID ADA6025 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 403
ID ADA76456 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 404
ID ABJ72320 standard; protein; 250 AA.
DE Human PRO1279 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 405
ID ADA19106 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 406
ID ABO33797 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

ID ADA61729 standard; protein; 250 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 407
ID ADB19514 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 408
ID ADB28055 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 409
ID ADA86534 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 410
ID ADB16098 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 411
ID ADA47884 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 412
ID ABO44736 standard; protein; 250 AA.
DE Novel human secreted protein #179.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 413
ID ABO33632 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 414
ID ADA67679 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 415
ID ADB30686 standard; protein; 250 AA.
DE Homo sapiens.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 416
ID ADA85982 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 417
ID ADA97194 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 418
ID ADA79498 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 419
ID ADA87637 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 420
ID ADB16839 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 421
ID ADA1931 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 422
ID ADB14994 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 423
ID ADB18955 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 424
ID ADA94170 standard; protein; 250 AA.
DE Human PRO polypeptide #253.


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PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 425
ID ADB20066 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 426
ID ADB13378 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 427
ID ABO43401 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 428
ID ADA74632 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 429
ID ADB24865 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 430
ID ADA82389 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 431
ID ADA75352 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 432
ID ADA85430 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 433
ID ADA84878 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082708-A1.

PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 434
ID ADB30134 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 435
ID ADA80662 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 436
ID ADA75904 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 437
ID ADA47129 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 438
ID ADB25425 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 439
ID ADA93601 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 440
ID ADB26951 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 441
ID ADB31238 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 442
ID ABJ72448 standard; protein; 250 AA.
DE Human PRO1279 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
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PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 443
ID ADA61166 standard; protein; 250 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 444
ID ADB24313 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077114-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 445
ID ADA96642 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 446
ID ADA81214 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 447
ID ADA96090 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 448
ID ADB26399 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 449
ID ADB21884 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 450
ID ABO34343 standard; protein; 250 AA.
DE Human secreted/transmembrane polypeptide PRO 1279.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 451
ID ADA77663 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 452
ID ADB18403 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003077110-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 453
ID ADA87086 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 454
ID ABO44485 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 455
ID ADA88189 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 456
ID ADA46577 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 457
ID ADB28607 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 458
ID ADB29159 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 459
ID ABO26216 standard; protein; 250 AA.
DE Human protein from novel secreted protein gene 179.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 460
ID ADA77111 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;

Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 461
ID ABO33509 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 462
ID ADA88741 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 463
ID ADA97746 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 464
ID ADB27503 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 465
ID ADB22436 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 466
ID ABU72150 standard; protein; 250 AA.
DE Human membrane bound receptor/protein PRO1279 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 467
ID ADA67127 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 468
ID ADB22988 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 469
ID ADB23761 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 470
ID ADA92483 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 471
ID ADB15546 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 472
ID ADB83676 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 473
ID ADB80782 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 474
ID ADB73323 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 475
ID ADB38798 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 476
ID ADB78405 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 477
ID ADB38246 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 478
ID ADB66718 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 479
ID ADB85053 standard; protein; 250 AA.
DE Human PRO polypeptide #93.

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PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 480
ID ADB89798 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 481
ID ADB90530 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 482
ID ADB90596 standard; protein; 250 AA.
DE Ovarian cancer-associated protein #81.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 483
ID ADB39631 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 484
ID ADB78159 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 485
ID ADB37225 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 486
ID ADB84807 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 487
ID ADB47254 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 488
ID ADB33922 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003069397-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 489
ID ADB86861 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 490
ID ADB73077 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 491
ID ADB77466 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 492
ID ADB75388 standard; protein; 250 AA.
DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 493
ID ADB34623 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 494
ID ADB35727 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 495
ID ADB34071 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 496
ID ADB35175 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.0%; Score 618.5; DB 7; Length 250;
  Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 497
ID ADB36279 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077720-A1.
PD 24-APR-2003.
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PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 498
ID ADB46674 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 499
ID ADC18039 standard; protein; 250 AA.
DE Human PRO polypeptide #51.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 500
ID ADC36915 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 501
ID ADC21905 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 502
ID ADC50547 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 503
ID ADC72094 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 504
ID ADC60073 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 505
ID ADC49936 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 506
ID ADC49135 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 507
ID ADC49652 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 508
ID ADC47513 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 509
ID ADC53080 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein Seq ID506.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 510
ID ADC57434 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein Seq ID506.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 511
ID ADC60625 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 512
ID ADC51100 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 513
ID ADC65627 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 514
ID ADC54725 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein Seq ID506.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 515
ID ADC53686 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein Seq ID506.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 516
ID ADC49135 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

ID ADD11457 standard; protein; 250 AA.
DE Human secreted/transmembrane PRO polypeptide #104.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 535
ID ADD09608 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 536
ID ADD50850 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 537
ID ADD41321 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 538
ID ADD52460 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 539
ID ADD51096 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 540
ID ADD70685 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US200309625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 541
ID ADD39762 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 542
ID ADD53200 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 543
ID ADD53752 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.

DE Novel human secreted and transmembrane protein PRO1279.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 544
ID ADD70208 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 545
ID ADD37250 standard; protein; 250 AA.
DE Human secreted/transmembrane PRO polypeptide #104.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 546
ID ADD38329 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 547
ID ADD39285 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 548
ID ADD51908 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 549
ID ADD02707 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 550
ID ADD50577 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 551
ID ADD02141 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 552
ID ADD54323 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.

PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 553
ID ADD50331 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 554
ID ADD38808 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 555
ID ADD40239 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 556
ID ADD51342 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 557
ID ADE50460 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 558
ID ADD92640 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 559
ID ADD91536 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 560
ID ADE04150 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 561
ID ADE20072 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003092883-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 562
ID ADE32447 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 563
ID ADE22379 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 564
ID ADD79603 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 565
ID ADE42139 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 566
ID ADE17956 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 567
ID ADD92088 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 568
ID ADE33551 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 569
ID ADE34103 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 570
ID ADD80155 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207417-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 571
ID ADE4993 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 572
ID ADD93192 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 573
ID ADE19612 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 574
ID ADE21541 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 575
ID ADE19060 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 576
ID ADE43256 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 577
ID ADD96045 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 578
ID ADE22931 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 579
ID ADD79049 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 580
ID ADE32999 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 581
ID ADE42691 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 582
ID ADD80707 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 583
ID ADD89735 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 584
ID ADE41019 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 585
ID ADE04818 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 586
ID ADE92947 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 587
ID ADF29966 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 588
ID ADF55859 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

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Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 589
ID ADG21656 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 590
ID ADG323297 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 591
ID ADF97632 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 592
ID ADG80696 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 593
ID ADG80144 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 594
ID ADH55436 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 595
ID ADH55988 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 596
ID ADH99363 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 597
ID ADI64207 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 598
ID ADI65156 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 599
ID ADH82069 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 600
ID ADH81517 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 601
ID ADM82686 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 602
ID ADNI6085 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 603
ID ADNI6714 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 604
ID ADN39242 standard; protein; 250 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:560.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 605
ID ADNI5533 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 606
ID ADNI4981 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 607
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ID ADI63655 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 608
ID ADC48899 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 609
ID ADC81243 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 610
ID ADE21060 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 611
ID ADE05904 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 612
ID ADD76691 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 613
ID ADD75133 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 614
ID ADD75879 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 615
ID ADD85111 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 616
ID ADD86937 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 617
ID ADE20814 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 618
ID ADE39111 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 619
ID ADDB8055 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 620
ID ADDB6459 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 621
ID ADE05658 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 622
ID ADD73643 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 623
ID ADE75907 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 624
ID ADD78483 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 625
ID ADE41458 standard; protein; 250 AA.
DE Human secreted/transmembrane PRO polypeptide #104.

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PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 626
ID ADE23483 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 627
ID ADE21306 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 628
ID ADD77421 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 629
ID ADE20568 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 630
ID ADD75633 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 631
ID ADD74149 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 632
ID ADD74395 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 633
ID ADD76125 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 634
ID ADD85617 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100721-A1.

PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 635
ID ADE24035 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 636
ID ADE24678 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 637
ID ADD87503 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 638
ID ADE05166 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 639
ID ADD75379 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 640
ID ADD76923 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 641
ID ADD86691 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 642
ID ADE89369 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 643
ID ADD78159 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100731-A1.
PD 29-MAY-2003.
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PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 644
ID ADE18508 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 645
ID ADE88817 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 646
ID ADD77667 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 647
ID ADD77913 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 648
ID ADD85371 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 649
ID ADD73903 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 650
ID ADD74641 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 651
ID ADD77169 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 652
ID ADD85863 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 653
ID ADE05412 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 654
ID ADD74887 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 655
ID ADE96543 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 656
ID ADE94837 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 657
ID ADE91248 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 658
ID ADF25854 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 659
ID ADE95389 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 660
ID ADE93499 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 661
ID ADF24753 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 662
ID ADE95863 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 662
ID ADF29489 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 663
ID ADF35080 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 664
ID ADE97020 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 665
ID ADE92395 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 666
ID ADE90696 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 667
ID ADE91843 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 668
ID ADG05699 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 669
ID ADG27253 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 670
ID ADG02422 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 671
ID ADG22208 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 672
ID ADG20278 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 673
ID ADF98184 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 674
ID ADG24401 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 675
ID ADF98755 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 676
ID ADG03586 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 677
ID ADF99307 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 678
ID ADG16892 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 679
ID ADG05351 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 680

ID ADG19618 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 681
ID ADG11316 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 682
ID ADG13455 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 683
ID ADG08512 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 684
ID ADG15682 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 685
ID ADG12095 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 686
ID ADF97080 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 687
ID ADG06265 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 688
ID ADG23849 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 689
ID ADG04138 standard; protein; 250 AA.

DE Human PRO polypeptide #253.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 690
ID ADG25039 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 691
ID ADF94652 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 692
ID ADG07336 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 693
ID ADG07888 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 694
ID ADG06748 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 695
ID ADG55383 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 696
ID ADG61047 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 697
ID ADG62151 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 698
ID ADH03058 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.

PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 699
ID ADG82352 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 700
ID ADG57591 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 701
ID ADG57039 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 702
ID ADG55935 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 703
ID ADG58695 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 704
ID ADG71061 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 705
ID ADH04012 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 706
ID ADH03535 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 707
ID ADH39092 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096965-A1.

PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 708
ID ADG58143 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 709
ID ADG53727 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 710
ID ADG71613 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 711
ID ADG81800 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 712
ID ADH30762 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 713
ID ADH12129 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 714
ID ADG52551 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 715
ID ADG54279 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 716
ID ADG81248 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 717
ID ADG56487 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 718
ID ADH12753 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 719
ID ADG61599 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 720
ID ADH28686 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 721
ID ADG54831 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 722
ID ADG59871 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 723
ID ADH43641 standard; protein; 250 AA.
DE Human PRO polypeptide #104.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 724
ID ADG34182 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 725
ID ADH04489 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;

Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 726
ID ADI81295 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 727
ID ADI33652 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 728
ID ADH69746 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 729
ID ADH61490 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 730
ID ADG10038 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 731
ID ADI15509 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 732
ID ADG09386 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 733
ID ADI14841 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 734
ID ADI29907 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

RESULT 735
ID ADI18436 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207349-A1.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 736
ID ADM27304 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 737
ID ADJ63717 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 738
ID ADJ77612 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 739
ID ADK32986 standard; protein; 250 AA.
DE Human PRO polypeptide #104.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 740
ID ADK66662 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 741
ID ADJ65734 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 742
ID ADM27870 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 743
ID ADM42594 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 744
ID AAY43636 standard; protein; 282 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 745
ID ADM28456 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 746
ID ADI95938 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 747
ID ADI96490 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 748
ID ADR72632 standard; protein; 250 AA.
DE Human renal cell carcinoma-related kallikrein 11 (hK11) protein 2.
PN WO2004077060-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 749
ID ADR72890 standard; protein; 250 AA.
DE Human ovarian cancer-related tumour marker kallikrein 11 (hK11) protein2.
PN WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 750
ID ADS34892 standard; protein; 250 AA.
DE Human autoimmune disease-related protein - SEQ ID 106.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 751
ID AAY42439 standard; protein; 282 AA.
DE CAS812 amino acid sequence.
PN WO9949055-A1.
PD 30-SEP-1999.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 45.0%; Score 618.5; DB 2; Length 282;
Best Local Similarity 48.2%; Pred. No. 9.9e-40;
RESULT 752
ID AAB11712 standard; protein; 282 AA.
DE Human serine protease BSSP6 (hBSSP6) SEQ ID NO:2.
PN WO200031257-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 45.0%; Score 618.5; DB 3; Length 282;
Best Local Similarity 48.2%; Pred. No. 9.9e-40;
RESULT 753
ID AAY43636 standard; protein; 282 AA.

DE A human prostate-associated serum protease (PRASP).
PN WO941387-A2.
PD 19-AUG-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 45.0%; Score 618.5; DB 3; Length 282;
Best Local Similarity 48.2%; Pred. No. 9.9e-40;
RESULT 754
ID ADN11325 standard; protein; 282 AA.
DE Human kallikrein-11, marker for prostate cancer.
PN WO2004029616-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 45.0%; Score 618.5; DB 8; Length 282;
Best Local Similarity 48.2%; Pred. No. 9.9e-40;
RESULT 755
ID ADQ17587 standard; protein; 282 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 404.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 45.0%; Score 618.5; DB 8; Length 282;
Best Local Similarity 48.2%; Pred. No. 9.9e-40;
RESULT 756
ID ADR72631 standard; protein; 282 AA.
DE Human renal cell carcinoma-related kallikrein 11 (hK11) protein 1.
PN WO2004077060-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 45.0%; Score 618.5; DB 8; Length 282;
Best Local Similarity 48.2%; Pred. No. 9.9e-40;
RESULT 757
ID ADR72889 standard; protein; 282 AA.
DE Human ovarian cancer-related tumour-marker kallikrein 11 (hK11) protein1.
PN WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 45.0%; Score 618.5; DB 8; Length 282;
Best Local Similarity 48.2%; Pred. No. 9.9e-40;
RESULT 758
ID ADS34893 standard; protein; 282 AA.
DE Human autoimmune disease-related protein - SEQ ID 107.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 45.0%; Score 618.5; DB 8; Length 282;
Best Local Similarity 48.2%; Pred. No. 9.9e-40;
RESULT 759
ID AAY42440 standard; protein; 281 AA.
DE CASB12 polypeptide derived from Expressed Sequence Tag products.
PN WO9949055-A1.
PD 30-SEP-1999.
PA (SMUK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 44.6%; Score 612.5; DB 2; Length 281;
Best Local Similarity 48.0%; Pred. No. 2.8e-39;
RESULT 760
ID AAB36482 standard; protein; 288 AA.
DE Fusion gene with human serine protease catalytic domain protein #13.
PN WO200066709-A2.
PD 09-NOV-2000.
PA (ORTH) ORTHO-MCNEIL PHARM RES INC.
Query Match 43.9%; Score 602.5; DB 3; Length 288;
Best Local Similarity 51.1%; Pred. No. 1.7e-38;
RESULT 761
ID AAB67542 standard; protein; 288 AA.
DE Amino acid sequence of catalytic domain in PFEK1-6XHIS-TAG.
PN WO200116289-A2.
PD 08-MAR-2001.
PA (ORTH) ORTHO-MCNEIL PHARM INC.
Query Match 43.9%; Score 602.5; DB 4; Length 288;
Best Local Similarity 51.1%; Pred. No. 1.7e-38;
RESULT 762
ID AAY36093 standard; protein; 250 AA.
DE Extended human secreted protein sequence, SEQ ID NO. 478.
PN WO9931236-A2.
PD 24-JUN-1999.
PA (GEST) GENSET.
Query Match 43.8%; Score 601.5; DB 2; Length 250;
Best Local Similarity 47.4%; Pred. No. 1.8e-38;
RESULT 763
ID ADP19401 standard; protein; 250 AA.
DE Human secreted polypeptide #252.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Query Match 43.8%; Score 601.5; DB 8; Length 250;
Best Local Similarity 47.4%; Pred. No. 1.8e-38;
RESULT 764
ID AAB11714 standard; protein; 275 AA.
DE Human serine protease BSSP6 (hBSSP6) SEQ ID NO:6.
PN WO200031257-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 43.7%; Score 601; DB 3; Length 275;
Best Local Similarity 44.2%; Pred. No. 2.1e-38;
RESULT 765
ID AAU82732 standard; protein; 320 AA.
DE Amino acid sequence of novel human protease #31.
PN WO200200860-A2.
PD 03-JAN-2002.
PA (SUGE-) SUGEN INC.
Query Match 43.6%; Score 599.5; DB 5; Length 320;
Best Local Similarity 46.4%; Pred. No. 3.3e-38;
RESULT 766
ID AAE19166 standard; protein; 320 AA.
DE Human protease, PRTS-3 protein.
PN WO200208396-A2.
PD 31-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 43.6%; Score 599.5; DB 5; Length 320;
Best Local Similarity 46.4%; Pred. No. 3.3e-38;
RESULT 767
ID ADI17075 standard; protein; 225 AA.
DE Murine NOVX protein homologue SeqID 611.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 43.6%; Score 599; DB 5; Length 225;
Best Local Similarity 49.8%; Pred. No. 2.5e-38;
RESULT 768
ID AAU93930 standard; protein; 256 AA.
DE Novel human kallikrein KUK15.
PN WO200214485-A2.
PD 21-FEB-2002.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 43.6%; Score 599; DB 5; Length 256;
Best Local Similarity 47.1%; Pred. No. 2.8e-38;
RESULT 769
ID ADN10932 standard; protein; 256 AA.
DE Human kallikrein 15, marker of endocrine cancer.
PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 43.6%; Score 599; DB 8; Length 256;
Best Local Similarity 47.1%; Pred. No. 2.8e-38;
RESULT 770
ID AAB36483 standard; protein; 289 AA.
DE Fusion gene with human serine protease catalytic domain protein #14.
PN WO200066709-A2.
PD 09-NOV-2000.
PA (ORTH) ORTHO-MCNEIL PHARM RES INC.
Query Match 43.6%; Score 598.5; DB 3; Length 289;
Best Local Similarity 49.1%; Pred. No. 3.5e-38;
RESULT 771
ID AAB67543 standard; protein; 289 AA.
DE Amino acid sequence of catalytic domain in PFEK1-6XHIS-TAG.
PN WO200116289-A2.

PD 08-MAR-2001.
PA (ORTH) ORTHO-MCNEIL PHARM INC.
Query Match 43.6%; Score 598.5; DB 4; Length 289;
Best Local Similarity 49.1%; Pred. No. 3.5e-38;
RESULT 772
ID AAE08017 standard; protein; 248 AA.
DE Human F5133 consensus protein sequence.
PN US6232456-B1.
PD 15-MAY-2001.
PA (ABSO) ABBOTT LAB.
Query Match 43.5%; Score 597.5; DB 4; Length 248;
Best Local Similarity 47.8%; Pred. No. 3.6e-38;
RESULT 773
ID AAB11713 standard; protein; 276 AA.
DE Mouse serine protease BSSP6 (mBSSP6) SEQ ID NO:4.
PN WO200031257-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 43.5%; Score 597.5; DB 3; Length 276;
Best Local Similarity 47.0%; Pred. No. 4e-38;
RESULT 774
ID ADC31389 standard; protein; 298 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1471.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSEQ) HYSEQ INC.
Query Match 43.3%; Score 595; DB 7; Length 298;
Best Local Similarity 48.1%; Pred. No. 6.8e-38;
RESULT 775
ID ADI17077 standard; protein; 260 AA.
DE Human NOVX protein homologue SeqID 613.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA) CURAGEN CORP.
Query Match 43.2%; Score 593.5; DB 5; Length 260;
Best Local Similarity 48.6%; Pred. No. 7.7e-38;
RESULT 776
ID AAB21312 standard; protein; 228 AA.
DE Human TLSP.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 43.1%; Score 592; DB 3; Length 228;
Best Local Similarity 49.3%; Pred. No. 8.7e-38;
RESULT 777
ID AAW08475 standard; protein; 247 AA.
DE Porcine trypsinogen.
PN WO9700316-A1.
PD 03-JAN-1997.
PA (NOVO) NOVO-NORDISK AS.
Query Match 41.7%; Score 573; DB 2; Length 247;
Best Local Similarity 45.6%; Pred. No. 2.8e-36;
RESULT 778
ID ABB98258 standard; protein; 247 AA.
DE Pig trypsinogen SEQ ID NO 1.
PN WO200261064-A2.
PD 08-AUG-2002.
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 41.7%; Score 573; DB 5; Length 247;
Best Local Similarity 45.6%; Pred. No. 2.8e-36;
RESULT 779
ID ADJ92132 standard; protein; 247 AA.
DE Pig pro-trypsin.
PN US2004043455-A1.
PD 04-MAR-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match 41.7%; Score 573; DB 8; Length 247;
Best Local Similarity 45.6%; Pred. No. 2.8e-36;
RESULT 780
ID AAB21306 standard; protein; 251 AA.
DE Human KLK-L6 protein #2.
PN WO200053776-A2.

PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.4%; Score 569.5; DB 3; Length 251;
Best Local Similarity 46.9%; Pred. No. 5.2e-36;
RESULT 781
ID ADN10930 standard; protein; 251 AA.
DE Human kallikrein 14, marker of endocrine cancer.
PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.4%; Score 569.5; DB 8; Length 251;
Best Local Similarity 46.9%; Pred. No. 5.2e-36;
RESULT 782
ID ABJ26666 standard; protein; 267 AA.
DE Human protein modification + maintenance molecule protein SEQ ID NO 20.
PN WO200300844-A2.
PD 03-JAN-2003.
PA (INCY) INCYTE GENOMICS INC.
Query Match 41.4%; Score 569.5; DB 6; Length 267;
Best Local Similarity 46.9%; Pred. No. 5.6e-36;
RESULT 783
ID AAB21298 standard; protein; 250 AA.
DE Human KLK-L3 protein #2.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.4%; Score 568.5; DB 3; Length 250;
Best Local Similarity 46.7%; Pred. No. 6.2e-36;
RESULT 784
ID ABP64969 standard; protein; 250 AA.
DE Human protein SEQ ID 629.
PN WO200259260-A2.
PD 01-AUG-2002.
PA (HYSEQ) HYSEQ INC.
Query Match 41.4%; Score 568.5; DB 5; Length 250;
Best Local Similarity 46.7%; Pred. No. 6.2e-36;
RESULT 785
ID ABR55400 standard; protein; 250 AA.
DE Amino acid sequence of human kallikrein 9 (hk9).
PN WO200303731-A2.
PD 24-APR-2003.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.4%; Score 568.5; DB 6; Length 250;
Best Local Similarity 46.7%; Pred. No. 6.2e-36;
RESULT 786
ID ADN05516 standard; protein; 250 AA.
DE Antipsoriatic protein sequence #924.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 41.4%; Score 568.5; DB 8; Length 250;
Best Local Similarity 46.7%; Pred. No. 6.2e-36;
RESULT 787
ID AAB21300 standard; protein; 277 AA.
DE Human KLK-L4 protein #2.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.3%; Score 567; DB 3; Length 277;
Best Local Similarity 46.8%; Pred. No. 9e-36;
RESULT 788
ID ABO00554 standard; protein; 277 AA.
DE Novel human polypeptide #141.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSEQ) HYSEQ INC.
Query Match 41.3%; Score 567; DB 6; Length 277;
Best Local Similarity 46.8%; Pred. No. 9e-36;
RESULT 789
ID ADL71094 standard; protein; 277 AA.
DE Human kallikrein 13 protein SEQ ID NO:1.
PN WO2004021009-A2.
PD 11-MAR-2004.

PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.1%; Score 567; DB 8; Length 277;
Best Local Similarity 46.8%; Pred. No. 9e-36;
RESULT 790
ID ADN04184 standard; protein; 277 AA.
DE Antipeptidic protein sequence #287.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 41.3%; Score 567; DB 8; Length 277;
Best Local Similarity 46.8%; Pred. No. 9e-36;
RESULT 791
ID ADRI4575 standard; protein; 277 AA.
DE Human NF-kappaB pathway-associated protein SeqID576.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 41.3%; Score 567; DB 8; Length 277;
Best Local Similarity 46.8%; Pred. No. 9e-36;
RESULT 792
ID AAU16971 standard; protein; 251 AA.
DE Human novel secreted protein, SEQ ID 212.
PN WO200155441-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.2%; Score 566.5; DB 4; Length 251;
Best Local Similarity 46.9%; Pred. No. 8.9e-36;
RESULT 793
ID AAU23217 standard; protein; 247 AA.
DE Novel human enzyme polypeptide #303.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 4; Length 247;
Best Local Similarity 46.9%; Pred. No. 1.3e-35;
RESULT 794
ID AAY16777 standard; protein; 293 AA.
DE Human keratinocyte derived protease (KDP).
PN WO9918219-A1.
PD 15-APR-1999.
PA (PROCT) PROCTER & GAMBLE CO.
Query Match 41.1%; Score 564.5; DB 2; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 795
ID AAY30524 standard; protein; 293 AA.
DE Human PDSP-1 protein.
PN WO9946391-A2.
PD 16-SEP-1999.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 41.1%; Score 564.5; DB 2; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 796
ID AAY38412 standard; protein; 293 AA.
DE Human secreted protein encoded by gene No. 27.
PN WO9935158-A1.
PD 15-JUL-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 2; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 797
ID AAY38426 standard; protein; 293 AA.
DE Human secreted protein encoded by gene No. 27.
PN WO9935158-A1.
PD 15-JUL-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 2; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 798
ID AAY66726 standard; protein; 293 AA.
DE Membrane-bound protein PRO1132.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 800
ID AAB65249 standard; protein; 293 AA.
DE Human PRO1132 (UNQ570) protein sequence SEQ ID NO:309.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 4; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 801
ID AAU12399 standard; protein; 293 AA.
DE Human PRO1132 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 4; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 802
ID AAU81966 standard; protein; 293 AA.
DE Human PRO1132.
PN WO200109327-A2.
PD 08-FEB-2001.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 5; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 803
ID ABUS8064 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 804
ID ABUS9142 standard; protein; 293 AA.
DE Novel human secreted or transmembrane protein PRO1132.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 805
ID ABUS2654 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 806
ID ABO17843 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003032156-A1.
PD 13-FEB-2003.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 807
ID ADA57425 standard; protein; 293 AA.
DE Human secreted protein #257.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 808

ID ADA56974 standard; protein; 293 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 809
ID ADA57427 standard; protein; 293 AA.
DE Human secreted protein #257.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 810
ID ADA57428 standard; protein; 293 AA.
DE Human secreted protein #257.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 811
ID ABU60573 standard; protein; 293 AA.
DE Human secreted/transmembrane protein, #130.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 812
ID ABU13955 standard; protein; 293 AA.
DE Human PRO1132 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 813
ID ABU81097 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 814
ID ABU72540 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 815
ID ABU66797 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 816
ID ADA41303 standard; protein; 293 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
ID ADA41305 standard; protein; 293 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
ID ADA40825 standard; protein; 293 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 819
ID ADA41306 standard; protein; 293 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 820
ID ABU59878 standard; protein; 293 AA.
DE Novel secreted and transmembrane protein PRO1132.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 821
ID ABU59289 standard; protein; 293 AA.
DE Human secreted/transmembrane protein, #130.
PN US2003027162-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 822
ID ABO25986 standard; protein; 293 AA.
DE Human PRO1132 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 823
ID ABO25068 standard; protein; 293 AA.
DE Human secreted/transmembrane protein (PRO) #228.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 824
ID ABUS8995 standard; protein; 293 AA.
DE Human secreted/transmembrane protein, #130.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 825
ID ABU92373 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 826
ID ABUS9438 standard; protein; 293 AA.
DE Novel human secreted or transmembrane protein PRO1346.
PN US2003027985-A1.
PD 06-FEB-2003.

Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 827
ID ABUG7073 standard; protein; 293 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 456.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 828
ID ABUG2204 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 829
ID ABU10910 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 830
ID ABU81662 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 831
ID ABU88601 standard; protein; 293 AA.
DE Human secreted and transmembrane polypeptide PRO1132.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 832
ID ABO34115 standard; protein; 293 AA.
DE Human PRO1132 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 833
ID ADA45975 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003023328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 834
ID ADA76406 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 835
ID ADA19056 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 836
ID ADA67629 standard; protein; 293 AA.
DE Human PRO polypeptide #228.

ID ADA61679 standard; protein; 293 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 837
ID ADB19464 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 838
ID ADB28005 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 839
ID ADA86484 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 840
ID ADB16048 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 841
ID ADA37820 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003082937-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 842
ID ADA47834 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 843
ID ADA21506 standard; protein; 293 AA.
DE Human secreted/transmembrane polypeptide PRO1132.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 844
ID ADA10293 standard; protein; 293 AA.
DE Human secreted/transmembrane protein, PRO1132.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 6; Length 293;
RESULT 845
ID ADA67629 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003068795-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 846
ID ADB30636 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 847
ID ADA85932 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 848
ID ADA17837 standard; protein; 293 AA.
DE Human PRO1132 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 849
ID ADA97144 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 850
ID ADA79448 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 851
ID ADA87587 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 852
ID ADB16789 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 853
ID ADA27945 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 854
ID ADA91881 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 855
ID ADB14944 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 856
ID ADB18905 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 857
ID ADA94120 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 858
ID ADB20016 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 859
ID ADB13328 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 860
ID ABO43376 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 861
ID ADA94525 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 862
ID ADA74582 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 863
ID ADB24815 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 864
ID ADB24815 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;

ID ADA82339 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 865
ID ADA75302 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 866
ID ADA85380 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 867
ID ADA84828 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 868
ID ADB30084 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 869
ID ADA80612 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 870
ID ADA75854 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 871
ID ADA38750 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 872
ID ADA47079 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 873
ID ADB25375 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.

PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 874
ID ADA33551 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 875
ID ADB26901 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 876
ID ADB31188 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 877
ID ADA92871 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 878
ID ADA61116 standard; protein; 293 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 879
ID ADB24263 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 880
ID ADA96592 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 881
ID ADA81164 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 882
ID ADA96040 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082759-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 893
ID ADB26349 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 894
ID ADB21834 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 895
ID ADA77613 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 896
ID ADB18353 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US200307710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 897
ID ADA87036 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 898
ID ADA98139 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 899
ID ADA46527 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 900
ID ADB28557 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 901
ID ADB29109 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 892
ID ABO53201 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 893
ID ADA77061 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 894
ID ADA22432 standard; protein; 293 AA.
DE Human secreted/transmembrane polypeptide PRO1132.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 895
ID ADA88691 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 896
ID ADA37696 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 897
ID ADB27453 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 898
ID ADB22386 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 899
ID ABO22571 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 900
ID ADA06598 standard; protein; 293 AA.
DE Human secreted/transmembrane PRO polypeptide #96.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 901
ID ADA39291 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003059782-A1.
PD 27-MAR-2003.

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Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 902
ID ADA67077 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 903
ID ADB22938 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 904
ID ADB23711 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 905
ID ADA92433 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 906
ID ADB15496 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 907
ID ADB38748 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 908
ID ADB96317 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 909
ID ADB38196 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 910
ID ADB66668 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 911
ID ADB89748 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 912
ID ADB30480 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 913
ID ADB80490 standard; protein; 293 AA.
DE Ovarian cancer-associated protein #27.
PN WO2002102335-A2.
PD 27-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 914
ID ADB39581 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 915
ID ADB47204 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 916
ID ADB86811 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 917
ID ADB77416 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 918
ID ADB34573 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 919
ID ADB35677 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 920
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ID ADB34021 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 921
ID ADB35125 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 922
ID ADB36229 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 923
ID ADB46624 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 924
ID ADC57789 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 925
ID ADC55153 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 926
ID ADC12020 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 927
ID ADC56442 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 928
ID ADC07497 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 929
ID ADC11487 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 930
ID ADC50497 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 931
ID ADC72044 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 932
ID ADC60023 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 933
ID ADC53030 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 934
ID ADC57384 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 935
ID ADC60575 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 936
ID ADC51050 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 937
ID ADC65577 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 938
ID ADC34675 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 939

ID ADC53636 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 940
ID ADC59159 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 941
ID ADC56037 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 942
ID ADC5607 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 943
ID ADC14609 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 944
ID ADD08141 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 945
ID ADD03281 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 946
ID ADC90273 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 947
ID ADC81966 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 948
ID ADC69692 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194770-A1.
PD 16-OCT-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 949
ID ADC48581 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 950
ID ADD10110 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 951
ID ADD07608 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 952
ID ADD04685 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 953
ID ADC82499 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 954
ID ADC80641 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 955
ID ADD11148 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 956
ID ADC48029 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 957
ID ADD08679 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;

RESULT 958
ID ADC80089 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 959
ID ADD06928 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 960
ID ADD09558 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 961
ID ADC83175 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 962
ID ADD41271 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 963
ID ADD52410 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 964
ID ADD53150 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 965
ID ADD53702 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 966
ID ADD55282 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 967
ID ADD56240 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003087304-A1.
PD 08-MAY-2003.

PN US2003077594-A1.
PD 24-APR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 968
ID ADD51858 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 969
ID ADD02657 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 970
ID ADD02091 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 971
ID ADD54273 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 972
ID ADD54678 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 973
ID ADD92590 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 974
ID ADD91486 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 975
ID ADE04100 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 976
ID ADE26832 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087304-A1.
PD 08-MAY-2003.

Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 977
ID ADE32397 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 978
ID ADE22329 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 979
ID ADD79553 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 980
ID ADE42089 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 981
ID ADE17906 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 982
ID ADD92038 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 983
ID ADE33501 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 984
ID ADE34053 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 985
ID ADD80105 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;

Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 986
ID ADD93142 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 987
ID ADE19562 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 988
ID ADE19010 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 989
ID ADE43206 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 990
ID ADD95995 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 991
ID ADE22881 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 992
ID ADD78999 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 993
ID ADE26299 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 994
ID ADE32949 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 995

ID ADE42641 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 996
ID AD80657 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 997
ID AD89685 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 998
ID ADE4069 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 999
ID ADE04768 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1000
ID ADE2897 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1001
ID ADF67236 standard; protein; 293 AA.
DE Human PRO1132 amino acid sequence SEQ ID NO:309.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1002
ID ADG21606 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1003
ID ADG23247 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1004
ID ADF97582 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207388-A1.

DE Human PRO polypeptide #228.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1005
ID ADG80646 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1006
ID ADG80094 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1007
ID ADH55386 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1008
ID ADH55938 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1009
ID ADI35490 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1010
ID ADI64157 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1011
ID ADI65106 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1012
ID ADI63605 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1013
ID ADH82019 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207388-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1014
ID ADH99982 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1015
ID ADH81467 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1016
ID ADM82636 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1017
ID ADN16035 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1018
ID ADN16664 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1019
ID ADN39198 standard; protein; 293 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:516.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOBB-) EOS BIOTECHNOLOGY INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1020
ID ADN15483 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1021
ID ADN14931 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1022
ID ADC81193 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1023
ID ADD76641 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1024
ID ADD88005 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1025
ID ADD86409 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1026
ID ADE75857 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1027
ID ADE23433 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1028
ID ADE23985 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1029
ID ADE24628 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1030
ID ADD87453 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1031
ID ADE89319 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;

Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1032
ID ADE18458 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1033
ID ADE88767 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1034
ID ADE94787 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1035
ID ADE91198 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1036
ID ADF35435 standard; protein; 293 AA.
DE Human PRO1132 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1037
ID ADE95339 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1038
ID ADE93449 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1039
ID ADF35030 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1040
ID ADE92345 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1041

ID ADE90646 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1042
ID ADE91793 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1043
ID ADG11685 standard; protein; 293 AA.
DE Human PRO1132 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1044
ID ADG02372 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1045
ID ADG22158 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1046
ID ADG20228 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1047
ID ADF98134 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1048
ID ADG24351 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1049
ID ADF98705 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1050
ID ADG03536 standard; protein; 293 AA.

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DE Human PRO polypeptide #228.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1051
ID ADF99257 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1052
ID ADG16842 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1053
ID ADG05301 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1054
ID ADG19568 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1055
ID ADG13405 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1056
ID ADG08462 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1057
ID ADG15632 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1058
ID ADF97030 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1059
ID ADG06215 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207358-A1.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1060
ID ADG23799 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1061
ID ADG04088 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1062
ID ADG24989 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1063
ID ADG07286 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1064
ID ADG07838 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1065
ID ADG55333 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1066
ID ADG60997 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1067
ID ADG62101 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1068
ID ADG82302 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207358-A1.
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PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1078
ID ADH19555 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1079
ID ADH30712 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1080
ID ADH12079 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1081
ID ADG52501 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1082
ID ADG54229 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1083
ID ADG81198 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1084
ID ADG56437 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1085
ID ADH12703 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1086
ID ADH21048 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1076
ID ADG71563 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1075
ID ADG53677 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1074
ID ADG58093 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1073
ID ADG71011 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1072
ID ADG58645 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1071
ID ADG55885 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1070
ID ADG56989 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1069
ID ADG57541 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1068
ID ADH19555 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1067
ID ADG81750 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207805-A1.
PD 06-NOV-2003.

RESULT 1087
ID ADG61549 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1088
ID ADH20088 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1089
ID ADH28636 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1090
ID ADG54781 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1091
ID ADG59821 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1092
ID ADI81245 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1093
ID ADG09988 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1094
ID ADI15459 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1095
ID ADG09336 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1096
ID ADI14791 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1097
ID ADI18386 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1098
ID ADJ63667 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1099
ID ADJ77562 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1100
ID ADJ65684 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1101
ID ADM27820 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1102
ID ADK52481 standard; protein; 293 AA.
DE Human kallikrein 5 protein.
PN WO2004021008-A2.
PD 11-MAR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
PA (YOUS/) YOUSEF G.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1103
ID ADM42544 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1104
ID ADM28406 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1105

ID ADI95888 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1106
ID ADI96440 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US200307354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1107
ID ADR72621 standard; protein; 293 AA.
DE Human renal cell carcinoma-related kallikrein 5 (hk5) protein.
PN WO2004077060-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1108
ID ADR72873 standard; protein; 293 AA.
DE Human ovarian cancer-related tumour marker kallikrein 5 (hk5) protein.
PN WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1109
ID AAY14072 standard; protein; 322 AA.
DE Human BS247 specific epitope.
PN WO9922027-A1.
PD 06-MAY-1999.
PA (ABBOT) ABBOTT LAB.
Query Match 41.1%; Score 564.5; DB 2; Length 322;
Best Local Similarity 45.3%; Pred. No. 1.6e-35;
RESULT 1110
ID AAW07620 standard; protein; 276 AA.
DE Human NES1 polypeptide.
PN WO9639175-A1.
PD 12-DEC-1996.
PA (NEVE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
Query Match 41.0%; Score 564; DB 2; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1111
ID AAB21327 standard; protein; 276 AA.
DE Human NES1.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.0%; Score 564; DB 3; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1112
ID ABG96356 standard; protein; 276 AA.
DE Human ovarian cancer marker OV32.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.0%; Score 564; DB 5; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1113
ID AAU82729 standard; protein; 276 AA.
DE Amino acid sequence of novel human protease #28.
PN WO200200860-A2.
PD 03-JAN-2002.
PA (SUGR-) SUGEN INC.
Query Match 41.0%; Score 564; DB 5; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1114
ID ADB80527 standard; protein; 276 AA.

DE Ovarian cancer-associated protein #46.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 41.0%; Score 564; DB 7; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1115
ID ADE40473 standard; protein; 276 AA.
DE Human kallikrein 10 (gene ID 2045) protein.
PN WO2003070883-A2.
PD 28-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.0%; Score 564; DB 7; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1116
ID ADN39880 standard; protein; 276 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C250.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 41.0%; Score 564; DB 7; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1117
ID ADN04446 standard; protein; 276 AA.
DE Antipsoriatic protein sequence #416.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 41.0%; Score 564; DB 8; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1118
ID ADQ9070 standard; protein; 276 AA.
DE Human urological disorder related protein 2045 SEQ:22.
PN WO2004065576-A2.
PD 05-AUG-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.0%; Score 564; DB 8; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1119
ID ADR72628 standard; protein; 276 AA.
DE Human renal cell carcinoma-related kallikrein 10 (hk10) protein.
PN WO2004077060-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.0%; Score 564; DB 8; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1120
ID ADR72886 standard; protein; 276 AA.
DE Human ovarian cancer-related tumour marker kallikrein 10 (hk10) protein.
PN WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.0%; Score 564; DB 8; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1121
ID AAB21305 standard; protein; 237 AA.
DE Human KIK-L6 protein #1.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.9%; Score 562; DB 3; Length 237;
Best Local Similarity 48.1%; Pred. No. 1.9e-35;
RESULT 1122
ID AAB21299 standard; protein; 256 AA.
DE Human KIK-L4 protein #1.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.9%; Score 561.5; DB 3; Length 256;
Best Local Similarity 49.1%; Pred. No. 2.2e-35;
RESULT 1123
ID AAB21309 standard; protein; 287 AA.
DE Human KIK-L2.

PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.9%; Score 561.5; DB 3; Length 287;
Best Local Similarity 46.1%; Pred. No. 2.5e-35;
RESULT 1124
ID ABB98259 standard; protein; 228 AA.
DE Synthetic shortened trypsinogen SEQ ID NO 23.
PN WO200261064-A2.
PD 08-AUG-2002.
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 40.8%; Score 561; DB 5; Length 228;
Best Local Similarity 46.7%; Pred. No. 2.1e-35;
RESULT 1125
ID AAB21310 standard; protein; 239 AA.
DE Human zyme.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.8%; Score 561; DB 3; Length 239;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1126
ID AAR44532 standard; protein; 244 AA.
DE Zyme APP-cleaving protease.
PN EP576152-A1.
PD 29-DEC-1993.
PA (ELIL) LILLY & CO ELI.
Query Match 40.8%; Score 561; DB 2; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1127
ID AAW22985 standard; protein; 244 AA.
DE Human serine protease 59 (SP59).
PN JP09149790-A.
PD 10-JUN-1997.
PA (SUNR) SUNTORY LTD.
Query Match 40.8%; Score 561; DB 2; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1128
ID AAW51006 standard; protein; 244 AA.
DE Protease M, a novel serine protease.
PN WO9811238-A2.
PD 19-MAR-1998.
PA (DAND) DANA FARRER CANCER INST INC.
Query Match 40.8%; Score 561; DB 2; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1129
ID AAB21323 standard; protein; 244 AA.
DE Human zyme.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.8%; Score 561; DB 3; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1130
ID AAE37572 standard; protein; 244 AA.
DE Human 2047 protein.
PN WO2003037258-A2.
PD 08-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 40.8%; Score 561; DB 6; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1131
ID ADB80567 standard; protein; 244 AA.
DE Ovarian cancer-associated protein #66.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 40.8%; Score 561; DB 7; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1132
ID ADN39212 standard; protein; 244 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:530.

PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 40.8%; Score 561; DB 7; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1133
ID ADN04074 standard; protein; 244 AA.
DE Antipsoriatic protein sequence #232.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 40.8%; Score 561; DB 8; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1134
ID ADN29289 standard; protein; 244 AA.
DE Human kallikrein 6 associated protein.
PN US2004097452-A1.
PD 20-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 40.8%; Score 561; DB 8; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1135
ID ADQ89076 standard; protein; 244 AA.
DE Human urological disorder related protein 2047 SEQ:28.
PN WO2004065576-A2.
PD 05-AUG-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 40.8%; Score 561; DB 8; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1136
ID ADR72624 standard; protein; 244 AA.
DE Human renal cell carcinoma-related kallikrein 6 (hk6) protein.
PN WO2004077060-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.8%; Score 561; DB 8; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1137
ID ADR72876 standard; protein; 244 AA.
DE Human ovarian cancer-related tumour marker kallikrein 6 (hk6) protein.
PN WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.8%; Score 561; DB 8; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1138
ID ABG96357 standard; protein; 244 AA.
DE Human ovarian cancer marker OV33.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 40.8%; Score 560; DB 5; Length 244;
Best Local Similarity 46.9%; Pred. No. 2.7e-35;
RESULT 1139
ID AAB21297 standard; protein; 296 AA.
DE Human KIK-L3 protein #1.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.5%; Score 557; DB 3; Length 296;
Best Local Similarity 46.1%; Pred. No. 5.7e-35;
RESULT 1140
ID AAR67888 standard; protein; 253 AA.
DE Human stratum corneum chymotrophic recombinant enzyme (SCCE).
PN WO9500851-A1.
PD 05-JAN-1995.
PA (SYMB-) SYMBICOM AB.
Query Match 40.4%; Score 555; DB 2; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1141
ID AAW05383 standard; protein; 253 AA.
DE Human amyloid precursor protein protease.
PN WO9631122-A1.

PD 10-OCT-1996.
PA (ELIL) LILLY & CO ELI.
Query Match 40.4%; Score 555; DB 2; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1142
ID ABB84421 standard; peptide; 253 AA.
DE Human SCCE protein N-terminal fragment SEQ ID 48.
PD 15-AUG-2002.
PA (EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
Query Match 40.4%; Score 555; DB 5; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1143
ID ABB84406 standard; protein; 253 AA.
DE Human SCCE protein.
PD WO200262135-A2.
PD 15-AUG-2002.
PA (EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
Query Match 40.4%; Score 555; DB 5; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1144
ID ABB84406 standard; protein; 253 AA.
DE Amino acid sequence of novel human protease #39.
PD 03-JAN-2002.
PA (SUGE-) SUGEN INC.
Query Match 40.4%; Score 555; DB 5; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1145
ID ABU07440 standard; protein; 253 AA.
DE Protein differentially regulated in prostate cancer #43.
PD WO200281638-A2.
PD 17-OCT-2002.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 40.4%; Score 555; DB 6; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1146
ID ABU07471 standard; protein; 253 AA.
DE Protein differentially regulated in prostate cancer #74.
PD WO200281638-A2.
PD 17-OCT-2002.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 40.4%; Score 555; DB 6; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1147
ID ABR58471 standard; protein; 253 AA.
DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
PD WO2003029468-A1.
PD 10-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 40.4%; Score 555; DB 6; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1148
ID ADB80484 standard; protein; 253 AA.
DE Ovarian cancer-associated protein #24.
PD WO2002102235-A2.
PD 27-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 40.4%; Score 555; DB 7; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1149
ID ADJ68833 standard; protein; 253 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID639.
PD WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 40.4%; Score 555; DB 7; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1150
ID ADN39180 standard; protein; 253 AA.

DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:498.
PD WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 40.4%; Score 555; DB 7; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1151
ID ADL06515 standard; protein; 253 AA.
DE Human tumour-associated antigenic target (TAT) polypeptide #14.
PD WO2004016225-A2.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 40.4%; Score 555; DB 8; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1152
ID ADN04182 standard; protein; 253 AA.
DE Antipsoriatic protein sequence #286.
PD WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 40.4%; Score 555; DB 8; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1153
ID ADR72880 standard; protein; 253 AA.
DE Human ovarian cancer-related tumour marker kallikrein 7 (hk7) protein.
PD WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.4%; Score 555; DB 8; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1154
ID ADA05734 standard; protein; 252 AA.
DE Human NOV18b protein SEQ ID NO:94.
PD WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 40.3%; Score 553.5; DB 6; Length 252;
Best Local Similarity 46.6%; Pred. No. 9e-35;
RESULT 1155
ID ADN62898 standard; protein; 252 AA.
DE Human NOV18b.
PD US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KERUDA R.
PA (JUJ/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIP/) DIPIPPO V A.

PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 40.3%; Score 553.5; DB 8; Length 252;
Best Local Similarity 46.8%; Pred. No. 9e-35;
RESULT 1156
ID AAY08025 standard; protein; 253 AA.
DE Mouse protease-related protein (PVP).
PN DE19736198-CL.
PD 24-DEC-1998.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
Query Match 40.3%; Score 553.5; DB 2; Length 253;
Best Local Similarity 43.5%; Pred. No. 9e-35;
RESULT 1157
ID ADN62896 standard; protein; 250 AA.
DE Human NOV18a.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUUG/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGE E M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 40.2%; Score 553; DB 8; Length 250;
Best Local Similarity 44.8%; Pred. No. 9.8e-35;
RESULT 1158
ID AAY77494 standard; protein; 229 AA.
DE Bovine trypsinogen.
PN WO200005384-A1.
PD 03-FEB-2000.
PA (PROD-) PRODIGENE INC.
Query Match 40.2%; Score 552; DB 3; Length 229;
Best Local Similarity 46.3%; Pred. No. 1.1e-34;
RESULT 1159
ID AAR53638 standard; protein; 230 AA.
DE Bovine trypsinogen.
PN EP597681-A1.
PD 18-MAY-1994.
PA (ELIL/) LILLY & CO ELI.
Query Match 40.2%; Score 552; DB 2; Length 230;
Best Local Similarity 47.5%; Pred. No. 1.1e-34;
RESULT 1160
ID AAY91926 standard; protein; 231 AA.
DE Recombinant trypsin.
PN WO200017332-A1.
PD 30-MAR-2000.
PA (ELIL/) LILLY & CO ELI.
Query Match 40.2%; Score 552; DB 3; Length 231;
Best Local Similarity 46.3%; Pred. No. 1.1e-34;
RESULT 1161
ID AAB80953 standard; protein; 231 AA.
DE Bovine met-phe-trypsinogen.
PN WO200119970-A2.
PD 22-MAR-2001.
PA (ELIL/) LILLY & CO ELI.
Query Match 40.2%; Score 552; DB 4; Length 231;
Best Local Similarity 46.3%; Pred. No. 1.1e-34;
RESULT 1162
ID ADA05732 standard; protein; 250 AA.
DE Human NOV18a protein SEQ ID NO:92.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 40.2%; Score 552; DB 6; Length 250;
Best Local Similarity 44.8%; Pred. No. 1.2e-34;
RESULT 1163
ID ABB84420 standard; peptide; 249 AA.
DE Porcine SCCE protein N-terminal fragment SEQ ID 47.
PN WO200262135-A2.
PD 15-AUG-2002.
PA (EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
Query Match 40.1%; Score 550.5; DB 5; Length 249;
Best Local Similarity 46.7%; Pred. No. 1.5e-34;
RESULT 1164
ID AAB35701 standard; protein; 247 AA.
DE Human trypsin hL amino acid sequence.
PN JP2000253887-A.
PD 19-SEP-2000.
PA (TTPH-) TT PHARMA KK.
Query Match 40.0%; Score 549.5; DB 3; Length 247;
Best Local Similarity 44.0%; Pred. No. 1.8e-34;
RESULT 1165
ID AAU86677 standard; protein; 247 AA.
DE Novel human connective tissue related polypeptide #243.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 547.5; DB 4; Length 247;
Best Local Similarity 46.1%; Pred. No. 2.6e-34;
RESULT 1166
ID AAU23752 standard; protein; 247 AA.
DE Novel human enzyme polypeptide #838.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 547.5; DB 4; Length 247;
Best Local Similarity 46.1%; Pred. No. 2.6e-34;
RESULT 1167
ID AAU17043 standard; protein; 247 AA.
DE Human novel secreted protein, SEQ ID 284.
PN WO200155441-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 547.5; DB 4; Length 247;
Best Local Similarity 46.1%; Pred. No. 2.6e-34;
RESULT 1168
ID ADB60011 standard; protein; 247 AA.
DE Connective tissue antigen (CTA) #243.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 547.5; DB 7; Length 247;
Best Local Similarity 46.1%; Pred. No. 2.6e-34;
RESULT 1169
ID AAW81767 standard; peptide; 223 AA.

DE Bovine TRYP peptide fragment.
PN JP10287696-A.
PD 27-OCT-1998.
PA (IYAK-) IYAKU BUNSHI SEKKEI KENKYUSHO KK.
Query Match 39.8%; Score 547; DB 2; Length 223;
Best Local Similarity 46.1%; Pred. No. 2.5e-34;
RESULT 1170
ID AAY69973 standard; protein; 223 AA.
DE TRYP protein.
PN WO9962004-A1.
PD 02-DEC-1999.
PA (MEDI-) INST MEDICINAL MOLECULAR DESIGN INC.
Query Match 39.8%; Score 547; DB 3; Length 223;
Best Local Similarity 46.1%; Pred. No. 2.5e-34;
RESULT 1171
ID ABG31841 standard; protein; 223 AA.
DE Example protein #3 used in three-dimensional structure analysis method.
PN WO200257954-A1.
PD 25-JUL-2002.
PA (MITU) MITSUBISHI CHEM CORP.
PA (UMEY/) UMEYAMA H.
Query Match 39.8%; Score 547; DB 5; Length 223;
Best Local Similarity 46.1%; Pred. No. 2.5e-34;
RESULT 1172
ID ADC73287 standard; protein; 223 AA.
DE Bovine 2PTC E protein - SEQ ID 13.
PN WO2003060765-A1.
PD 24-JUL-2003.
PA (AJIN) AJINOMOTO CO INC.
PA (UMEY/) UMEYAMA H.
Query Match 39.8%; Score 547; DB 7; Length 223;
Best Local Similarity 46.1%; Pred. No. 2.5e-34;
RESULT 1173
ID ADD5545 standard; protein; 223 AA.
DE Cationic bovine trypsinogen TRY1.
PN WO2003040093-A2.
PD 15-MAY-2003.
PA (FARB) BAYER AG.
Query Match 39.8%; Score 547; DB 7; Length 223;
Best Local Similarity 46.1%; Pred. No. 2.5e-34;
RESULT 1174
ID AAR53637 standard; protein; 224 AA.
DE Bovine trypsin.
PN EP597681-A1.
PD 18-MAY-1994.
PA (LILLY) LILLY & CO ELI.
Query Match 39.8%; Score 547; DB 2; Length 224;
Best Local Similarity 46.1%; Pred. No. 2.5e-34;
RESULT 1175
ID AAY91925 standard; protein; 233 AA.
DE Trypsinogen analogue.
PN WO200017332-A1.
PD 30-MAR-2000.
PA (LILLY) LILLY & CO ELI.
Query Match 39.8%; Score 547; DB 3; Length 233;
Best Local Similarity 46.1%; Pred. No. 2.6e-34;
RESULT 1176
ID ADI39734 standard; protein; 244 AA.
DE Human protease M (proM) protein.
PN US6642013-B1.
PD 04-NOV-2003.
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.
Query Match 39.7%; Score 546; DB 8; Length 244;
Best Local Similarity 45.8%; Pred. No. 3.3e-34;
RESULT 1177
ID ADI37158 standard; protein; 244 AA.
DE Human protease m (Protm).
PN US2003199010-A1.
PD 23-OCT-2003.
PA (UYAR-) UNIV ARKANSAS
Query Match 39.7%; Score 546; DB 8; Length 244;
Best Local Similarity 45.8%; Pred. No. 3.3e-34;
RESULT 1178
ID AAY78974 standard; protein; 247 AA.
DE Canine cationic trypsinogen amino acid sequence.
PN WO200009739-A1.
PD 24-FEB-2000.
PA (FUJY) FUJY YAKUHIIN KOGYO KK.
Query Match 39.7%; Score 546; DB 3; Length 247;
Best Local Similarity 45.6%; Pred. No. 3.3e-34;
RESULT 1179
ID ADA05742 standard; protein; 247 AA.
DE Human NOV18f protein SEQ ID NO:102.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 39.7%; Score 546; DB 6; Length 247;
Best Local Similarity 45.5%; Pred. No. 3.3e-34;
RESULT 1180
ID ADN62906 standard; protein; 247 AA.
DE Human NOV18f.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJY/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 39.7%; Score 546; DB 8; Length 247;
Best Local Similarity 45.5%; Pred. No. 3.3e-34;
RESULT 1181
ID AAB98502 standard; protein; 225 AA.
DE Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.
PN WO200129056-A1.
PD 26-APR-2001.
PA (UYAR-) UNIV ARKANSAS.
Query Match 39.7%; Score 545; DB 4; Length 225;
Best Local Similarity 46.5%; Pred. No. 3.6e-34;
RESULT 1182
ID AAY78975 standard; protein; 246 AA.
DE Canine anionic trypsinogen amino acid sequence.
PN WO200009739-A1.
PD 24-FEB-2000.
PA (FUJY) FUJY YAKUHIIN KOGYO KK.
Query Match 39.7%; Score 545; DB 3; Length 246;
Best Local Similarity 44.2%; Pred. No. 4e-34;
RESULT 1183

ID AAB21326 standard; protein; 257 AA.
DE Human HSCBE.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 39.6%; Score 544; DB 3; Length 257;
Best Local Similarity 44.1%; Pred. No. 5e-34;
RESULT 1184
ID AAW64260 standard; protein; 246 AA.
DE Human amyloid beta-protein precursor inhibitor.
PN WO9824886-A1.
PD 11-JUN-1998.
PA (BGMH) BRIGHAM & WOMENS HOSPITAL.
Query Match 39.5%; Score 543; DB 2; Length 246;
Best Local Similarity 44.5%; Pred. No. 5.7e-34;
RESULT 1185
ID ADC73299 standard; protein; 220 AA.
DE Stereostereorelated 2PTC_E protein.
PN WO2003060765-A1.
PD 24-JUL-2003.
PA (AJIN) AJINOMOTO CO INC.
PA (UMEY/) UMEYAMA H.
Query Match 39.4%; Score 541; DB 7; Length 220;
Best Local Similarity 46.8%; Pred. No. 7.2e-34;
RESULT 1186
ID ADC73301 standard; protein; 279 AA.
DE Stereostereorelated 2PTC protein.
PN WO2003060765-A1.
PD 24-JUL-2003.
PA (AJIN) AJINOMOTO CO INC.
PA (UMEY/) UMEYAMA H.
Query Match 39.4%; Score 541; DB 7; Length 279;
Best Local Similarity 46.8%; Pred. No. 9.2e-34;
RESULT 1187
ID ADI16686 standard; protein; 259 AA.
DE Human NOVX protein to treat human pathological conditions SeqID222.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 39.3%; Score 539.5; DB 5; Length 259;
Best Local Similarity 44.4%; Pred. No. 1.1e-33;
RESULT 1188
ID ADN42340 standard; protein; 259 AA.
DE Human novel proteinNOV 62.
PN US2004033493-A1.
PD 19-FEB-2004.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (GANG/) GANGOLLI E A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELLI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUF/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENA C E A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
Query Match 39.3%; Score 539.5; DB 8; Length 259;
Best Local Similarity 44.4%; Pred. No. 1.1e-33;
RESULT 1189
ID ABB78122 standard; peptide; 223 AA.
DE Amino acid sequence of trypsin.
PN US2002072863-A1.
PD 13-JUN-2002.
PA (FUITSU) FUJITSU LTD.
Query Match 39.2%; Score 538; DB 5; Length 223;
Best Local Similarity 45.6%; Pred. No. 1.2e-33;
RESULT 1190
ID ABB83322 standard; protein; 223 AA.
DE Partial trypsin sequence.
PN US2002035434-A1.
PD 21-MAR-2002.
PA (FUITSU) FUJITSU LTD.
Query Match 39.2%; Score 538; DB 5; Length 223;
Best Local Similarity 45.6%; Pred. No. 1.2e-33;
RESULT 1191
ID ABB84419 standard; peptide; 243 AA.
DE Bovine SCCE protein N-terminal fragment SEQ ID 46.
PN WO200262135-A2.
PD 15-AUG-2002.
PA (EGEL/) EGELRUUD T.
PA (HANS/) HANSSON L.
Query Match 38.7%; Score 531.5; DB 5; Length 243;
Best Local Similarity 43.8%; Pred. No. 4.3e-33;
RESULT 1192
ID ABB04644 standard; protein; 240 AA.
DE Engraulis japonicus trypsinogen (atry I) SEQ ID NO:1.
PN JP2001269173-A.
PD 02-OCT-2001.
PA (NISE) JAPAN TOBACCO INC.
Query Match 38.2%; Score 525; DB 5; Length 240;
Best Local Similarity 45.7%; Pred. No. 1.3e-32;
RESULT 1193
ID AAW64261 standard; protein; 232 AA.
DE Kallikrein substrate binding site.
PN WO9824886-A1.
PD 11-JUN-1998.
PA (BGMH) BRIGHAM & WOMENS HOSPITAL.
Query Match 38.1%; Score 524; DB 2; Length 232;
Best Local Similarity 43.6%; Pred. No. 1.6e-32;
RESULT 1194
ID ABB84423 standard; peptide; 249 AA.
DE Murine SCCE protein N-terminal fragment SEQ ID 50.
PN WO200262135-A2.
PD 15-AUG-2002.
PA (EGEL/) EGELRUUD T.
PA (HANS/) HANSSON L.
Query Match 38.0%; Score 521.5; DB 5; Length 249;
Best Local Similarity 43.0%; Pred. No. 2.6e-32;
RESULT 1195
ID ABR96164 standard; protein; 261 AA.
DE Human NOV13a protein SEQ ID NO:70.
PN WO200290568-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 37.8%; Score 519.5; DB 6; Length 261;
Best Local Similarity 40.0%; Pred. No. 3.9e-32;
RESULT 1196
ID ADL15205 standard; protein; 232 AA.
DE Pancreatic kallikrein #1.
PN CN1384199-A.
PD 11-DEC-2002.
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.
Query Match 37.8%; Score 519; DB 7; Length 232;
Best Local Similarity 44.5%; Pred. No. 3.8e-32;
RESULT 1197
ID ABG70276 standard; protein; 247 AA.
DE Human Serine Protease TLSP-like protein.
PN WO200255702-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 37.6%; Score 516; DB 5; Length 247;
Best Local Similarity 42.5%; Pred. No. 6.9e-32;
RESULT 1198

ID AAW94493 standard; protein; 268 AA.
DE Human kallikrein.
PN WO9842849-A1.
PD 01-OCT-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match 37.4%; Score 514; DB 2; Length 268;
Best Local Similarity 46.4%; Pred. No. 1.1e-31;
RESULT 1199
ID ABB04645 standard; protein; 241 AA.
DE Engraulis japonicus trypsinogen (aTry II) SEQ ID NO:2.
PN JP2001269173-A.
PD 02-OCT-2001.
PA (NISE) JAPAN TOBACCO INC.
Query Match 36.7%; Score 504; DB 5; Length 241;
Best Local Similarity 45.9%; Pred. No. 5.6e-31;
RESULT 1200
ID AAU87693 standard; protein; 247 AA.
DE Human pancreatic tumour protein #5.
PN WO200212331-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 36.5%; Score 501; DB 5; Length 247;
Best Local Similarity 43.3%; Pred. No. 9.8e-31;
RESULT 1201
ID ADN04140 standard; protein; 247 AA.
DE Antipsoriatic protein sequence #265.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 36.5%; Score 501; DB 8; Length 247;
Best Local Similarity 43.3%; Pred. No. 9.8e-31;
RESULT 1202
ID ADN99594 standard; protein; 247 AA.
DE Novel human protein sequence #410.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 36.5%; Score 501; DB 8; Length 247;
Best Local Similarity 43.3%; Pred. No. 9.8e-31;
RESULT 1203
ID ADQ30589 standard; protein; 247 AA.
DE Pancreas cancer marker - trypsin II precursor.
PN WO200405519-A2.
PD 01-JUL-2004.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.
Query Match 36.5%; Score 501; DB 8; Length 247;
Best Local Similarity 43.3%; Pred. No. 9.8e-31;
RESULT 1204
ID ABR41530 standard; protein; 261 AA.
DE Human DITP protein modification/maintenance protein.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 36.5%; Score 501; DB 6; Length 261;
Best Local Similarity 43.3%; Pred. No. 1e-30;
RESULT 1205
ID AAB03862 standard; protein; 223 AA.
DE Human neurosin amino acid sequence.
PN WO200031284-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 36.4%; Score 500; DB 3; Length 223;
Best Local Similarity 43.5%; Pred. No. 1.1e-30;
RESULT 1206
ID AAB21294 standard; protein; 254 AA.
DE Human KIK-L1 protein #2.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 36.2%; Score 498; DB 3; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1207
ID AAM01174 standard; protein; 254 AA.
DE Human prostate-specific amino acid sequence P703P.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 36.2%; Score 498; DB 4; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1208
ID AAU69819 standard; protein; 254 AA.
DE Human prostate cDNA encoded protein #27.
PN WO200173032-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 36.2%; Score 498; DB 4; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1209
ID AAG99059 standard; protein; 254 AA.
DE Human prostate-specific amino acid of P703P.
PN WO200134802-A2.
PD 17-MAY-2001.
PA (CORI-) CORIXA CORP.
Query Match 36.2%; Score 498; DB 4; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1210
ID ABU71710 standard; protein; 254 AA.
DE Prostate cancer specific antigen P703P #7.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ) XU J.
PA (DILL) DILLON D C.
PA (MITC) MITCHAM J L.
PA (HARL) HARLOCKER S L.
PA (JIAN) JIANG Y.
PA (KALO) KALOS M D.
PA (FANG) FANGER G R.
PA (RETT) RETTER M W.
PA (STOL) STOLK J A.
PA (DAYC) DAY C H.
PA (VEDV) VEDVICK T S.
PA (CART) CARTER D.
PA (LISX) LI S X.
PA (WANG) WANG A.
PA (SKEI) SKEIKY Y A W.
PA (HEPL) HEPLER W T.
PA (HEND) HENDERSON R A.
PA (HURA) HURAL J.
PA (MCNE) MCNEILL P D.
PA (HOUG) HOUGHTON R L.
PA (DBAS) Y DE BASSOLS C V.
PA (FOYT) FOY T M.
Query Match 36.2%; Score 498; DB 4; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1211
ID ABB95279 standard; protein; 254 AA.
DE Human P703P putative full length protein SEQ ID NO 525.
PN US200202248-A1.
PD 21-FEB-2002.
PA (XUJ) XU J.
PA (DILL) DILLON D C.
PA (MITC) MITCHAM J L.
PA (HARL) HARLOCKER S L.
PA (JIAN) JIANG Y.
PA (KALO) KALOS M D.
PA (FANG) FANGER G R.
PA (RETT) RETTER M W.
PA (STOL) STOLK J A.
PA (DAYC) DAY C H.
PA (VEDV) VEDVICK T S.
PA (CART) CARTER D.
PA (LISX) LI S X.
PA (WANG) WANG A.
PA (SKEI) SKEIKY Y A W.
PA (HEPL) HEPLER W T.

PA (HEND/) HENDERSON R A. 36.2%; Score 498; DB 5; Length 254;
Query Match 43.1%; Pred. No. 1.7e-30;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1212
ID ABP54360 standard; protein; 254 AA.
DE Human KLK4 protein SEQ ID NO:13.
PN WO200277243-A1.
PD 03-OCT-2002.
PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
Query Match 36.2%; Score 498; DB 6; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1213
ID ABP54357 standard; protein; 254 AA.
DE Human KLK4 protein SEQ ID NO:6.
PN WO200277243-A1.
PD 03-OCT-2002.
PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
Query Match 36.2%; Score 498; DB 6; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1214
ID ABR54391 standard; protein; 254 AA.
DE Prostate tumour specific protein sequence SEQ ID 525.
PN WO200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 36.2%; Score 498; DB 6; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1215
ID ADB13975 standard; protein; 254 AA.
DE Human prostate specific protein P703P.
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 36.2%; Score 498; DB 7; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1216
ID ADG26391 standard; protein; 254 AA.
DE Human prostate-specific polypeptide #60.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match 36.2%; Score 498; DB 7; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1217
ID AAB74830 standard; protein; 1079 AA.
DE Prostate tumour antigen amino acid sequence for a fusion protein.
PN WO200125272-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match 36.2%; Score 498; DB 4; Length 1079;
Best Local Similarity 43.1%; Pred. No. 7.6e-30;
RESULT 1218
ID ABU71860 standard; protein; 1079 AA.
DE Prostate specific antigen fusion protein #2.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISK/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.

PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match 36.2%; Score 498; DB 4; Length 1079;
Best Local Similarity 43.1%; Pred. No. 7.6e-30;
RESULT 1219
ID ADI17268 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 804.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 36.2%; Score 497.5; DB 5; Length 230;
Best Local Similarity 47.4%; Pred. No. 1.7e-30;
RESULT 1220
ID ADI17276 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 812.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 36.2%; Score 497.5; DB 5; Length 230;
Best Local Similarity 47.4%; Pred. No. 1.7e-30;
RESULT 1221
ID ADJ33075 standard; protein; 230 AA.
DE Trypsin-like serine protease protein - SEQ ID 66.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUK/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPLY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 36.2%; Score 497.5; DB 7; Length 230;
Best Local Similarity 47.4%; Pred. No. 1.7e-30;
RESULT 1222
ID ADL27345 standard; peptide; 280 AA.
DE Amino acid sequence of trypsinogen.
PN WO2004019878-A2.
PD 11-MAR-2004.
PA (COMP-) COMPOUND THERAPEUTICS INC.
PA (AFEY/) AFEYAN N B.
Query Match 36.2%; Score 497.5; DB 8; Length 280;
Best Local Similarity 42.7%; Pred. No. 2.1e-30;
RESULT 1223
ID ADL27346 standard; peptide; 461 AA.
DE Amino acid sequence of trypsinogen-0aa-sp55.
PN WO2004019878-A2.
PD 11-MAR-2004.
PA (COMP-) COMPOUND THERAPEUTICS INC.
PA (AFEY/) AFEYAN N B.
Query Match 36.2%; Score 497.5; DB 8; Length 461;

Best Local Similarity 42.7%; Pred. No. 3.5e-30;
RESULT 1224
ID ADL27347 standard; peptide; 464 AA.
DE Amino acid sequence of trypsinogen-3aa-sp55.
PN WO2004019878-A2.
PD 11-MAR-2004.
PA (COMP-) COMPOUND THERAPEUTICS INC.
PA (AFXY/) AFEYAN N B.
Query Match 36.2%; Score 497.5; DB 8; Length 464;
Best Local Similarity 42.7%; Pred. No. 3.5e-30;
RESULT 1225
ID ADL27348 standard; peptide; 485 AA.
DE Amino acid sequence of trypsinogen-20aa-sp55.
PN WO2004019878-A2.
PD 11-MAR-2004.
PA (COMP-) COMPOUND THERAPEUTICS INC.
PA (AFXY/) AFEYAN N B.
Query Match 36.2%; Score 497.5; DB 8; Length 485;
Best Local Similarity 42.7%; Pred. No. 3.6e-30;
RESULT 1226
ID AAB21307 standard; protein; 249 AA.
DE Human prostatic.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 36.2%; Score 497; DB 3; Length 249;
Best Local Similarity 43.1%; Pred. No. 2e-30;
RESULT 1227
ID AAB21320 standard; protein; 254 AA.
DE Human prostatic.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 36.2%; Score 497; DB 3; Length 254;
Best Local Similarity 43.1%; Pred. No. 2.1e-30;
RESULT 1228
ID AAY72525 standard; protein; 254 AA.
DE Human prostatic antigen #3.
PN WO200104143-A2.
PD 18-JAN-2001.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.
Query Match 36.2%; Score 497; DB 4; Length 254;
Best Local Similarity 43.1%; Pred. No. 2.1e-30;
RESULT 1229
ID AAU74901 standard; protein; 254 AA.
DE Protein sequence of prostate homologue #3.
PN WO200200708-A2.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 36.2%; Score 497; DB 5; Length 254;
Best Local Similarity 43.1%; Pred. No. 2.1e-30;
RESULT 1230
ID AAU74932 standard; protein; 254 AA.
DE Amino acid sequence of prostate protein fragment #3.
PN WO200200867-A1.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 36.2%; Score 497; DB 5; Length 254;
Best Local Similarity 43.1%; Pred. No. 2.1e-30;
RESULT 1231
ID AAW60592 standard; protein; 248 AA.
DE Human prostate-specific kallikrein (HPSK) protein.
PN WO9820117-A1.
PD 14-MAY-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match 36.1%; Score 496.5; DB 2; Length 248;
Best Local Similarity 43.4%; Pred. No. 2.2e-30;
RESULT 1232
ID AAY72524 standard; protein; 248 AA.
DE Human prostatic antigen #2.
PN WO200104143-A2.
PD 18-JAN-2001.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 36.1%; Score 496.5; DB 4; Length 248;
Best Local Similarity 43.4%; Pred. No. 2.2e-30;
RESULT 1233
ID AAU74770 standard; protein; 248 AA.
DE Protein sequence of prostate homologue #2.
PN WO200200708-A2.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 36.1%; Score 496.5; DB 5; Length 248;
Best Local Similarity 43.4%; Pred. No. 2.2e-30;
RESULT 1234
ID AAU74931 standard; protein; 248 AA.
DE Amino acid sequence of prostate protein fragment #2.
PN WO200200867-A1.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 36.0%; Score 495; DB 5; Length 262;
Best Local Similarity 40.4%; Pred. No. 3e-30;
RESULT 1235
ID ABG76997 standard; protein; 262 AA.
DE Human kallikrein protein variant #1.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUIL/) HUI L.
Query Match 36.0%; Score 495; DB 5; Length 262;
Best Local Similarity 40.4%; Pred. No. 3e-30;
RESULT 1236
ID ADR90673 standard; protein; 246 AA.
DE Human trypsinogen partial protein.
PN WO200407877-A2.
PD 16-SEP-2004.
PA (BIOR-) BIOREXIS PHARM CORP.
Query Match 36.0%; Score 494.5; DB 8; Length 246;
Best Local Similarity 41.9%; Pred. No. 3.1e-30;
RESULT 1237
ID AAB21321 standard; protein; 247 AA.
DE Human trypsinogen.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 36.0%; Score 494.5; DB 3; Length 247;
Best Local Similarity 41.9%; Pred. No. 3.1e-30;
RESULT 1238
ID ABR54239 standard; protein; 247 AA.
DE Human NOV35a protein SEQ ID NO:146.
PN WO2003023001-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 36.0%; Score 494.5; DB 6; Length 247;
Best Local Similarity 41.9%; Pred. No. 3.1e-30;
RESULT 1239
ID ABR54241 standard; protein; 247 AA.
DE Human NOV35c protein SEQ ID NO:150.
PN WO2003023001-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 36.0%; Score 494.5; DB 6; Length 247;
Best Local Similarity 41.9%; Pred. No. 3.1e-30;
RESULT 1240
ID ADQ30588 standard; protein; 247 AA.
DE Pancreas cancer marker - trypsin I precursor.
PN WO2004055519-A2.
PD 01-JUL-2004.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.
Query Match 36.0%; Score 494.5; DB 8; Length 247;
Best Local Similarity 41.9%; Pred. No. 3.1e-30;
RESULT 1241
ID AAM01173 standard; protein; 254 AA.

DE Human prostate-specific amino acid mature form of P703P.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 36.0%; Score 494; DB 4; Length 254;
Best Local Similarity 42.7%; Pred. No. 3.5e-30;
RESULT 1242
ID AAU69818 standard; protein; 254 AA.
DE Human prostate cDNA encoded protein #26.
PN WO200173032-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 36.0%; Score 494; DB 4; Length 254;
Best Local Similarity 42.7%; Pred. No. 3.5e-30;
RESULT 1243
ID AAG99058 standard; protein; 254 AA.
DE Human prostate-specific mature protein of P703P.
PN WO200134802-A2.
PD 17-MAY-2001.
PA (CORI-) CORIXA CORP.
Query Match 36.0%; Score 494; DB 4; Length 254;
Best Local Similarity 42.7%; Pred. No. 3.5e-30;
RESULT 1244
ID ABU71709 standard; protein; 254 AA.
DE Prostate cancer associated protein #12.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (KUGJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match 36.0%; Score 494; DB 4; Length 254;
Best Local Similarity 42.7%; Pred. No. 3.5e-30;
RESULT 1245
ID ABB95278 standard; protein; 254 AA.
DE Human P703P mature protein SEQ ID NO 523.
PN US200202248-A1.
PD 21-FEB-2002.
PA (KUGJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.

Query Match 36.0%; Score 494; DB 5; Length 254;
Best Local Similarity 42.7%; Pred. No. 3.5e-30;
RESULT 1246
ID ABR54390 standard; protein; 254 AA.
DE Prostate tumour specific protein sequence SEQ ID 523.
PN WO200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 36.0%; Score 494; DB 6; Length 254;
Best Local Similarity 42.7%; Pred. No. 3.5e-30;
RESULT 1247
ID ADB13973 standard; protein; 254 AA.
DE Human mature prostate specific protein P703P.
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 36.0%; Score 494; DB 7; Length 254;
Best Local Similarity 42.7%; Pred. No. 3.5e-30;
RESULT 1248
ID ADG26389 standard; protein; 254 AA.
DE Human prostate-specific polypeptide #59.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match 36.0%; Score 494; DB 7; Length 254;
Best Local Similarity 42.7%; Pred. No. 3.5e-30;
RESULT 1249
ID AAB21319 standard; protein; 262 AA.
DE Human KLK2.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 36.0%; Score 494; DB 3; Length 262;
Best Local Similarity 40.4%; Pred. No. 3.6e-30;
RESULT 1250
ID ABG76996 standard; protein; 262 AA.
DE Human kallikrein protein.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUIL/) HUI L.
Query Match 36.0%; Score 494; DB 5; Length 262;
Best Local Similarity 40.4%; Pred. No. 3.6e-30;
RESULT 1251
ID ADL15197 standard; protein; 262 AA.
DE Human pancreatic kallikrein.
PN CN1384199-A.
PD 11-DEC-2002.
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.
Query Match 36.0%; Score 494; DB 7; Length 262;
Best Local Similarity 40.4%; Pred. No. 3.6e-30;
RESULT 1252
ID ADL49699 standard; protein; 262 AA.
DE Human kallikrein protein (KLK1).
PN US2004033582-A1.
PD 19-FEB-2004.
PA (EDMO/) EDMONDS M.
PA (HUIL/) HUI L.
PA (PERR/) PERRONE M.
PA (POWE/) POWELL J R.
PA (RAMA/) RAMANATHAN C S.
PA (SWAN/) SWANSON B.
PA (TSUC/) TSUCHIHASHI Z.
PA (ZERR/) ZERBA K.
Query Match 36.0%; Score 494; DB 8; Length 262;
Best Local Similarity 40.4%; Pred. No. 3.6e-30;
RESULT 1253
ID ADQ39654 standard; protein; 262 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1317.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.

Query Match
Best Local Similarity 36.0%; Score 494; DB 8; Length 262;
RESULT 1254
ID AD534891 standard; protein; 262 AA.
DE Human autoimmune disease-related protein - SEQ ID 105.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 36.0%; Score 494; DB 8; Length 262;
RESULT 1255
ID ABR54277 standard; protein; 240 AA.
DE Human trypsinogen protein SEQ ID NO:341.
PN WO2003023001-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 35.9%; Score 493.5; DB 6; Length 240;
RESULT 1256
ID AAB21316 standard; protein; 241 AA.
DE Human trypsinogen.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match
Best Local Similarity 35.9%; Score 493.5; DB 3; Length 241;
RESULT 1257
ID ADN04297 standard; protein; 247 AA.
DE Antipsoriatic protein sequence #343.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GENTH) GENENTECH INC.
Query Match
Best Local Similarity 35.9%; Score 493; DB 8; Length 247;
RESULT 1258
ID AAB21308 standard; protein; 253 AA.
DE Human EMSP.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match
Best Local Similarity 35.9%; Score 493; DB 3; Length 253;
RESULT 1259
ID AAB21324 standard; protein; 258 AA.
DE Human EMSP.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match
Best Local Similarity 35.9%; Score 493; DB 3; Length 259;
RESULT 1260
ID AAW71005 standard; protein; 262 AA.
DE Human prostate-associated kallikrein designated HPAK.
PN WO9832865-A1.
PD 30-JUL-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match
Best Local Similarity 35.9%; Score 493; DB 2; Length 262;
RESULT 1261
ID ABP74711 standard; protein; 262 AA.
DE Human glandular kallikrein 1 precursor protein SEQ ID NO:600.
PN WO200281646-A2.
PD 17-OCT-2002.
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
Query Match
Best Local Similarity 35.9%; Score 493; DB 6; Length 262;
RESULT 1262
ID ADL15204 standard; protein; 262 AA.
DE Pancreatic kallikrein #1.
PN CN1384199-A.
PD 11-DEC-2002.
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.
Query Match
Best Local Similarity 35.9%; Score 493; DB 7; Length 262;

Best Local Similarity 40.4%; Pred. No. 4.3e-30;
RESULT 1263
ID ADM72846 standard; protein; 263 AA.
DE Human glandular kallikrein 1 protein SEQ ID NO:105.
PN WO2004022709-A2.
PD 18-MAR-2004.
PA (MANN-) MANNKIND CORP.
Query Match
Best Local Similarity 35.9%; Score 493; DB 8; Length 263;
RESULT 1264
ID AAB98503 standard; protein; 225 AA.
DE Human trypsin serine protease catalytic domain.
PN WO200129056-A1.
PD 26-APR-2001.
PA (UYAR-) UNIV ARKANSAS.
Query Match
Best Local Similarity 35.8%; Score 492; DB 4; Length 225;
RESULT 1265
ID AAW93488 standard; protein; 230 AA.
DE Human TRYI trypsinogen variant protein.
PN WO9910503-A1.
PD 04-MAR-1999.
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
Query Match
Best Local Similarity 35.8%; Score 492; DB 2; Length 230;
RESULT 1266
ID AAB21315 standard; protein; 256 AA.
DE Human KIK1.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match
Best Local Similarity 35.8%; Score 492; DB 3; Length 256;
RESULT 1267
ID AAP95121 standard; protein; 262 AA.
DE Kallikrein encoded by clone lambda HK65a.
PN EP297913-A.
PD 04-JAN-1989.
PA (AMGE-) AMGEN.
Query Match
Best Local Similarity 35.8%; Score 492; DB 1; Length 262;
RESULT 1268
ID ABG76998 standard; protein; 262 AA.
DE Human kallikrein protein variant #2.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUIL/) HUI L.
Query Match
Best Local Similarity 35.8%; Score 492; DB 5; Length 262;
RESULT 1269
ID AAB54293 standard; protein; 267 AA.
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:745.
PN WO200055320-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 35.8%; Score 492; DB 3; Length 267;
RESULT 1270
ID ABG77002 standard; protein; 262 AA.
DE Human kallikrein 1 polymorphic sequence.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUIL/) HUI L.
Query Match
Best Local Similarity 35.7%; Score 491; DB 5; Length 262;
RESULT 1271
ID ADA05744 standard; protein; 224 AA.
DE Human NOV18g protein SEQ ID NO:104.
PN WO2003029424-A2.


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PD 10-APR-2003.
PA (CURA-) CURAGEN CORP. 35.7%; Score 490; DB 6; Length 224;
Query Match 35.7%; Score 488; DB 8; Length 247;
Best Local Similarity 45.3%; Pred. No. 6.3e-30;
RESULT 1272
ID ADN62908 standard; protein; 224 AA.
DE Human NOV189.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KERODA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JINW/) JI W.
PA (MILL/) MILLER C E.
PA (RASI/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 35.7%; Score 490; DB 8; Length 224;
Best Local Similarity 45.3%; Pred. No. 6.3e-30;
RESULT 1273
ID AAE00397 standard; protein; 234 AA.
DE Human serine protease, PROST 07.
PD 12-APR-2001.
PA (SCHD/) SCHERING AG. 35.6%; Score 489.5; DB 4; Length 234;
Query Match 35.6%; Score 488.5; DB 2; Length 231;
Best Local Similarity 43.0%; Pred. No. 7.2e-30;
RESULT 1274
ID AAY25510 standard; protein; 231 AA.
DE Human prostate serine protease protein.
PD 18-AUG-1999.
PA (BADI/) BASF AG.
Query Match 35.6%; Score 488.5; DB 2; Length 231;
Best Local Similarity 43.9%; Pred. No. 8.4e-30;
RESULT 1275
ID ADN04725 standard; protein; 247 AA.
DE Antipsoriatic protein sequence #544.
PD 08-APR-2004.
PA (GETH/) GENENTECH INC.
Query Match 35.5%; Score 488; DB 8; Length 247;
Best Local Similarity 42.3%; Pred. No. 9.9e-30;
RESULT 1276
ID ADN99593 standard; protein; 247 AA.
DE Novel human protein sequence #409.
PD 08-APR-2004.
PA (GETH/) GENENTECH INC.
Query Match 35.5%; Score 487.5; DB 5; Length 449;
Best Local Similarity 44.1%; Pred. No. 2e-29;

PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 35.5%; Score 488; DB 8; Length 247;
Best Local Similarity 42.3%; Pred. No. 9.9e-30;
RESULT 1277
ID AAM01227 standard; protein; 449 AA.
DE P703P and PSA fusion amino acid sequence.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 35.5%; Score 487.5; DB 4; Length 449;
Best Local Similarity 44.1%; Pred. No. 2e-29;
RESULT 1278
ID AAU69872 standard; protein; 449 AA.
DE Human prostate serum antigen/P703P fusion protein.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 35.5%; Score 487.5; DB 4; Length 449;
Best Local Similarity 44.1%; Pred. No. 2e-29;
RESULT 1279
ID ABU71763 standard; protein; 449 AA.
DE Prostate cancer specific antigen fusion protein #1.
PD 19-DEC-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match 35.5%; Score 487.5; DB 4; Length 449;
Best Local Similarity 44.1%; Pred. No. 2e-29;
RESULT 1280
ID ABB95332 standard; protein; 449 AA.
DE Human P703P/PSA fusion protein SEQ ID NO 617.
PD 21-FEB-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (FOYT/) FOY T M.
Query Match 35.5%; Score 487.5; DB 5; Length 449;
Best Local Similarity 44.1%; Pred. No. 2e-29;

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RESULT 1281
ID ABR54444 standard; protein; 449 AA.
DE Prostate tumour specific protein sequence SEQ ID 617.
PN WO200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 35.5%; Score 487.5; DB 6; Length 449;
PA (FOYT/) FOY T M. 44.1%; Pred. No. 2e-29;
RESULT 1282
ID ADB14067 standard; protein; 449 AA.
DE Human prostate specific protein P703P/PSA fusion protein.
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 35.5%; Score 487.5; DB 7; Length 449;
PA (FOYT/) FOY T M. 44.1%; Pred. No. 2e-29;
RESULT 1283
ID ADG26483 standard; protein; 449 AA.
DE Human prostate-specific polypeptide #113.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 35.5%; Score 487.5; DB 7; Length 449;
PA (FOYT/) FOY T M. 44.1%; Pred. No. 2e-29;
RESULT 1284
ID ABU71889 standard; protein; 585 AA.
DE Prostate cancer specific antigen fusion protein #3.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match
Best Local Similarity 35.5%; Score 487.5; DB 4; Length 585;
PA (HEPL/) HEPLER W T. 44.1%; Pred. No. 2.6e-29;
RESULT 1285
ID ABU71888 standard; protein; 585 AA.
DE Prostate cancer associated protein #72.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match
Best Local Similarity 35.5%; Score 487.5; DB 4; Length 585;
PA (HEPL/) HEPLER W T. 44.1%; Pred. No. 2.6e-29;
RESULT 1286
ID ABU71890 standard; protein; 801 AA.
DE Prostate cancer specific antigen fusion protein #4.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match
Best Local Similarity 35.5%; Score 487.5; DB 7; Length 585;
PA (HEPL/) HEPLER W T. 44.1%; Pred. No. 2.6e-29;
RESULT 1287
ID ADB14470 standard; protein; 585 AA.
DE FOPF/hPAP fusion protein, FOPF3.
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 35.5%; Score 487.5; DB 6; Length 585;
PA (FOYT/) FOY T M. 44.1%; Pred. No. 2.6e-29;
RESULT 1288
ID ADG26993 standard; protein; 585 AA.
DE Human prostate-specific polypeptide #249.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 35.5%; Score 487.5; DB 7; Length 585;
PA (FOYT/) FOY T M. 44.1%; Pred. No. 2.6e-29;
RESULT 1289
ID ABU71890 standard; protein; 801 AA.
DE Prostate cancer specific antigen fusion protein #4.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match
Best Local Similarity 35.5%; Score 487.5; DB 4; Length 801;
PA (HEPL/) HEPLER W T. 44.1%; Pred. No. 3.6e-29;
RESULT 1290
ID AAV31160 standard; protein; 224 AA.
DE Human trypsin serine protease protein domain.
PN US5948892-A.
PD 07-SEP-1999.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 35.4%; Score 487; DB 2; Length 224;
PA (AMGE-) AMGEN INC. 43.4%; Pred. No. 1.1e-29;
RESULT 1291
ID ADL15207 standard; protein; 261 AA.
DE Pancreatic kallikrein #3.
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PN CN1384199-A.
PD 11-DEC-2002.
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.
Query Match 35.3%; Score 484.5; DB 7; Length 261;
Best Local Similarity 40.2%; Pred. No. 1.9e-29;
RESULT 1292
ID ABM83249 standard; protein; 261 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3498.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 35.2%; Score 484; DB 8; Length 261;
Best Local Similarity 43.5%; Pred. No. 2.1e-29;
RESULT 1293
ID ABM83250 standard; protein; 333 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3499.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 35.2%; Score 484; DB 8; Length 333;
Best Local Similarity 43.5%; Pred. No. 2.7e-29;
RESULT 1294
ID AAW57740 standard; protein; 240 AA.
DE Trypsinogen-like protein.
PN JP10099080-A.
PD 21-APR-1998.
PA (SHIS-) SHISEIDO CO LTD.
Query Match 35.2%; Score 483.5; DB 2; Length 240;
Best Local Similarity 42.5%; Pred. No. 2.1e-29;
RESULT 1295
ID ADL15206 standard; protein; 260 AA.
DE Pancreatic kallikrein #2.
PN CN1384199-A.
PD 11-DEC-2002.
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.
Query Match 35.2%; Score 483; DB 7; Length 260;
Best Local Similarity 39.8%; Pred. No. 2.5e-29;
RESULT 1296
ID AAB21293 standard; protein; 237 AA.
DE Human KLK-L1 protein #1.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN-) MOUNT SINAI HOSPITAL.
Query Match 35.1%; Score 482.5; DB 3; Length 237;
Best Local Similarity 42.2%; Pred. No. 2.5e-29;
RESULT 1297
ID AAP70568 standard; protein; 262 AA.
DE Human kallikrein-like substance has hypotensive activity.
PN JP62126980-A.
PD 09-JUN-1987.
PA (NAKA-) NAKANISHI S.
Query Match 35.0%; Score 481; DB 1; Length 262;
Best Local Similarity 40.0%; Pred. No. 3.6e-29;
RESULT 1298
ID AAU01290 standard; protein; 216 AA.
DE Human serine protease HETAA37p.
PN WO200123587-A2.
PD 05-APR-2001.
PA (SMIK-) SMITHKLINE BEECHAM PLC.
Query Match 34.8%; Score 477.5; DB 4; Length 216;
Best Local Similarity 44.3%; Pred. No. 5.5e-29;
RESULT 1299
ID AAY72526 standard; protein; 226 AA.
DE Human prostatic antigen P703PDE5 sequence.
PN WO200104143-A2.
PD 18-JAN-2001.
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.
Query Match 34.8%; Score 477.5; DB 4; Length 226;
Best Local Similarity 43.8%; Pred. No. 5.8e-29;
DE Protein sequence of prostate homologue #4.
PN CN1384199-A.
PD 11-DEC-2002.
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.
Query Match 35.3%; Score 484.5; DB 7; Length 261;
Best Local Similarity 40.2%; Pred. No. 1.9e-29;
RESULT 1292
ID ABM83249 standard; protein; 261 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3498.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 35.2%; Score 484; DB 8; Length 261;
Best Local Similarity 43.5%; Pred. No. 2.1e-29;
RESULT 1293
ID ABM83250 standard; protein; 333 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3499.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 35.2%; Score 484; DB 8; Length 333;
Best Local Similarity 43.5%; Pred. No. 2.7e-29;
RESULT 1294
ID AAW57740 standard; protein; 240 AA.
DE Trypsinogen-like protein.
PN JP10099080-A.
PD 21-APR-1998.
PA (SHIS-) SHISEIDO CO LTD.
Query Match 35.2%; Score 483.5; DB 2; Length 240;
Best Local Similarity 42.5%; Pred. No. 2.1e-29;
RESULT 1295
ID ADL15206 standard; protein; 260 AA.
DE Pancreatic kallikrein #2.
PN CN1384199-A.
PD 11-DEC-2002.
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.
Query Match 35.2%; Score 483; DB 7; Length 260;
Best Local Similarity 39.8%; Pred. No. 2.5e-29;
RESULT 1296
ID AAB21293 standard; protein; 237 AA.
DE Human KLK-L1 protein #1.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN-) MOUNT SINAI HOSPITAL.
Query Match 35.1%; Score 482.5; DB 3; Length 237;
Best Local Similarity 42.2%; Pred. No. 2.5e-29;
RESULT 1297
ID AAP70568 standard; protein; 262 AA.
DE Human kallikrein-like substance has hypotensive activity.
PN JP62126980-A.
PD 09-JUN-1987.
PA (NAKA-) NAKANISHI S.
Query Match 35.0%; Score 481; DB 1; Length 262;
Best Local Similarity 40.0%; Pred. No. 3.6e-29;
RESULT 1298
ID AAU01290 standard; protein; 216 AA.
DE Human serine protease HETAA37p.
PN WO200123587-A2.
PD 05-APR-2001.
PA (SMIK-) SMITHKLINE BEECHAM PLC.
Query Match 34.8%; Score 477.5; DB 4; Length 216;
Best Local Similarity 44.3%; Pred. No. 5.5e-29;
RESULT 1299
ID AAY72526 standard; protein; 226 AA.
DE Human prostatic antigen P703PDE5 sequence.
PN WO200104143-A2.
PD 18-JAN-2001.
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.
Query Match 34.8%; Score 477.5; DB 4; Length 226;
Best Local Similarity 43.8%; Pred. No. 5.8e-29;
DE Protein sequence of prostate homologue #4.
PN WO200200708-A2.
PD 03-JAN-2002.
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 34.8%; Score 477.5; DB 5; Length 226;
Best Local Similarity 43.8%; Pred. No. 5.8e-29;
RESULT 1301
ID AAU74933 standard; protein; 226 AA.
DE Amino acid sequence of prostate protein fragment #4.
PN WO200200867-A1.
PD 03-JAN-2002.
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 34.8%; Score 477.5; DB 5; Length 226;
Best Local Similarity 43.8%; Pred. No. 5.8e-29;
RESULT 1302
ID AAY72522 standard; protein; 312 AA.
DE NS1-P703P-His fusion protein.
PN WO200104143-A2.
PD 18-JAN-2001.
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.
Query Match 34.8%; Score 477.5; DB 4; Length 312;
Best Local Similarity 43.8%; Pred. No. 8.1e-29;
RESULT 1303
ID AAU74768 standard; protein; 312 AA.
DE Amino acid sequence of wild-type NS1-p703-His fusion protein.
PN WO200200708-A2.
PD 03-JAN-2002.
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 34.8%; Score 477.5; DB 5; Length 312;
Best Local Similarity 43.8%; Pred. No. 8.1e-29;
RESULT 1304
ID AAU74929 standard; protein; 312 AA.
DE Amino acid sequence of wild-type NS1-P703P-His fusion protein.
PN WO200200867-A1.
PD 03-JAN-2002.
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 34.8%; Score 477.5; DB 5; Length 312;
Best Local Similarity 43.8%; Pred. No. 8.1e-29;
RESULT 1305
ID ABU71886 standard; protein; 344 AA.
DE Human prostate specific antigen (PSA) epitope #26.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ-) XU J.
PA (DILL-) DILLON D C.
PA (MITC-) MITCHAM J L.
PA (HARL-) HARLOCKER S L.
PA (JIAN-) JIANG Y.
PA (KALO-) KALOS M D.
PA (FANG-) FANGER G R.
PA (RETT-) RETTER M W.
PA (STOL-) STOLK J A.
PA (DAYC-) DAY C H.
PA (VEDV-) VEDVICK T S.
PA (CART-) CARTER D.
PA (LISK-) LI S X.
PA (WANG-) WANG A.
PA (SKEI-) SKEIKY Y A W.
PA (HEPL-) HEPLER W T.
PA (HEND-) HENDERSON R A.
PA (HURA-) HURAL J.
PA (MCNE-) MCNEILL P D.
PA (HOUG-) HOUGHTON R L.
PA (DEAS-) Y DE BASSOLS C V.
PA (FOYT-) FOY T M.
Query Match 34.8%; Score 477.5; DB 4; Length 344;
Best Local Similarity 43.8%; Pred. No. 8.9e-29;
RESULT 1306
ID ABM82601 standard; protein; 239 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2850.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.

Query Match
Best Local Similarity 34.6%; Score 475.5; DB 8; Length 239;
RESULT 1307
ID ABM82602 standard; protein; 239 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2851.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 34.6%; Score 475.5; DB 8; Length 239;
RESULT 1308
ID ABM82603 standard; protein; 239 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2852.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 34.6%; Score 475.5; DB 8; Length 239;
RESULT 1309
ID ADN99649 standard; protein; 280 AA.
DE Novel human protein sequence #465.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 34.4%; Score 473; DB 8; Length 280;
RESULT 1310
ID AAY82008 standard; protein; 220 AA.
DE Human immunogenic prostate tumour protein sequence SEQ ID NO:327.
PN WO200004149-A2.
PD 27-JAN-2000.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 3; Length 220;
RESULT 1311
ID AAM01123 standard; protein; 220 AA.
DE Human prostate-specific amino acid sequence P703PDE6.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;
RESULT 1312
ID AAU69768 standard; protein; 220 AA.
DE Human prostate cDNA encoded protein #8.
PN WO200173032-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;
RESULT 1313
ID AAB74806 standard; protein; 220 AA.
DE Prostate tumour antigen predicted amino acid sequence for P703PDE5.
PN WO200125272-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;
RESULT 1314
ID AAG99008 standard; protein; 220 AA.
DE Human prostate-specific amino acid sequence P703PDE5.
PN WO200134802-A2.
PD 17-MAY-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;
RESULT 1315
ID AAG62147 standard; protein; 220 AA.
DE Human P703P inventive antigen SEQ ID NO: 330.
PN WO200125273-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;

Best Local Similarity 43.8%; Pred. No. 1.4e-28;
RESULT 1316
ID ABU71659 standard; protein; 220 AA.
DE Prostate cancer specific antigen P703P #4.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ-) XU J.
PA (DILL-) DILLON D C.
PA (MITC-) MITCHAM J L.
PA (HARL-) HARLOCKER S L.
PA (JIAN-) JIANG Y.
PA (KALO-) KALOS M D.
PA (FANG-) FANGER G R.
PA (RETT-) RETTER M W.
PA (STOL-) STOLK J A.
PA (DAYC-) DAY C H.
PA (VEDV-) VEDVICK T S.
PA (CART-) CARTER D.
PA (LISX-) LI S X.
PA (WANG-) WANG A.
PA (SKEI-) SKEIKY Y A W.
PA (HEPL-) HEPLER W T.
PA (HEND-) HENDERSON R A.
PA (HURA-) HURAL J.
PA (MCNE-) MCNEILL P D.
PA (HOUG-) HOUGHTON R L.
PA (DBAS-) Y DE BASSOLS C V.
PA (FOYT-) FOY T M.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;
RESULT 1317
ID ABB95228 standard; protein; 220 AA.
DE Human P703PDES protein SEQ ID NO 327.
PN US200202248-A1.
PD 21-FEB-2002.
PA (XUJ-) XU J.
PA (DILL-) DILLON D C.
PA (MITC-) MITCHAM J L.
PA (HARL-) HARLOCKER S L.
PA (JIAN-) JIANG Y.
PA (KALO-) KALOS M D.
PA (FANG-) FANGER G R.
PA (RETT-) RETTER M W.
PA (STOL-) STOLK J A.
PA (VEDV-) VEDVICK T S.
PA (CART-) CARTER D.
PA (LISX-) LI S X.
PA (WANG-) WANG A.
PA (SKEI-) SKEIKY Y A W.
PA (HEPL-) HEPLER W T.
PA (HEND-) HENDERSON R A.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 5; Length 220;
RESULT 1318
ID ABR54340 standard; protein; 220 AA.
DE Prostate tumour specific protein sequence SEQ ID 327.
PN WO200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 6; Length 220;
RESULT 1319
ID ADB13777 standard; protein; 220 AA.
DE Human prostate specific protein P703PDE5.
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 7; Length 220;
RESULT 1320
ID ADG26193 standard; protein; 220 AA.
DE Human prostate-specific polypeptide #9.

PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match 34.4%; Score 472.5; DB 7; Length 220;
Best Local Similarity 43.8%; Pred. No. 1.4e-28;
RESULT 1321
ID ADI39732 standard; protein; 262 AA.
DE Human glandular kallikrein (HK2) protein.
PN US6642013-B1.
PD 04-NOV-2003.
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.
Query Match 34.4%; Score 472.5; DB 8; Length 262;
Best Local Similarity 38.9%; Pred. No. 1.6e-28;
RESULT 1322
ID ADI37156 standard; protein; 262 AA.
DE Human glandular kallikrein (hHK2) protein.
PN US2003199010-A1.
PD 23-OCT-2003.
PA (UYAR-) UNIV ARKANSAS.
Query Match 34.4%; Score 472.5; DB 8; Length 262;
Best Local Similarity 38.9%; Pred. No. 1.6e-28;
RESULT 1323
ID ABR96163 standard; protein; 274 AA.
DE Human NOV12a protein SEQ ID NO:68.
PN WO200290568-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 34.4%; Score 472.5; DB 6; Length 274;
Best Local Similarity 40.7%; Pred. No. 1.7e-28;
RESULT 1324
ID AAP92314 standard; protein; 245 AA.
DE Human recombinant kallikrein gene.
PN EP297913-A.
PD 04-JAN-1989.
PA (AMGE-) AMGEN.
Query Match 34.3%; Score 471; DB 1; Length 245;
Best Local Similarity 40.2%; Pred. No. 2e-28;
RESULT 1325
ID AAB21313 standard; protein; 255 AA.
DE Human PSA.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 34.2%; Score 470.5; DB 3; Length 255;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1326
ID AAU06276 standard; protein; 257 AA.
DE Prostate specific Antigen (PSA) polypeptide.
PN WO200145728-A2.
PD 28-JUN-2001.
PA (EPIM-) EPIMUNE INC.
Query Match 34.2%; Score 470.5; DB 4; Length 257;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1327
ID AAW13649 standard; protein; 261 AA.
DE Human prostatic specific antigen.
PN WO9711172-A1.
PD 27-MAR-1997.
PA (WORC-) WORCESTER FOUND BIOMEDICAL RES.
Query Match 34.2%; Score 470.5; DB 2; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1328
ID AAY56048 standard; protein; 261 AA.
DE Human prostate-specific antigen.
PN WO9961068-A1.
PD 02-DEC-1999.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 34.2%; Score 470.5; DB 3; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1329
ID AAY77842 standard; protein; 261 AA.
DE Human prostate-specific antigen (PSA) sequence.
PN WO9960984-A2.

PD 02-DEC-1999.
PA (ENTR-) ENTREMED INC.
Query Match 34.2%; Score 470.5; DB 3; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1330
ID AAB21317 standard; protein; 261 AA.
DE Human PSA.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 34.2%; Score 470.5; DB 3; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1331
ID AAB74821 standard; protein; 261 AA.
DE Prostate tumour antigen amino acid sequence for PSA.
PN WO200125272-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match 34.2%; Score 470.5; DB 4; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1332
ID AAG62144 standard; protein; 261 AA.
DE Human prostate specific membrane antigen SEQ ID NO: 327.
PN WO200125273-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match 34.2%; Score 470.5; DB 4; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1333
ID AAG62146 standard; protein; 261 AA.
DE Human prostate specific antigen SEQ ID NO: 329.
PN WO200125273-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match 34.2%; Score 470.5; DB 4; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1334
ID ABU71859 standard; protein; 261 AA.
DE Human prostatic specific membrane antigen (PSMA).
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ) XU J.
PA (DILL) DILLON D C.
PA (MITC) MITCHAM J L.
PA (HARL) HARLOCKER S L.
PA (JIAN) JIANG Y.
PA (KALO) KALOS M D.
PA (FANG) FANGER G R.
PA (RETT) RETTER M W.
PA (STOL) STOLK J A.
PA (DAYC) DAY C H.
PA (VEDV) VEDVICK T S.
PA (CAST) CARTER D.
PA (LISX) LI S X.
PA (WANG) WANG A.
PA (SKEI) SKEIKY Y A W.
PA (HEPL) HEPLER W T.
PA (HEND) HENDERSON R A.
PA (HURA) HURAL J.
PA (MCNE) MCNEILL P D.
PA (HOUG) HOUGHTON R L.
PA (DBAS) Y DE BASSOLS C V.
PA (FOYT) FOY T M.
Query Match 34.2%; Score 470.5; DB 4; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1335
ID ABP74202 standard; protein; 261 AA.
DE Human PSA protein SEQ ID NO:78.
PN WO200281645-A2.
PD 17-OCT-2002.
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
Query Match 34.2%; Score 470.5; DB 6; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;

RESULT 1336
ID ADB82777 standard; protein; 261 AA.
DE Human protein sequence useful for the treatment of cancer (SeqID 1558).
PN WO2003050236-A2.
PD 19-JUN-2003.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 34.2%; Score 470.5; DB 7; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1337
ID ADC09580 standard; protein; 261 AA.
DE PSA protein #SEQ ID 78.
PN WO2003008537-A2.
PD 30-JAN-2003.
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
Query Match 34.2%; Score 470.5; DB 7; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1338
ID ADJ59022 standard; protein; 261 AA.
DE Human PSA precursor protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 34.2%; Score 470.5; DB 7; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1339
ID ADI39733 standard; protein; 261 AA.
DE Human prostate specific antigen (PSA) protein.
PN US6642013-B1.
PD 04-NOV-2003.
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.
Query Match 34.2%; Score 470.5; DB 8; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1340
ID ADI37157 standard; protein; 261 AA.
DE Human prostate specific antigen (hPSA).
PN US2003199010-A1.
PD 23-OCT-2003.
PA (UYAR-) UNIV ARKANSAS.
Query Match 34.2%; Score 470.5; DB 8; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1341
ID ADM72819 standard; protein; 261 AA.
DE Human PSA protein SEQ ID NO:78.
PN WO2004022709-A2.
PD 18-MAR-2004.
PA (MANN-) MANNKIND CORP.
Query Match 34.2%; Score 470.5; DB 8; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1342
ID ABM82166 standard; protein; 261 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO2109, SEQ:5591.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 34.2%; Score 470.5; DB 8; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1343
ID AAB08449 standard; protein; 375 AA.
DE A human prostate specific antigen variant polypeptide.
PN WO2000049158-A2.
PD 24-AUG-2000.
PA (COMP-) COMPUGEN LTD.
Query Match 34.2%; Score 470.5; DB 3; Length 375;
Best Local Similarity 40.4%; Pred. No. 3.4e-28;
RESULT 1344
ID AAG62154 standard; protein; 692 AA.
DE Human wt1/PSA fusion protein SEQ ID NO: 357.
PN WO200125273-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match 34.2%; Score 470.5; DB 4; Length 692;
Best Local Similarity 40.4%; Pred. No. 6.3e-28;

RESULT 1345
ID AAB67545 standard; protein; 284 AA.
DE Amino acid sequence of protease MH2 catalytic domain in PFEK2-6XHIS-TAG.
PN WO200116289-A2.
PD 08-MAR-2001.
PA (ORTH) ORTHO-MCNEIL PHARM INC.
Query Match 34.1%; Score 469; DB 4; Length 284;
Best Local Similarity 43.8%; Pred. No. 3.3e-28;
RESULT 1346
ID ADJ59024 standard; protein; 261 AA.
DE Human PSA precursor protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 34.1%; Score 468.5; DB 7; Length 261;
Best Local Similarity 40.4%; Pred. No. 3.3e-28;
RESULT 1347
ID AAU74903 standard; protein; 231 AA.
DE Amino acid sequence of p703 mutated-His fusion protein.
PN WO200200708-A2.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 34.0%; Score 467.5; DB 5; Length 231;
Best Local Similarity 43.4%; Pred. No. 3.5e-28;
RESULT 1348
ID AAU74934 standard; protein; 231 AA.
DE Amino acid sequence of P703p mutated-His fusion protein.
PN WO200200867-A1.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 34.0%; Score 467.5; DB 5; Length 231;
Best Local Similarity 43.4%; Pred. No. 3.5e-28;
RESULT 1349
ID AAU72521 standard; protein; 312 AA.
DE NS1-P703p mutated-His fusion protein.
PN WO200104143-A2.
PD 18-JAN-2001.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.
Query Match 34.0%; Score 467.5; DB 4; Length 312;
Best Local Similarity 43.4%; Pred. No. 4.8e-28;
RESULT 1350
ID AAU74767 standard; protein; 312 AA.
DE Amino acid sequence of NS1-p703 mutated-His fusion protein.
PN WO200200708-A2.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 34.0%; Score 467.5; DB 5; Length 312;
Best Local Similarity 43.4%; Pred. No. 4.8e-28;
RESULT 1351
ID AAU74928 standard; protein; 312 AA.
DE Amino acid sequence of NS1-P703p mutated-His fusion protein.
PN WO200200867-A1.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 34.0%; Score 467.5; DB 5; Length 312;
Best Local Similarity 43.4%; Pred. No. 4.8e-28;
RESULT 1352
ID AAP81243 standard; protein; 247 AA.
DE Human spleen trypsin III (trypsinogen III).
PN JP63160582-A.
PD 04-JUL-1988.
PA (SANY) SANKYO CO LTD.
Query Match 34.0%; Score 467; DB 1; Length 247;
Best Local Similarity 40.9%; Pred. No. 4.1e-28;
RESULT 1353
ID AAR82703 standard; protein; 247 AA.
DE Human pancreatic trypsin III.
PN JP07184655-A.
PD 25-JUL-1995.
PA (SANY) SANKYO CO LTD.
Query Match 34.0%; Score 467; DB 2; Length 247;
Best Local Similarity 40.9%; Pred. No. 4.1e-28;

RESULT 1354
ID ADJ59026 standard; protein; 261 AA.
DE Human PSA analogue (Y154) precursor protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 34.0%; Score 466.5; DB 7; Length 261;
Best Local Similarity 40.4%; Pred. No. 4.7e-28;
RESULT 1355
ID ABB84422 standard; peptide; 226 AA.
DE Rat SCCE protein N-terminal fragment SEQ ID 48.
PN WO200262135-A2.
PD 15-AUG-2002.
PA (EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
Query Match 33.8%; Score 464.5; DB 5; Length 226;
Best Local Similarity 42.7%; Pred. No. 5.8e-28;
RESULT 1356
ID ADJ59028 standard; protein; 261 AA.
DE Human PSA analogue (Y155/Y154) precursor protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 33.8%; Score 464.5; DB 7; Length 261;
Best Local Similarity 40.4%; Pred. No. 6.8e-28;
RESULT 1357
ID ADA50549 standard; protein; 237 AA.
DE Rhesus macaque prostate specific antigen (PSA/KLK3), SEQ ID NO:4.
PN WO2003031569-A2.
PD 17-APR-2003.
PA (CENZ) CENTOCOR INC.
Query Match 33.8%; Score 464; DB 6; Length 237;
Best Local Similarity 42.6%; Pred. No. 6.7e-28;
RESULT 1358
ID ADM12395 standard; protein; 261 AA.
DE Human prostate-specific antigen protein.
PN US2003235594-A1.
PD 25-DEC-2003.
PA (ANTI-) ANTIGEN EXPRESS INC.
Query Match 33.7%; Score 463.5; DB 8; Length 261;
Best Local Similarity 40.8%; Pred. No. 8.1e-28;
RESULT 1359
ID ADR66838 standard; protein; 248 AA.
DE Human prostatic carcinoma derived DNA SEQ ID 131 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 33.7%; Score 462.5; DB 8; Length 248;
Best Local Similarity 40.2%; Pred. No. 9.2e-28;
RESULT 1360
ID ADR66277 standard; protein; 248 AA.
DE Human prostatic carcinoma derived protein SEQ ID 131 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 33.7%; Score 462.5; DB 8; Length 248;
Best Local Similarity 40.2%; Pred. No. 9.2e-28;
RESULT 1361
ID ADR66934 standard; protein; 251 AA.
DE Human prostatic carcinoma derived DNA SEQ ID 232 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.

PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 33.7%; Score 462.5; DB 8; Length 251;
Best Local Similarity 40.2%; Pred. No. 9.3e-28;
RESULT 1362
ID ADR66036 standard; protein; 251 AA.
DE Human prostatic carcinoma derived protein SEQ ID 232 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 33.7%; Score 462.5; DB 8; Length 251;
Best Local Similarity 40.2%; Pred. No. 9.3e-28;
RESULT 1363
ID ADP27546 standard; protein; 281 AA.
DE Human kallikrein-3 (KLK-3) EHT103 protien b variant SeqID 20.
PN FR2848569-A1.
PD 18-JUN-2004.
PA (EXON-) EXONHIT THERAPEUTICS SA.
Query Match 33.6%; Score 462; DB 8; Length 281;
Best Local Similarity 41.0%; Pred. No. 1.1e-27;
RESULT 1364
ID ADP27545 standard; protein; 297 AA.
DE Human kallikrein-3 (KLK-3) EHT103 protien a variant SeqID 19.
PN FR2848569-A1.
PD 18-JUN-2004.
PA (EXON-) EXONHIT THERAPEUTICS SA.
Query Match 33.6%; Score 462; DB 8; Length 297;
Best Local Similarity 41.0%; Pred. No. 1.2e-27;
RESULT 1365
ID AAR84668 standard; protein; 261 AA.
DE Prepro-hk2 kallikrein.
PN WO9530758-A1.
PD 16-NOV-1995.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match 33.5%; Score 460.5; DB 2; Length 261;
Best Local Similarity 40.2%; Pred. No. 1.4e-27;
RESULT 1366
ID AAW10600 standard; protein; 261 AA.
DE Human prepro-Trp226-glandular kallikrein-2.
PN WO9701630-A1.
PD 16-JAN-1997.
PA (ORIN) ORION YHTYMAE OY.
Query Match 33.5%; Score 460.5; DB 2; Length 261;
Best Local Similarity 40.2%; Pred. No. 1.4e-27;
RESULT 1367
ID AAU98921 standard; protein; 245 AA.
DE Human prostate specific antigen (PSA) variant.
PN WO200240059-A2.
PD 23-MAY-2002.
PA (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.
PA (MINC/) MINCHEFF M S.
PA (LOUK/) LOUKINOV D I.
PA (ZOUB/) ZOUBAK S.
Query Match 33.4%; Score 459.5; DB 5; Length 245;
Best Local Similarity 41.4%; Pred. No. 1.5e-27;
RESULT 1368
ID AAY08894 standard; protein; 238 AA.
DE Chimeric serine protease FXT protein.
PN EP927764-A2.
PD 07-JUL-1999.
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
Query Match 33.4%; Score 459; DB 2; Length 238;
Best Local Similarity 40.5%; Pred. No. 1.6e-27;
RESULT 1369
ID AAB21314 standard; protein; 255 AA.
DE Human KLK2.
PN WO200053776-A2.
PD 14-SEP-2000.

PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 33.4%; Score 458.5; DB 3; Length 255;
Best Local Similarity 40.8%; Pred. No. 1.9e-27;
RESULT 1370
ID AAW06971 standard; protein; 261 AA.
DE Prostate-specific glandular kallikrein prepro-hk2.
PN WO9634964-A2.
PD 07-NOV-1996.
PA (HYBR-) HYBRITECH INC.
PA (MAYO-) MAYO FOUNDATION.
Query Match 33.4%; Score 458.5; DB 2; Length 261;
Best Local Similarity 40.8%; Pred. No. 2e-27;
RESULT 1371
ID AAW83203 standard; protein; 261 AA.
DE Prostate-specific glandular kallikrein protein pphk2.
PN WO9846795-A1.
PD 22-OCT-1998.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (MAYO-) MAYO FOUNDATION.
Query Match 33.4%; Score 458.5; DB 2; Length 261;
Best Local Similarity 40.8%; Pred. No. 2e-27;
RESULT 1372
ID AAW96187 standard; protein; 237 AA.
DE Human prostate specific antigen (PSA).
PN WO9859073-A1.
PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (YOUNG) YOUNG C Y F.
PA (TIND/) TINDALL D J.
PA (KLEE/) KLEE G G.
Query Match 33.4%; Score 458.5; DB 2; Length 261;
Best Local Similarity 40.8%; Pred. No. 2e-27;
RESULT 1373
ID AAW45397 standard; protein; 261 AA.
DE Prostate-specific glandular kallikrein precursor prepro-hk2.
PN WO9802748-A1.
PD 22-JAN-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITECH INC.
Query Match 33.4%; Score 458.5; DB 2; Length 261;
Best Local Similarity 40.8%; Pred. No. 2e-27;
RESULT 1374
ID AAW6189 standard; protein; 261 AA.
DE Prepro human Kallikrein 2 (preprohk2).
PN WO9859073-A1.
PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (YOUNG) YOUNG C Y F.
PA (TIND/) TINDALL D J.
PA (KLEE/) KLEE G G.
Query Match 33.4%; Score 458.5; DB 2; Length 261;
Best Local Similarity 40.8%; Pred. No. 2e-27;
RESULT 1375
ID AAB21318 standard; protein; 261 AA.
DE Human KLK2.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 33.4%; Score 458.5; DB 3; Length 261;
Best Local Similarity 40.8%; Pred. No. 2e-27;
RESULT 1376
ID AAU06279 standard; protein; 261 AA.
DE Human kallikrein2 polypeptide.
PN WO200145728-A2.
PD 28-JUN-2001.
PA (EPIM-) EPIMUNE INC.
Query Match 33.4%; Score 458.5; DB 4; Length 261;
Best Local Similarity 40.8%; Pred. No. 2e-27;
RESULT 1377
ID ADB75390 standard; protein; 261 AA.
DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 33.4%; Score 458.5; DB 7; Length 261;

Best Local Similarity 40.8%; Pred. No. 2e-27;
RESULT 1378
ID AAW83213 standard; protein; 237 AA.
DE Prostate-specific antigen protein hk3.
PN WO9846795-A1.
PD 22-OCT-1998.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (MAYO-) MAYO FOUNDATION.
Query Match 33.3%; Score 457.5; DB 2; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1379
ID AAW56086 standard; protein; 237 AA.
DE Human prostate specific antigen protein.
PN WO9810292-A1.
PD 12-MAR-1998.
PA (CENZ) CENTOCOR INC.
Query Match 33.3%; Score 457.5; DB 2; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1380
ID AAW96187 standard; protein; 237 AA.
DE Human prostate specific antigen (PSA).
PN WO9859073-A1.
PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (YOUNG) YOUNG C Y F.
PA (TIND/) TINDALL D J.
PA (KLEE/) KLEE G G.
Query Match 33.3%; Score 457.5; DB 2; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1381
ID AAB11041 standard; peptide; 237 AA.
DE Human prostate-specific antigen N-terminal fragment #2.
PN EP1043394-A2.
PD 11-OCT-2000.
PA (SERA-) SERATEC GES BIOTECHNOLOGIE MBH.
Query Match 33.3%; Score 457.5; DB 3; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1382
ID AAB19819 standard; protein; 237 AA.
DE Prostate specific antigen specific to benign prostatic hyperplasia.
PN WO200067030-A1.
PD 09-NOV-2000.
PA (HYBR-) HYBRITECH INC.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 33.3%; Score 457.5; DB 4; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1383
ID AAB19818 standard; protein; 237 AA.
DE Prostate specific antigen elevated in benign prostatic hyperplasia.
PN WO200066718-A1.
PD 09-NOV-2000.
PA (HYBR-) HYBRITECH INC.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 33.3%; Score 457.5; DB 4; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1384
ID ADA50546 standard; protein; 237 AA.
DE Human prostate specific antigen (PSA/KLK3), SEQ ID NO:1.
PN WO2003031569-A2.
PD 17-APR-2003.
PA (CENZ) CENTOCOR INC.
Query Match 33.3%; Score 457.5; DB 6; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1385
ID ADA09840 standard; protein; 237 AA.
DE Human mature prostate specific antigen (PSA).
PN US2003059864-A1.
PD 27-MAR-2003.
PA (MIKO/) MIKOLAJCZYK S D.
PA (RITT/) RITTENHOUSE H G.
Query Match 33.3%; Score 457.5; DB 6; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1386

ID ADJ59023 standard; protein; 237 AA.
DE Human PSA mature protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 33.3%; Score 457.5; DB 7; Length 237;
Best Local Similarity 41.8%; Pred. No. 2.1e-27;
RESULT 1387
ID ADF60980 standard; protein; 237 AA.
DE Human prostate specific antigen (PSA).
PN US2003166036-A1.
PD 04-SEP-2003.
PA (MIKO/) MIKOLAJCZYK S D.
PA (KIT7/) RITTENHOUSE H G.
Query Match 33.3%; Score 457.5; DB 8; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1388
ID AAP70677 standard; protein; 245 AA.
DE Human kallikrein gene product.
PN WO8702709-A.
PD 07-MAY-1987.
PA (BIOT-) BIOTECHN RES PARTN.
PA (CALB-) CALIF BIOTECHNOL INC.
Query Match 33.2%; Score 456; DB 1; Length 245;
Best Local Similarity 39.7%; Pred. No. 2.9e-27;
RESULT 1389
ID AAW45398 standard; protein; 237 AA.
DE Prostate-specific antigen protein hK3 (PSA).
PN WO9802748-A1.
PD 22-JAN-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITECH INC.
Query Match 33.2%; Score 455.5; DB 2; Length 237;
Best Local Similarity 41.6%; Pred. No. 3e-27;
RESULT 1390
ID ADJ59025 standard; protein; 237 AA.
DE Human PSA mature protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 33.2%; Score 455.5; DB 7; Length 237;
Best Local Similarity 41.6%; Pred. No. 3e-27;
RESULT 1391
ID AAW6972 standard; protein; 261 AA.
DE Kallikrein prepro-hK2v217 variant.
PN WO9634964-A2.
PD 07-NOV-1996.
PA (HYBR-) HYBRITECH INC.
PA (MAYO-) MAYO FOUNDATION.
Query Match 33.2%; Score 455.5; DB 2; Length 261;
Best Local Similarity 40.8%; Pred. No. 3.3e-27;
RESULT 1392
ID AAW45400 standard; protein; 261 AA.
DE Prostate-specific glandular kallikrein hK2v217.
PN WO9802748-A1.
PD 22-JAN-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITECH INC.
Query Match 33.2%; Score 455.5; DB 2; Length 261;
Best Local Similarity 40.8%; Pred. No. 3.3e-27;
RESULT 1393
ID AAW59129 standard; protein; 232 AA.
DE Homo sapiens Tub Interactor (hTI-1) protein.
PN WO9812302-A1.
PD 26-MAR-1998.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 33.1%; Score 454.5; DB 2; Length 232;
Best Local Similarity 43.8%; Pred. No. 3.5e-27;
RESULT 1394
ID AAY72523 standard; protein; 232 AA.
DE Human prostate antigen #1.
PN WO200104143-A2.
PD 18-JAN-2001.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.
Query Match 33.1%; Score 454.5; DB 4; Length 232;
Best Local Similarity 43.8%; Pred. No. 3.5e-27;
RESULT 1395
ID AAU74769 standard; protein; 232 AA.
DE Protein sequence of prostate homologue #1.
PN WO200200708-A2.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 33.1%; Score 454.5; DB 5; Length 232;
Best Local Similarity 43.8%; Pred. No. 3.5e-27;
RESULT 1396
ID AAU74930 standard; protein; 232 AA.
DE Amino acid sequence of prostate protein fragment #1.
PN WO200200867-A1.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 33.1%; Score 454.5; DB 5; Length 232;
Best Local Similarity 43.8%; Pred. No. 3.5e-27;
RESULT 1397
ID AAR84669 standard; protein; 244 AA.
DE Pro-hK2 kallikrein.
PN WO9530758-A1.
PD 16-NOV-1995.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITECH INC.
Query Match 33.1%; Score 454.5; DB 2; Length 244;
Best Local Similarity 41.2%; Pred. No. 3.7e-27;
RESULT 1398
ID ADO38617 standard; protein; 261 AA.
DE Prostate Specific Antigen (PSA).
PN US2004058881-A1.
PD 25-MAR-2004.
PA (ANTI-) ANTIGEN EXPRESS INC.
Query Match 33.1%; Score 454.5; DB 8; Length 261;
Best Local Similarity 39.6%; Pred. No. 4e-27;
RESULT 1399
ID ADJ59027 standard; protein; 237 AA.
DE Human PSA analogue (Y154) mature protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 33.0%; Score 453.5; DB 7; Length 237;
Best Local Similarity 41.6%; Pred. No. 4.3e-27;
RESULT 1400
ID AAW83204 standard; protein; 244 AA.
DE Prostate-specific glandular kallikrein protein phK2.
PN WO9846795-A1.
PD 22-OCT-1998.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (MAYO-) MAYO FOUNDATION.
Query Match 32.9%; Score 452.5; DB 2; Length 244;
Best Local Similarity 41.8%; Pred. No. 5.3e-27;
RESULT 1401
ID AAW45396 standard; protein; 244 AA.
DE Prostate-specific glandular kallikrein precursor pro-hK2.
PN WO9802748-A1.
PD 22-JAN-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITECH INC.
Query Match 32.9%; Score 452.5; DB 2; Length 244;
Best Local Similarity 41.8%; Pred. No. 5.3e-27;
RESULT 1402
ID AAW96188 standard; protein; 244 AA.
DE Pro human Kallikrein 2 (prohK2).
PN WO9859073-A1.
PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (YOUN/) YOUNG C Y F.
PA (TIND/) TINDALL D J.
PA (KLEE/) KLEE G G.
Query Match 32.9%; Score 452.5; DB 2; Length 244;

Best Local Similarity 41.8%; Pred. No. 5.3e-27;
RESULT 1403
ID AAW03130 standard; protein; 250 AA.
DE Prostate-specific antigen.
PN WO9821042-A2.
PD 11-JUL-1996.
PA (UYBO-) UNIV BOSTON.
Query Match 32.9%; Score 452.5; DB 2; Length 250;
Best Local Similarity 40.5%; Pred. No. 5.4e-27;
RESULT 1404
ID ADP27538 standard; protein; 281 AA.
DE Human kallikrein-2 (KLK-2) EHT102 protein b variant SeqID 12.
PN FR2848569-A1.
PD 18-JUN-2004.
PA (EXON-) EXONHIT THERAPEUTICS SA.
Query Match 32.9%; Score 452.5; DB 8; Length 281;
Best Local Similarity 41.8%; Pred. No. 6.1e-27;
RESULT 1405
ID ADP27537 standard; protein; 297 AA.
DE Human kallikrein-2 (KLK-2) EHT102 protein a variant SeqID 11.
PN FR2848569-A1.
PD 18-JUN-2004.
PA (EXON-) EXONHIT THERAPEUTICS SA.
Query Match 32.9%; Score 452.5; DB 8; Length 297;
Best Local Similarity 41.8%; Pred. No. 6.5e-27;
RESULT 1406
ID ADJ59029 standard; protein; 236 AA.
DE Human PSA analogue (L155/Y154) mature protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 32.9%; Score 451.5; DB 7; Length 236;
Best Local Similarity 41.6%; Pred. No. 6.1e-27;
RESULT 1407
ID AAR77098 standard; protein; 237 AA.
DE Prostate-specific antigen.
PN WO9528498-A1.
PD 26-OCT-1995.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 32.8%; Score 450.5; DB 2; Length 237;
Best Local Similarity 40.7%; Pred. No. 7.4e-27;
RESULT 1408
ID AAW83202 standard; protein; 237 AA.
DE Prostate-specific glandular kallikrein protein hK2.
PN WO9846795-A1.
PD 22-OCT-1998.
PA (BAYO) BAYLOR COLLEGE MEDICINE.
PA (MAYO-) MAYO FOUNDATION.
Query Match 32.8%; Score 450.5; DB 2; Length 237;
Best Local Similarity 42.0%; Pred. No. 7.4e-27;
RESULT 1409
ID AAW45395 standard; protein; 237 AA.
DE Mature prostate-specific glandular kallikrein hK2.
PN WO9802748-A1.
PD 22-JAN-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match 32.8%; Score 450.5; DB 2; Length 237;
Best Local Similarity 42.0%; Pred. No. 7.4e-27;
RESULT 1410
ID AAW96186 standard; protein; 237 AA.
DE Mature human kallikrein 2 (hK2).
PN WO9859073-A1.
PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (YOUNG) YOUNG C Y F.
PA (TIND) TINDALL D J.
PA (KLEE) KLEE G G.
Query Match 32.8%; Score 450.5; DB 2; Length 237;
Best Local Similarity 42.0%; Pred. No. 7.4e-27;
RESULT 1411
ID ADA50561 standard; protein; 237 AA.
DE Kallikrein KLK2, SEQ ID NO:16.
PN WO2003031569-A2.
PD 17-APR-2003.
PA (CENZ) CENTOCOR INC.
Query Match 32.8%; Score 450.5; DB 6; Length 237;
Best Local Similarity 42.0%; Pred. No. 7.4e-27;
RESULT 1412
ID AAR84667 standard; protein; 237 AA.
DE Mature kallikrein hK2.
PN WO9530758-A1.
PD 16-NOV-1995.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match 32.6%; Score 448.5; DB 2; Length 237;
Best Local Similarity 42.0%; Pred. No. 1e-26;
RESULT 1413
ID ADI17277 standard; protein; 217 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 813.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 32.6%; Score 447.5; DB 5; Length 217;
Best Local Similarity 44.4%; Pred. No. 1.1e-26;
RESULT 1414
ID ADI17269 standard; protein; 217 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 805.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 32.6%; Score 447.5; DB 5; Length 217;
Best Local Similarity 44.4%; Pred. No. 1.1e-26;
RESULT 1415
ID ADJ83076 standard; protein; 217 AA.
DE Trypsin protein which is related to human NOVX protein - SEQ ID 67.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO) ALSOBROOK J P.
PA (TCHE) TCHERNEV V T.
PA (LIUX) LIU X.
PA (SPYT) SPYTEK K A.
PA (ZERH) ZERHUSEN B D.
PA (PATI) PAITURAJAN M.
PA (LEPL) LEPLEY D M.
PA (BURG) BURGESS C E.
PA (SHIM) SHIMKETS R A.
PA (GROS) GROSSE W M.
PA (SZEK) SZEKERES E S.
PA (VERN) VERNET C A M.
PA (LILL) LI L.
PA (CASM) CASMAN S J.
PA (BOLD) BOLDOG F L.
PA (GORM) GORMAN L.
PA (GANG) GANGOLLI E A.
PA (FERN) FERNANDES E R.
PA (RIEG) RIEGER D K.
PA (EDIN) EDINGER S R.
PA (GUNT) GUNTHER E.
PA (MILL) MILLET I.
PA (SCIO) SCIORE P.
PA (ELLE) ELLERMAN K.
PA (MACD) MACDOUGALL J R.
PA (SMIT) SMITHSON G.
Query Match 32.6%; Score 447.5; DB 7; Length 217;
Best Local Similarity 44.4%; Pred. No. 1.1e-26;
RESULT 1416
ID AAW83212 standard; protein; 237 AA.
DE hK2 variant A217V.
PN WO9846795-A1.
PD 22-OCT-1998.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (MAYO-) MAYO FOUNDATION.
Query Match 32.6%; Score 447.5; DB 2; Length 237;
Best Local Similarity 42.0%; Pred. No. 1.3e-26;
RESULT 1417

ID AAW49087 standard; protein; 237 AA.
DE Mutant human kallikrein 2 (hk2) A217V.
PN WO9821365-A2.
PD 22-MAY-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match 32.6%; Score 447.5; DB 2; Length 237;
Best Local Similarity 42.0%; Pred. No. 1.3e-26;
RESULT 1418
ID AAW96190 standard; protein; 237 AA.
DE Variant human kallikrein 2 (hk2).
PN WO9859073-A1.
PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (YOUNG-) YOUNG C Y F.
PA (TINDALL-) TINDALL D J.
PA (KLEE-) KLEE G G.
Query Match 32.6%; Score 447.5; DB 2; Length 237;
Best Local Similarity 42.0%; Pred. No. 1.3e-26;
RESULT 1419
ID AAW11023 standard; protein; 240 AA.
DE Human prostate specific antigen.
PN WO9640754-A1.
PD 19-DEC-1996.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 32.4%; Score 445; DB 2; Length 240;
Best Local Similarity 41.0%; Pred. No. 2e-26;
RESULT 1420
ID AAR84671 standard; protein; 237 AA.
DE Mature kallikrein hk3.
PN WO9530758-A1.
PD 16-NOV-1995.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match 32.4%; Score 444.5; DB 2; Length 237;
Best Local Similarity 41.1%; Pred. No. 2.1e-26;
RESULT 1421
ID ABM82643 standard; protein; 227 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2892.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 32.2%; Score 443; DB 8; Length 227;
Best Local Similarity 39.6%; Pred. No. 2.7e-26;
RESULT 1422
ID AAR84670 standard; protein; 238 AA.
DE Mature kallikrein hk2.
PN WO9530758-A1.
PD 16-NOV-1995.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match 32.1%; Score 441.5; DB 2; Length 238;
Best Local Similarity 40.9%; Pred. No. 3.6e-26;
RESULT 1423
ID AAR94526 standard; protein; 279 AA.
DE Korean Viper Salmons thrombin-like protease, Halybin.
PN EP07067-A2.
PD 17-APR-1996.
PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
Query Match 32.0%; Score 439; DB 2; Length 279;
Best Local Similarity 37.7%; Pred. No. 6.7e-26;
RESULT 1424
ID AAG79000 standard; protein; 233 AA.
DE Mamushi fibrinolytic enzyme, brevinase.
PN KR2001045716-A.
PD 05-JUN-2001.
PA (LEEJ-) LEE J W.
PA (PARK-) PARK W.
Query Match 31.8%; Score 436.5; DB 4; Length 233;
Best Local Similarity 37.9%; Pred. No. 8.7e-26;
RESULT 1425
ID AAM52944 standard; protein; 260 AA.
DE Agkistrodon halys brevicaudus thrombin-like protease, salmobin.

PN KR98002267-A.
PD 30-MAR-1998.
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.
Query Match 31.7%; Score 436; DB 2; Length 260;
Best Local Similarity 36.1%; Pred. No. 1.1e-25;
RESULT 1426
ID AAB50447 standard; protein; 205 AA.
DE Human prostate cancer-related intracellular protein #1.
PN WO200071711-A2.
PD 30-NOV-2000.
PA (SAAT-) SAATCIOGLU F.
Query Match 31.4%; Score 431.5; DB 4; Length 205;
Best Local Similarity 44.2%; Pred. No. 1.8e-25;
RESULT 1427
ID ADE78966 standard; protein; 227 AA.
DE Human protein modification and maintenance molecule (PMMW)-4.
PN WO2003063688-A2.
PD 07-AUG-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 31.3%; Score 430; DB 7; Length 227;
Best Local Similarity 39.2%; Pred. No. 2.7e-25;
RESULT 1428
ID AAW69388 standard; protein; 205 AA.
DE Prostate tumour specific gene clone DE13 protein.
PN WO9837418-A2.
PD 27-AUG-1998.
PA (CORI-) CORIXA CORP.
Query Match 31.0%; Score 426.5; DB 2; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1429
ID AAW71872 standard; protein; 205 AA.
DE Protein encoded by prostate tumour clone P703 splice variant DE13.
PN WO9837093-A2.
PD 27-AUG-1998.
PA (CORI-) CORIXA CORP.
Query Match 31.0%; Score 426.5; DB 2; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1430
ID AAY82005 standard; protein; 205 AA.
DE Human immunogenic prostate tumour protein sequence SEQ ID NO:176.
PN WO200004149-A2.
PD 27-JAN-2000.
PA (CORI-) CORIXA CORP.
Query Match 31.0%; Score 426.5; DB 3; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1431
ID ABG94414 standard; protein; 205 AA.
DE Human prostate tumour protein partial variant sequence #2.
PN US2002090372-A1.
PD 11-JUL-2002.
PA (XUJ-) XU J.
PA (DILL-) DILLON D C.
Query Match 31.0%; Score 426.5; DB 3; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1432
ID AAM01120 standard; protein; 205 AA.
DE Human prostate-specific amino acid sequence P703P-DE13.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 31.0%; Score 426.5; DB 4; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1433
ID AAU69766 standard; protein; 205 AA.
DE Human prostate cDNA encoded protein #6.
PN WO200173032-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 31.0%; Score 426.5; DB 4; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1434
ID AAB74803 standard; protein; 205 AA.
DE Prostate tumour antigen predicted amino acid sequence for P703P-DE13.

PN WO200125272-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match 31.0%; Score 426.5; DB 4; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1435
ID AAG99005 standard; protein; 205 AA.
DE Human prostate-specific amino acid sequence P703P-DE13.
PN WO200134802-A2.
PD 17-MAY-2001.
PA (CORI-) CORIXA CORP.
Query Match 31.0%; Score 426.5; DB 4; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1436
ID ABU71656 standard; protein; 205 AA.
DE Prostate cancer specific antigen P703P #2.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match 31.0%; Score 426.5; DB 4; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1437
ID AAU04964 standard; protein; 205 AA.
DE Human prostate tumour protein DE13.
PN US6262245-B1.
PD 17-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 31.0%; Score 426.5; DB 4; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1438
ID ABB95225 standard; protein; 205 AA.
DE Human P703P-DE13 protein SEQ ID NO 176.
PN US2002022248-A1.
PD 21-FEB-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
Query Match 31.0%; Score 426.5; DB 5; Length 205;

Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1439
ID ABG76668 standard; protein; 205 AA.
DE Prostate tumour protein #6.
PN US2002081580-A1.
PD 27-JUN-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
Query Match 31.0%; Score 426.5; DB 5; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1440
ID ABR54337 standard; protein; 205 AA.
DE Prostate tumour specific protein sequence SEQ ID 176.
PN WO200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 31.0%; Score 426.5; DB 6; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1441
ID ADB13626 standard; protein; 205 AA.
DE Human prostate specific protein P703P-DE13.
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 31.0%; Score 426.5; DB 7; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1442
ID ADG26042 standard; protein; 205 AA.
DE Human prostate-specific polypeptide #6.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match 31.0%; Score 426.5; DB 7; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1443
ID ABB09589 standard; protein; 234 AA.
DE Deinagkistrodon acutus venom thrombin-like protein (234 residue variant).
PN CN1181421-A.
PD 13-MAY-1998.
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
Query Match 30.7%; Score 422.5; DB 5; Length 234;
Best Local Similarity 36.4%; Pred. No. 1e-24;
RESULT 1444
ID ADK36957 standard; protein; 281 AA.
DE Novel human polypeptide SeqID9039.
PN WO200216439-A2.
PD 28-FEB-2002.
PA (HYSE-) HYSEQ INC.
Query Match 30.7%; Score 422.5; DB 5; Length 281;
Best Local Similarity 39.3%; Pred. No. 1.3e-24;
RESULT 1445
ID ABU92024 standard; protein; 218 AA.
DE Human protein modification and maintenance molecule-4 (PMMW-4).
PN WO2003031939-A2.
PD 17-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 30.7%; Score 422; DB 6; Length 218;
Best Local Similarity 37.8%; Pred. No. 1.1e-24;
RESULT 1446
ID AAB31579 standard; peptide; 225 AA.
DE Amino acid sequence of cod trypsin isozyms.
PN WO200078332-A2.
PD 28-DEC-2000.
PA (BJAR/) BJARNASON J B.
Query Match 30.6%; Score 421; DB 4; Length 225;
Best Local Similarity 44.3%; Pred. No. 1.3e-24;
RESULT 1447
ID ADE15982 standard; protein; 218 AA.
DE G-coupled protein receptor related polypeptide, SEQ ID NO 12.
PN WO200283841-A2.
PD 24-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 30.6%; Score 420; DB 7; Length 218;

Best Local Similarity 37.8%; Pred. No. 1.5e-24;
ID ADL93921 standard; protein; 218 AA.
DE Human G-coupled protein receptor-related protein #6.
PN US2004006205-A1.
PD 08-JAN-2004.
PA (LILL/) LI L.
PA (GERL/) GERLACH V.
PA (LIUX/) LIU X.
PA (MILL/) MILLER C E.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (ZHON/) ZHONG H.
PA (SMIT/) SMITHSON G.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (VOSS/) VOSS E Z.
PA (VERN/) VERNET C A.
PA (MACD/) MACDOUGALL J R.
PA (RAST/) RASTELLI L.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (MEZE/) MEZES P S.
PA (FURT/) FURTAK K.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (MALY/) MALYANKAR U M.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (EDIN/) EDINGER S.
PA (MAZU/) MAZUR A.
Query Match 30.6%; Score 420; DB 8; Length 218;
Best Local Similarity 37.8%; Pred. No. 1.5e-24;
RESULT 1449
ID AAY28641 standard; protein; 207 AA.
DE Human secreted protein from cDNA clone HKAET41.
PN WO9940183-A1.
PD 12-AUG-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 30.4%; Score 418; DB 2; Length 207;
Best Local Similarity 46.1%; Pred. No. 2e-24;
RESULT 1450
ID AAW46773 standard; protein; 233 AA.
DE Amino acid sequence of Salmonase.
PN EP814164-A2.
PD 29-DEC-1997.
PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
Query Match 30.4%; Score 417.5; DB 2; Length 233;
Best Local Similarity 36.6%; Pred. No. 2.5e-24;
RESULT 1451
ID AAE21442 standard; protein; 226 AA.
DE Human trypsin domain consensus protein #2.
PN WO200226802-A2.
PD 04-APR-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 30.3%; Score 416.5; DB 5; Length 226;
Best Local Similarity 42.6%; Pred. No. 2.9e-24;
RESULT 1452
ID ABG75786 standard; protein; 226 AA.
DE Trypsin domain consensus sequence, SMART.
PN US2002165152-A1.
PD 07-NOV-2002.
PA (KAPE/) KAPPELLER-LIBERMANN R.
Query Match 30.3%; Score 416.5; DB 6; Length 226;
Best Local Similarity 42.6%; Pred. No. 2.9e-24;
RESULT 1453
ID ADA05736 standard; protein; 198 AA.
DE Human NOV18c protein SEQ ID NO:96.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.

Query Match 30.0%; Score 412.5; DB 6; Length 198;
Best Local Similarity 36.8%; Pred. No. 5.2e-24;
RESULT 1454
ID ADNG2900 standard; protein; 198 AA.
DE Human NOV18c.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJ/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIP/) DIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 29.8%; Score 409; DB 7; Length 215;
Best Local Similarity 37.1%; Pred. No. 1.1e-23;
RESULT 1457
ID ABM82829 standard; protein; 215 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3078.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 29.8%; Score 409; DB 8; Length 215;
Best Local Similarity 37.1%; Pred. No. 1.1e-23;
RESULT 1458
ID ABM83248 standard; protein; 299 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3497.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.

Query Match 29.8%; Score 409; DB 6; Length 194;
Best Local Similarity 38.7%; Pred. No. 9.5e-24;
RESULT 1456
ID ADG75684 standard; protein; 215 AA.
DE Human protein modification and maintenance molecule polypeptide SeqID8.
PN WO2003083084-A2.
PD 09-OCT-2003.
PA (INCY-) INCYTE CORP.

Query Match 29.8%; Score 409; DB 8; Length 299;
Best Local Similarity 38.6%; Pred. No. 1.5e-23;
RESULT 1459
ID ADA05738 standard; protein; 181 AA.
DE Human NOV18d protein SEQ ID NO:198.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 29.7%; Score 408.5; DB 6; Length 181;
Best Local Similarity 37.4%; Pred. No. 9.6e-24;
RESULT 1460
ID ADNG2902 standard; protein; 181 AA.
DE Human NOV18d.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUGJ/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PAT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGE E M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 29.7%; Score 408.5; DB 8; Length 181;
Best Local Similarity 37.4%; Pred. No. 9.6e-24;
RESULT 1461
ID ABM82641 standard; protein; 222 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2890.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 29.6%; Score 407; DB 8; Length 222;
Best Local Similarity 36.7%; Pred. No. 1.6e-23;
RESULT 1462
ID AAB08510 standard; protein; 230 AA.
DE A recombinant protein C activator polypeptide.
PN WO200050612-A2.
PD 31-AUG-2000.
PA (INLI-) INSTRUMENTATION LAB.
Query Match 29.6%; Score 406.5; DB 3; Length 230;
Best Local Similarity 36.2%; Pred. No. 1.8e-23;
RESULT 1463
ID AAW6538 standard; protein; 231 AA.
DE A. contortrix protein C activator protein fragment.
PN WO9842850-A1.
PD 01-OCT-1998.
PA (RPMS-) RPMS TECHNOLOGY LTD.

Query Match 29.6%; Score 406.5; DB 2; Length 231;
Best Local Similarity 36.2%; Pred. No. 1.8e-23;
RESULT 1464
ID ABB09590 standard; protein; 218 AA.
DE Deinagkistrodon acutus venom thrombin-like protein (218 residue variant).
PN CN1181421-A.
PD 13-MAY-1998.
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
Query Match 29.5%; Score 405.5; DB 5; Length 218;
Best Local Similarity 36.5%; Pred. No. 2e-23;
RESULT 1465
ID ABM84665 standard; protein; 220 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4914.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 29.5%; Score 405; DB 8; Length 220;
Best Local Similarity 36.7%; Pred. No. 2.2e-23;
RESULT 1466
ID AAB08511 standard; protein; 230 AA.
DE Biosynthetic variant of protein C activator polypeptide.
PN WO200050612-A2.
PD 31-AUG-2000.
PA (INLI-) INSTRUMENTATION LAB.
Query Match 29.4%; Score 403.5; DB 3; Length 230;
Best Local Similarity 37.0%; Pred. No. 3e-23;
RESULT 1467
ID AAR20557 standard; protein; 234 AA.
DE Fibrinogenolytic protein #4 from snake venom.
PN DE4023699-A.
PD 30-JAN-1992.
PA (BADI-) BASF AG.
Query Match 29.3%; Score 403; DB 2; Length 234;
Best Local Similarity 36.7%; Pred. No. 3.3e-23;
RESULT 1468
ID AAP81333 standard; protein; 255 AA.
DE Batroxobin.
PN JP63049084-A.
PD 01-MAR-1988.
PA (YAMA/) YAMASHINA I.
Query Match 29.3%; Score 402; DB 1; Length 255;
Best Local Similarity 32.9%; Pred. No. 4.3e-23;
RESULT 1469
ID AAR05436 standard; protein; 255 AA.
DE Batroxobin gene product.
PN JP02124092-A.
PD 11-MAY-1990.
PA (FUJI-) FUJISAWA PHARM CO LTD.
Query Match 29.3%; Score 402; DB 2; Length 255;
Best Local Similarity 32.9%; Pred. No. 4.3e-23;
RESULT 1470
ID AAV17869 standard; protein; 255 AA.
DE Araraca batroxobin.
PN WO9929838-A1.
PD 17-JUN-1999.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 29.3%; Score 402; DB 2; Length 255;
Best Local Similarity 32.9%; Pred. No. 4.3e-23;
RESULT 1471
ID AAE21441 standard; protein; 249 AA.
DE Human trypsin domain consensus protein #1.
PN WO200226802-A2.
PD 04-APR-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 29.2%; Score 401.5; DB 5; Length 249;
Best Local Similarity 40.3%; Pred. No. 4.6e-23;
RESULT 1472
ID AAM52946 standard; protein; 231 AA.
DE Batroxobin, a snake venom protease.
PN KR98002267-A.
PD 30-MAR-1998.
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.
Query Match 29.1%; Score 400; DB 2; Length 231;

Best Local Similarity 34.2%; Pred. No. 5.6e-23;
RESULT 1473
ID AAB11711 standard; protein; 264 AA.
DE Mouse serine protease BSSP5 (mBSSP5) SEQ ID NO:4.
PN WO200031243-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 28.8%; Score 395.5; DB 3; Length 264;
Best Local Similarity 39.1%; Pred. No. 1.4e-22;
RESULT 1474
ID AAM52945 standard; protein; 236 AA.
DE Flabobobin, a snake venom protease.
PN KR98002267-A.
PD 30-MAR-1998.
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.
Query Match 28.7%; Score 394; DB 2; Length 236;
Best Local Similarity 36.8%; Pred. No. 1.7e-22;
RESULT 1475
ID AAR20556 standard; protein; 236 AA.
DE Fibrinogenolytic protein #3 from snake venom.
PN DE4023699-A.
PD 30-JAN-1992.
PA (BADI) BASF AG.
Query Match 28.6%; Score 393; DB 2; Length 236;
Best Local Similarity 37.3%; Pred. No. 2e-22;
RESULT 1476
ID ABM82831 standard; protein; 233 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3080.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 28.5%; Score 392; DB 8; Length 233;
Best Local Similarity 36.8%; Pred. No. 2.3e-22;
RESULT 1477
ID AAE39993 standard; protein; 253 AA.
DE Human adipsin protein #2.
PN US2003092620-A1.
PD 15-MAY-2003.
PA (GEST) GENSET SA.
Query Match 28.5%; Score 391; DB 7; Length 253;
Best Local Similarity 38.0%; Pred. No. 3e-22;
RESULT 1478
ID ABG75785 standard; protein; 227 AA.
DE Trypsin domain consensus sequence, PFAM.
PN US2002165152-A1.
PD 07-NOV-2002.
PA (KAPE/) KAPPELLER-LIBERMANN R.
Query Match 28.3%; Score 389; DB 6; Length 227;
Best Local Similarity 40.4%; Pred. No. 3.9e-22;
RESULT 1479
ID ADE58223 standard; protein; 253 AA.
DE Human Protein P00746, SEQ ID NO 4094.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 28.3%; Score 389; DB 7; Length 253;
Best Local Similarity 38.5%; Pred. No. 4.3e-22;
RESULT 1480
ID AAP70758 standard; protein; 269 AA.
DE Pig pancreas elastase-2.
PN JP62000276-A.
PD 06-JAN-1987.
PA (SANY) SANKYO CO LTD.
Query Match 28.2%; Score 388; DB 1; Length 269;
Best Local Similarity 38.5%; Pred. No. 5.5e-22;
RESULT 1481
ID AAE39992 standard; protein; 253 AA.
DE Human adipsin protein #1.
PN US2003092620-A1.
PD 15-MAY-2003.
PA (GEST) GENSET SA.
Query Match 28.2%; Score 387; DB 7; Length 253;

Best Local Similarity 38.5%; Pred. No. 6.2e-22;
RESULT 1482
ID AAB11710 standard; protein; 264 AA.
DE Human serine protease BSSP5 (hBSSP5) SEQ ID NO:2.
PN WO200031243-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 28.1%; Score 386.5; DB 3; Length 264;
Best Local Similarity 36.8%; Pred. No. 7e-22;
RESULT 1483
ID ABR39439 standard; protein; 264 AA.
DE Human GENSSET polypeptide clone name VCTRL-1.
PN WO2003014151-A2.
PD 20-FEB-2003.
PA (GEST) GENSET SA.
Query Match 28.1%; Score 386.5; DB 6; Length 264;
Best Local Similarity 36.8%; Pred. No. 7e-22;
RESULT 1484
ID ABU09382 standard; protein; 271 AA.
DE Consensus sequence of trypsin-like domain.
PN WO2003031463-A2.
PD 17-APR-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 28.1%; Score 386; DB 6; Length 271;
Best Local Similarity 39.1%; Pred. No. 7.9e-22;
RESULT 1485
ID ABM82830 standard; protein; 212 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3079.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 28.1%; Score 385.5; DB 8; Length 212;
Best Local Similarity 36.3%; Pred. No. 6.7e-22;
RESULT 1486
ID ABM82644 standard; protein; 212 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2893.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 28.1%; Score 385.5; DB 8; Length 212;
Best Local Similarity 36.3%; Pred. No. 6.7e-22;
RESULT 1487
ID ABM81778 standard; protein; 264 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO2719, SEQ:4580.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 28.1%; Score 385.5; DB 8; Length 264;
Best Local Similarity 36.8%; Pred. No. 8.4e-22;
RESULT 1488
ID ADR66037 standard; protein; 213 AA.
DE Human prostatic carcinoma derived protein SEQ ID 233 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 28.0%; Score 385; DB 8; Length 213;
Best Local Similarity 40.2%; Pred. No. 7.4e-22;
RESULT 1489
ID ADR66935 standard; protein; 213 AA.
DE Human prostatic carcinoma derived DNA SEQ ID 233 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 28.0%; Score 385; DB 8; Length 213;
Best Local Similarity 40.2%; Pred. No. 7.4e-22;

RESULT 1490
ID AAP61724 standard; protein; 269 AA.
DE Porcine elastase II.
PN JP61192289-A.
PD 26-AUG-1986.
PA (KIRI) KIRIN BREWERY KK.
Query Match 27.9%; Score 384; DB 1; Length 269;
Best Local Similarity 38.4%; Pred. No. 1.1e-21;
RESULT 1491
ID AAR07513 standard; protein; 258 AA.
DE Ancrod-like polypeptide #2.
PN EP395375-A.
PD 31-OCT-1990.
PA (GLAX) GLAXO INC.
PA (KNOL) KNOLL AG.
Query Match 27.9%; Score 383; DB 2; Length 258;
Best Local Similarity 34.3%; Pred. No. 1.3e-21;
RESULT 1492
ID AAR05775 standard; protein; 272 AA.
DE Snake venom ancrod polypeptide.
PN WO9006362-A.
PD 14-JUN-1990.
PA (BADI) BASF AG.
PA (BACH/) BACH A.
Query Match 27.9%; Score 383; DB 2; Length 272;
Best Local Similarity 33.9%; Pred. No. 1.4e-21;
RESULT 1493
ID AAU79393 standard; protein; 171 AA.
DE Novel human kallikrein KLIK15, splice variant #3.
PN WO200214485-A2.
PD 21-FEB-2002.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 27.8%; Score 382.5; DB 5; Length 171;
Best Local Similarity 35.8%; Pred. No. 9.2e-22;
RESULT 1494
ID ADNI0933 standard; protein; 171 AA.
DE Human kallikrein 15, marker of endocrine cancer.
PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 27.8%; Score 382.5; DB 8; Length 171;
Best Local Similarity 35.8%; Pred. No. 9.2e-22;
RESULT 1495
ID ABM82642 standard; protein; 212 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2891.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 27.8%; Score 382; DB 8; Length 212;
Best Local Similarity 35.5%; Pred. No. 1.2e-21;
RESULT 1496
ID AAR05772 standard; protein; 250 AA.
DE Human adipin gene product from the clone phg31.
PN WO9006365-A.
PD 14-JUN-1990.
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.
PA (DANA-) DANA-FARBER CANCER INST.
PA (META-) METABOLIC BIOSYSTEMS INC.
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.
Query Match 27.8%; Score 382; DB 2; Length 250;
Best Local Similarity 37.2%; Pred. No. 1.5e-21;
RESULT 1497
ID AAR05421 standard; protein; 250 AA.
DE Human adipin/D encoded by a cDNA.
PN WO9001540-A.
PD 22-FEB-1990.
PA (CALB-) CALIF BIOTECHN INC.
Query Match 27.8%; Score 382; DB 2; Length 250;
Best Local Similarity 38.4%; Pred. No. 1.5e-21;
RESULT 1498
ID ADE58221 standard; protein; 263 AA.
DE Rat Protein AAB31922, SEQ ID NO 4092.
PN WO2003016475-A2.

PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 27.7%; Score 381; DB 7; Length 263;
Best Local Similarity 37.6%; Pred. No. 1.9e-21;
RESULT 1499
ID ADN99596 standard; protein; 187 AA.
DE Novel human protein sequence #412.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 27.6%; Score 379.5; DB 8; Length 187;
Best Local Similarity 42.7%; Pred. No. 1.7e-21;
RESULT 1500
ID ABU92049 standard; protein; 220 AA.
DE Human protein modification and maintenance molecule-29 (PMMW-29).
PN WO2003031939-A2.
PD 17-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 27.6%; Score 379; DB 6; Length 220;
Best Local Similarity 37.2%; Pred. No. 2.2e-21;

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 5, 2005, 20:31:44 ; Search time 42 Seconds
(without alignments)
440.785 Million cell updates/sec

Title: US-10-015-385A-194

Perfect score: 1374

Sequence: 1 MGLSIFLLCVLGLSQAATP.....GVYICKYVDWIRMNRN 248

Scoring table: BLASUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5A COMB.pep:*

2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*

3: /cgn2_6/prodata/1/iaa/6A COMB.pep:*

4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*

5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep:*

6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1359.5	98.9	249	4	US-09-949-016-8151	Sequence 8151, Ap
2	1301	94.7	254	4	US-09-949-016-6948	Sequence 6948, Ap
3	811	59.0	162	4	US-09-244-111-6	Sequence 6, Appli
4	630.5	45.9	260	4	US-09-618-259-7	Sequence 7, Appli
5	626.5	45.6	260	3	US-09-070-526-2	Sequence 2, Appli
6	622.5	45.3	260	3	US-09-025-059-3	Sequence 3, Appli
7	622.5	45.3	260	3	US-09-008-271A-7	Sequence 7, Appli
8	622.5	45.3	260	4	US-09-618-259-8	Sequence 8, Appli
9	618.5	45.0	250	4	US-09-205-258-427	Sequence 427, App
10	618.5	45.0	282	3	US-09-025-059-1	Sequence 1, Appli
11	602.5	43.9	288	4	US-09-386-642-13	Sequence 13, Appl
12	598.5	43.6	289	4	US-09-386-642-14	Sequence 14, Appl
13	597.5	43.5	248	3	US-08-944-483-24	Sequence 24, Appl
14	573	41.7	247	2	US-08-956-267A-2	Sequence 2, Appli
15	567	41.3	290	4	US-09-949-016-8166	Sequence 8166, Ap
16	564.5	41.1	270	4	US-09-949-016-7712	Sequence 7712, Ap
17	564.5	41.1	293	4	US-09-509-908-2	Sequence 2, Appli
18	564	41.0	276	1	US-08-467-155A-1	Sequence 1, Appli
19	564	41.0	276	2	US-08-628-198-1	Sequence 1, Appli
20	564	41.0	276	3	US-09-201-038-1	Sequence 1, Appli
21	564	41.0	276	5	PCT-US96-07343-1	Sequence 1, Appli
22	563	41.0	325	4	US-09-949-016-7713	Sequence 7713, Ap
23	561	40.8	244	1	US-08-361-395-1	Sequence 1, Appli
24	555	40.4	253	2	US-08-557-146-2	Sequence 2, Appli
25	555	40.4	253	2	US-08-824-874-3	Sequence 3, Appli
26	555	40.4	253	2	US-09-154-344-2	Sequence 2, Appli
27	555	40.4	253	3	US-08-930-188-2	Sequence 2, Appli

101	494	36.0	254	4	US-09-685-166A-523	Sequence 523, App	174	458	33.3	228	2	US-08-296-149-7	Sequence 7, Appli
102	494	36.0	254	4	US-09-679-426-523	Sequence 523, App	175	458	33.3	228	2	US-08-801-499-7	Sequence 7, Appli
103	494	36.0	254	4	US-09-759-143-523	Sequence 523, App	176	458	33.3	228	2	US-08-615-271-7	Sequence 7, Appli
104	494	36.0	254	4	US-09-651-236-523	Sequence 523, App	177	458	33.3	228	3	US-09-074-660-7	Sequence 7, Appli
105	493	35.9	262	2	US-08-790-131-1	Sequence 1, Appli	178	458	33.3	228	3	US-09-074-659-7	Sequence 7, Appli
106	493	35.9	262	2	US-08-790-131-3	Sequence 3, Appli	179	458	33.3	228	3	US-09-106-468-7	Sequence 7, Appli
107	493	35.9	262	2	US-08-681-151-4	Sequence 4, Appli	180	458	33.3	228	3	US-09-106-466A-7	Sequence 7, Appli
108	493	35.9	262	2	US-08-824-874-4	Sequence 4, Appli	181	458	33.3	228	3	US-09-106-467-7	Sequence 7, Appli
109	493	35.9	262	3	US-08-807-151-4	Sequence 4, Appli	182	457.5	33.3	237	3	US-08-768-859A-1	Sequence 1, Appli
110	493	35.9	262	3	US-09-210-084-4	Sequence 4, Appli	183	457.5	33.3	237	3	US-08-767-820A-1	Sequence 1, Appli
111	493	35.9	262	3	US-09-478-957-4	Sequence 4, Appli	184	457.5	33.3	237	3	US-08-622-046B-7	Sequence 7, Appli
112	493	35.9	262	4	US-09-764-762-4	Sequence 4, Appli	185	457.5	33.3	237	3	US-08-944-483-38	Sequence 38, Appli
113	492	35.8	225	2	US-09-027-337-5	Sequence 5, Appli	186	457.5	33.3	237	3	US-09-100-264-3	Sequence 3, Appli
114	492	35.8	225	4	US-09-644-600-5	Sequence 5, Appli	187	457.5	33.3	237	4	US-09-303-339-2	Sequence 2, Appli
115	492	35.8	225	4	US-09-654-600A-5	Sequence 5, Appli	188	457.5	33.3	237	4	US-08-843-076D-7	Sequence 7, Appli
116	492	35.8	262	1	US-08-744-026-4	Sequence 4, Appli	189	457.5	33.3	237	4	US-09-303-208-1	Sequence 1, Appli
117	492	35.8	262	2	US-09-102-732-4	Sequence 4, Appli	190	455.5	33.2	237	1	US-08-096-946-11	Sequence 11, Appli
118	492	35.8	262	3	US-09-261-767-4	Sequence 4, Appli	191	455.5	33.2	237	5	PCT-US94-07329-11	Sequence 11, Appli
119	491	35.7	221	4	US-09-959-393-33	Sequence 33, Appli	192	455.5	33.2	237	5	PCT-US95-06157-1	Sequence 1, Appli
120	490	35.7	224	3	US-08-944-483-34	Sequence 34, Appli	193	455.5	33.2	261	3	US-08-768-859A-19	Sequence 19, Appli
121	487.5	35.5	449	4	US-09-636-215-617	Sequence 617, App	194	455.5	33.2	261	3	US-08-767-820A-19	Sequence 19, Appli
122	487.5	35.5	449	4	US-09-685-168A-617	Sequence 617, App	195	455.5	33.2	261	3	US-08-622-046B-3	Sequence 3, Appli
123	487.5	35.5	449	4	US-09-679-426-617	Sequence 617, App	196	454.5	33.1	232	2	US-08-897-340-31	Sequence 31, Appli
124	487.5	35.5	449	4	US-09-759-143-617	Sequence 617, App	197	454.5	33.1	232	3	US-09-253-329-31	Sequence 31, Appli
125	487.5	35.5	449	4	US-09-651-236-617	Sequence 617, App	198	454.5	33.1	244	5	PCT-US95-06157-10	Sequence 10, Appli
126	487	35.4	224	2	US-08-766-982-13	Sequence 13, Appli	199	452.5	32.9	238	5	PCT-US95-06157-8	Sequence 8, Appli
127	487	35.4	224	3	US-08-944-483-36	Sequence 36, Appli	200	452.5	32.9	244	3	US-08-768-859A-10	Sequence 10, Appli
128	487	35.4	224	3	US-09-296-219-13	Sequence 13, Appli	201	452.5	32.9	244	3	US-08-767-820A-10	Sequence 10, Appli
129	478	34.8	224	3	US-08-944-483-35	Sequence 35, Appli	202	452.5	32.9	244	3	US-08-622-046B-16	Sequence 16, Appli
130	472.5	34.4	220	3	US-09-439-313-327	Sequence 327, App	203	452.5	32.9	244	3	US-09-100-264-5	Sequence 5, Appli
131	472.5	34.4	220	3	US-09-352-616A-327	Sequence 327, App	204	452.5	32.9	244	3	US-08-843-076D-5	Sequence 5, Appli
132	472.5	34.4	220	4	US-09-232-149A-327	Sequence 327, App	205	450.5	32.8	237	2	US-08-844-024-2	Sequence 2, Appli
133	472.5	34.4	220	4	US-09-636-215-327	Sequence 327, App	206	450.5	32.8	237	2	US-08-718-547-2	Sequence 2, Appli
134	472.5	34.4	220	4	US-09-685-168A-327	Sequence 327, App	207	450.5	32.8	237	3	US-08-768-859A-16	Sequence 16, Appli
135	472.5	34.4	220	4	US-09-688-483-327	Sequence 327, App	208	450.5	32.8	237	3	US-08-767-820A-16	Sequence 16, Appli
136	472.5	34.4	220	4	US-09-679-426-327	Sequence 327, App	209	450.5	32.8	237	3	US-08-622-046B-12	Sequence 12, Appli
137	472.5	34.4	220	4	US-09-759-143-327	Sequence 327, App	210	450.5	32.8	237	3	US-08-944-483-37	Sequence 37, Appli
138	472.5	34.4	220	4	US-09-651-236-327	Sequence 327, App	211	450.5	32.8	237	4	US-09-100-264-1	Sequence 1, Appli
139	472.5	34.4	262	4	US-09-618-259-9	Sequence 9, Appli	212	450.5	32.8	237	4	US-08-843-076D-1	Sequence 1, Appli
140	470.5	34.2	261	1	US-08-744-026-5	Sequence 5, Appli	213	450.5	32.8	238	3	US-08-768-859A-8	Sequence 8, Appli
141	470.5	34.2	261	2	US-09-102-732-5	Sequence 5, Appli	214	450.5	32.8	238	3	US-08-767-820A-8	Sequence 8, Appli
142	470.5	34.2	261	3	US-09-083-521-6	Sequence 6, Appli	215	450	32.8	260	3	US-08-983-075D-9	Sequence 9, Appli
143	470.5	34.2	261	3	US-09-261-767-5	Sequence 5, Appli	216	449.5	32.7	244	3	US-08-622-046B-5	Sequence 5, Appli
144	470.5	34.2	261	4	US-09-413-049-1	Sequence 1, Appli	217	448.5	32.6	237	1	US-08-096-946-10	Sequence 10, Appli
145	470.5	34.2	261	4	US-09-907-402-1	Sequence 1, Appli	218	448.5	32.6	237	5	PCT-US94-07329-10	Sequence 10, Appli
146	470.5	34.2	261	4	US-09-618-259-10	Sequence 10, Appli	219	448.5	32.6	237	5	PCT-US95-06157-16	Sequence 16, Appli
147	470.5	34.2	375	4	US-09-755-100A-11	Sequence 11, Appli	220	447.5	32.6	237	3	US-08-768-859A-21	Sequence 21, Appli
148	470	34.2	238	3	US-08-944-483-39	Sequence 39, Appli	221	447.5	32.6	237	3	US-08-767-820A-21	Sequence 21, Appli
149	469.5	34.2	271	1	US-08-467-155A-10	Sequence 10, Appli	222	447.5	32.6	237	3	US-08-622-046B-1	Sequence 1, Appli
150	469.5	34.2	271	2	US-08-628-198-10	Sequence 10, Appli	223	447.5	32.6	237	4	US-08-843-076D-8	Sequence 8, Appli
151	469.5	34.2	271	3	US-09-201-038-10	Sequence 10, Appli	224	447.5	32.6	237	4	US-08-472-228A-1	Sequence 1, Appli
152	469.5	34.2	271	5	PCT-US96-07343-10	Sequence 10, Appli	225	445	32.4	240	3	US-09-146-831-1	Sequence 1, Appli
153	469	34.1	284	4	US-09-386-642-54	Sequence 54, Appli	226	445	32.4	240	3	PCT-US96-09303-1	Sequence 1, Appli
154	464.5	33.8	286	1	US-08-467-155A-9	Sequence 9, Appli	227	445	32.4	240	5	US-08-467-155A-8	Sequence 8, Appli
155	464.5	33.8	286	2	US-08-628-198-9	Sequence 9, Appli	228	430	31.3	299	2	US-08-628-198-8	Sequence 8, Appli
156	464.5	33.8	286	5	PCT-US96-07343-9	Sequence 9, Appli	229	430	31.3	299	2	US-09-201-038-8	Sequence 8, Appli
157	464.5	33.8	286	5	US-09-201-038-9	Sequence 9, Appli	230	430	31.3	299	5	PCT-US96-07343-8	Sequence 8, Appli
158	460.5	33.5	261	5	PCT-US95-06157-6	Sequence 6, Appli	231	430	31.3	299	5	US-09-020-956-176	Sequence 176, App
159	459	33.4	238	4	US-09-664-595A-15	Sequence 15, Appli	232	426.5	31.0	205	3	US-09-030-607-176	Sequence 176, App
160	459	33.4	262	3	US-09-025-059-4	Sequence 4, Appli	233	426.5	31.0	205	3	US-09-439-313-176	Sequence 176, App
161	459	33.4	262	4	US-09-755-100A-14	Sequence 14, Appli	234	426.5	31.0	205	3	US-09-352-616A-176	Sequence 176, App
162	458.5	33.4	261	3	US-08-768-859A-6	Sequence 6, Appli	235	426.5	31.0	205	3	US-09-233-149A-176	Sequence 176, App
163	458.5	33.4	261	3	US-08-767-820A-6	Sequence 6, Appli	236	426.5	31.0	205	4	US-09-159-813-176	Sequence 176, App
164	458.5	33.4	261	3	US-08-622-046B-14	Sequence 14, Appli	237	426.5	31.0	205	4	US-09-636-215-176	Sequence 176, App
165	458.5	33.4	261	3	US-09-100-264-7	Sequence 7, Appli	238	426.5	31.0	205	4	US-09-685-168A-176	Sequence 176, App
166	458.5	33.4	261	3	US-08-983-075D-7	Sequence 7, Appli	239	426.5	31.0	205	4	US-09-115-453-176	Sequence 176, App
167	458.5	33.4	261	4	US-08-843-076D-3	Sequence 3, Appli	240	426.5	31.0	205	4	US-09-688-489-176	Sequence 176, App
168	458.5	33.4	278	4	US-09-949-016-7711	Sequence 7711, Ap	241	426.5	31.0	205	4	US-09-679-426-176	Sequence 176, App
169	458	33.3	228	1	US-08-278-091-7	Sequence 7, Appli	242	426.5	31.0	205	4	US-09-759-143-176	Sequence 176, App
170	458	33.3	228	1	US-08-483-859-7	Sequence 7, Appli	243	426.5	31.0	205	4	US-09-651-236-176	Sequence 176, App
171	458	33.3	228	1	US-08-472-173-7	Sequence 7, Appli	244	426.5	31.0	205	4	US-09-244-111-4	Sequence 4, Appli
172	458	33.3	228	2	US-08-482-816-7	Sequence 7, Appli	245	418	30.4	237	2	US-08-738-413B-9	Sequence 9, Appli
173	458	33.3	228	2			246	417.5	30.4	233	2		

247	406.5	29.6	231	4	US-09-402-515A-16	Sequence 16, Appl	320	354	25.8	461	6	5270178-18	Patent No. 5270178
248	404	29.4	234	1	US-08-684-862-6	Sequence 6, Appl	321	354	25.8	461	6	5270178-17	Patent No. 5270178
249	393	28.6	236	1	US-08-684-862-5	Sequence 5, Appl	322	354	25.8	461	6	5270178-18	Patent No. 5270178
250	389	28.3	236	2	US-08-738-413B-10	Sequence 10, Appl	323	353.5	25.7	230	3	US-08-944-483-62	Sequence 62, Appl
251	387	28.2	253	6	5223425-8	Patent No. 5223425	324	353.5	25.7	270	2	US-08-978-404B-8	Sequence 8, Appl
252	387	28.2	253	6	5223425-8	Patent No. 5223425	325	353	25.7	274	2	US-08-978-404B-5	Sequence 5, Appl
253	385.5	28.1	267	4	US-09-949-016-9575	Sequence 9575, Ap	326	353	25.7	314	3	US-09-008-271A-3	Sequence 3, Appl
254	385	28.0	232	2	US-08-738-413B-11	Sequence 11, Appl	327	353	25.7	314	4	US-09-023-942A-6	Sequence 6, Appl
255	385	28.0	250	6	5223425-4	Patent No. 5223425	328	353	25.7	314	4	US-09-907-794A-257	Sequence 257, App
256	385	28.0	250	6	5223425-4	Patent No. 5223425	329	353	25.7	314	4	US-09-905-125A-257	Sequence 257, App
257	377.5	27.3	154	3	US-09-261-416-5	Sequence 5, Appl	330	353	25.7	314	4	US-09-902-775A-257	Sequence 257, App
258	374.5	27.3	238	6	5223425-5	Patent No. 5223425	331	353	25.7	314	4	US-09-906-700-257	Sequence 257, App
259	374.5	27.3	238	6	5223425-5	Patent No. 5223425	332	353	25.7	314	4	US-09-903-603A-257	Sequence 257, App
260	374.5	27.3	259	6	5223425-2	Patent No. 5223425	333	353	25.7	314	4	US-09-904-920A-257	Sequence 257, App
261	374.5	27.3	259	6	5223425-2	Patent No. 5223425	334	353	25.7	314	4	US-09-909-064-257	Sequence 257, App
262	374	27.2	260	6	5223425-10	Patent No. 5223425	335	353	25.7	314	4	US-09-905-381A-257	Sequence 257, App
263	374	27.2	260	6	5223425-10	Patent No. 5223425	336	353	25.7	314	4	US-09-906-618-257	Sequence 257, App
264	370.5	27.0	228	3	US-08-944-483-44	Sequence 44, Appl	337	351.5	25.6	814	1	US-08-750-711-1	Sequence 1, Appl
265	370	26.9	418	4	US-09-370-838-62	Sequence 62, Appl	338	349.5	25.4	166	4	US-09-636-215-838	Sequence 838, App
266	370	26.9	418	4	US-09-854-133-62	Sequence 62, Appl	339	349.5	25.4	166	4	US-09-685-166A-838	Sequence 838, App
267	368	26.8	418	1	US-08-508-448C-25	Sequence 25, Appl	340	349.5	25.4	166	4	US-09-679-426-838	Sequence 838, App
268	368	26.8	418	1	US-08-508-448C-25	Sequence 25, Appl	341	349.5	25.4	166	4	US-09-759-143-838	Sequence 838, App
269	368	26.8	418	4	US-09-370-838-82	Sequence 82, Appl	342	349.5	25.4	166	4	US-09-651-236-838	Sequence 838, App
270	368	26.8	418	4	US-09-854-133-83	Sequence 83, Appl	343	349	25.4	159	3	US-09-020-956-172	Sequence 172, App
271	368	26.8	418	4	US-09-854-133-83	Sequence 83, Appl	344	349	25.4	159	3	US-09-030-607-172	Sequence 172, App
272	366.5	26.7	149	3	US-09-518-046-20	Sequence 20, Appl	345	349	25.4	159	3	US-09-439-313-172	Sequence 172, App
273	366	26.6	232	1	US-08-508-448C-19	Sequence 19, Appl	346	349	25.4	159	3	US-09-352-616A-172	Sequence 172, App
274	366	26.6	234	2	US-08-738-413B-12	Sequence 12, Appl	347	349	25.4	159	4	US-09-233-149A-172	Sequence 172, App
275	365.5	26.6	245	3	US-08-906-769-121	Sequence 121, App	348	349	25.4	159	4	US-09-159-813-172	Sequence 172, App
276	365.5	26.6	245	3	US-08-906-616-121	Sequence 121, App	349	349	25.4	159	4	US-09-636-215-172	Sequence 172, App
277	365.5	26.6	245	3	US-08-906-616-121	Sequence 121, App	350	349	25.4	159	4	US-09-683-166A-172	Sequence 172, App
278	365.5	26.6	245	3	US-09-012-431-121	Sequence 121, App	351	349	25.4	159	4	US-09-115-453-172	Sequence 172, App
279	365.5	26.6	245	3	US-09-012-692-121	Sequence 121, App	352	349	25.4	159	4	US-09-688-489-172	Sequence 172, App
280	365.5	26.6	245	3	US-08-906-613-121	Sequence 121, App	353	349	25.4	159	4	US-09-679-426-172	Sequence 172, App
281	364.5	26.5	400	3	US-09-004-731-30	Sequence 30, Appl	354	349	25.4	159	4	US-09-759-143-172	Sequence 172, App
282	364.5	26.5	400	3	US-09-004-731-30	Sequence 30, Appl	355	349	25.4	159	4	US-09-651-236-172	Sequence 172, App
283	364.5	26.5	400	3	US-08-749-693-30	Sequence 30, Appl	356	349	25.4	1019	1	US-08-296-014A-4	Sequence 4, Appl
284	364.5	26.5	400	3	US-08-749-693-30	Sequence 30, Appl	357	349	25.4	1019	2	US-08-596-405-4	Sequence 4, Appl
285	364.5	26.5	400	3	US-09-004-729-30	Sequence 30, Appl	358	349	25.4	1019	2	US-08-877-620-4	Sequence 4, Appl
286	364.5	26.5	400	3	US-09-004-729-33	Sequence 33, Appl	359	349	25.4	1019	4	US-09-287-368-4	Sequence 4, Appl
287	362.5	26.4	242	3	US-09-004-731-36	Sequence 36, Appl	360	349	25.4	1019	4	US-09-626-795-4	Sequence 4, Appl
288	362.5	26.4	242	3	US-08-749-693-36	Sequence 36, Appl	361	349	25.4	1083	1	US-08-296-014A-2	Sequence 2, Appl
289	362.5	26.4	242	3	US-09-004-729-36	Sequence 36, Appl	362	349	25.4	1083	2	US-08-596-405-2	Sequence 2, Appl
290	362.5	26.4	319	4	US-09-386-642-12	Sequence 12, Appl	363	349	25.4	1083	2	US-08-877-620-2	Sequence 2, Appl
291	362.5	26.4	328	4	US-09-386-642-11	Sequence 11, Appl	364	349	25.4	1083	4	US-09-287-368-2	Sequence 2, Appl
292	361.5	26.3	387	3	US-09-032-215-8	Sequence 8, Appl	365	349	25.4	1083	4	US-09-626-795-2	Sequence 2, Appl
293	361.5	26.3	387	3	US-09-032-215-13	Sequence 13, Appl	366	348	25.3	461	6	5460953-3	Patent No. 5460953
294	361	26.3	236	1	US-08-684-862-4	Sequence 4, Appl	367	348	25.3	461	6	5460953-3	Patent No. 5460953
295	360.5	26.2	299	3	US-08-944-483-66	Sequence 66, Appl	368	347	25.3	262	1	US-07-720-189-1	Sequence 1, Appl
296	358.5	26.1	232	4	US-09-959-392-31	Sequence 31, Appl	369	347	25.3	356	4	US-09-054-272-18	Sequence 18, Appl
297	358	26.1	812	4	US-08-991-761A-7	Sequence 7, Appl	370	347	25.3	409	3	US-09-065-872-2	Sequence 2, Appl
298	357.5	26.0	232	3	US-08-906-769-81	Sequence 81, Appl	371	347	25.3	409	4	US-09-667-570A-2	Sequence 2, Appl
299	357.5	26.0	232	3	US-08-906-616-81	Sequence 81, Appl	372	347	25.3	410	3	US-09-065-872-1	Sequence 1, Appl
300	357.5	26.0	232	3	US-08-817-795-81	Sequence 81, Appl	373	347	25.3	410	4	US-09-667-570A-1	Sequence 1, Appl
301	357.5	26.0	232	3	US-08-639-075A-81	Sequence 81, Appl	374	347	25.3	419	1	US-08-295-411-1	Sequence 1, Appl
302	357.5	26.0	232	3	US-09-012-431-81	Sequence 81, Appl	375	347	25.3	419	2	US-08-955-471-1	Sequence 1, Appl
303	357.5	26.0	232	3	US-09-012-692-81	Sequence 81, Appl	376	347	25.3	419	4	US-09-667-570A-3	Sequence 3, Appl
304	357.5	26.0	232	3	US-08-906-613-81	Sequence 81, Appl	377	347	25.3	419	4	US-10-182-263-1	Sequence 1, Appl
305	357.5	26.0	232	5	PCT-US95-1442A-81	Sequence 81, Appl	378	347	25.3	419	5	PCT-US92-10242-1	Sequence 1, Appl
306	357	26.0	268	4	US-09-949-016-10712	Sequence 10712, A	379	347	25.3	460	2	US-08-756-506-2	Sequence 2, Appl
307	356.5	25.9	248	3	US-08-944-483-63	Sequence 63, Appl	380	347	25.3	460	2	US-08-756-506-2	Sequence 2, Appl
308	355.5	25.9	148	4	US-09-618-259-2	Sequence 2, Appl	381	347	25.3	461	4	US-10-182-263-2	Sequence 2, Appl
309	355.5	25.9	231	2	US-09-027-337-6	Sequence 6, Appl	382	347	25.3	461	4	US-09-054-272-32	Sequence 32, Appl
310	355.5	25.9	231	4	US-09-644-600-6	Sequence 6, Appl	383	347	25.3	461	4	US-09-949-016-5921	Sequence 5921, Ap
311	355.5	25.9	231	4	US-09-654-600A-6	Sequence 6, Appl	384	347	25.3	461	6	5225537-2	Patent No. 5225537
312	355.5	25.9	276	2	US-09-016-366A-5	Sequence 15, Appl	385	347	25.3	461	6	5225537-2	Patent No. 5225537
313	355.5	25.9	276	2	US-08-978-404B-21	Sequence 21, Appl	386	347	25.3	485	4	US-09-949-016-10882	Sequence 10882, A
314	354.5	25.8	461	6	5270178-2	Patent No. 5270178	387	346.5	25.2	791	1	US-08-643-219-1	Sequence 1, Appl
315	354.5	25.8	461	6	5270178-2	Patent No. 5270178	388	346.5	25.2	791	3	US-08-851-350-1	Sequence 1, Appl
316	354	25.8	229	2	US-08-557-146-13	Sequence 13, Appl	389	346	25.2	234	3	US-08-944-483-46	Sequence 46, Appl
317	354	25.8	229	2	US-09-154-344-13	Sequence 13, Appl	390	346	25.2	241	3	US-08-944-483-59	Sequence 59, Appl
318	354	25.8	312	4	US-09-023-942A-4	Sequence 4, Appl	391	346	25.2	419	4	US-10-182-263-5	Sequence 5, Appl
319	354	25.8	461	6	5270178-17	Patent No. 5270178	392	346	25.2	419	4	US-10-182-263-6	Sequence 6, Appl

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394	345.5	25.1	248	3	US-08-906-616-111	Sequence 111, App	467	339.5	24.7	258	1	US-07-990-301A-2	Sequence 2, Appli
395	345.5	25.1	248	3	US-08-817-795-111	Sequence 111, App	468	339.5	24.7	333	4	US-08-991-761A-8	Sequence 8, Appli
396	345.5	25.1	248	3	US-08-633-075A-111	Sequence 111, App	469	339	24.7	419	4	US-10-182-263-4	Sequence 4, Appli
397	345.5	25.1	248	3	US-09-012-431-111	Sequence 111, App	470	339	24.7	461	3	US-08-742-877-2	Sequence 2, Appli
398	345.5	25.1	248	3	US-09-012-692-111	Sequence 111, App	471	339	24.7	461	3	US-08-083-871A-21	Sequence 21, Appli
399	345.5	25.1	248	3	US-08-906-613-111	Sequence 111, App	472	339	24.7	461	6	US-10-133-907-5	Sequence 5, Appli
400	345.5	25.1	248	5	PCT-US95-14442A-111	Sequence 111, App	473	339	24.7	461	6	5521070-2	Patent No. 5521070
401	344	25.0	274	2	US-09-016-366A-21	Sequence 21, Appli	474	339	24.7	461	6	5521070-2	Patent No. 5521070
402	344	25.0	274	2	US-08-978-404B-16	Sequence 16, Appli	475	339	24.7	480	4	US-09-949-016-11123	Sequence 11123, A
403	343.5	25.0	273	2	US-08-978-404B-3	Sequence 3, Appli	476	339	24.7	481	4	US-09-949-016-9238	Sequence 9238, Ap
404	343.5	25.0	460	6	5270178-13	Patent No. 5270178	477	339	24.7	481	4	US-09-949-016-9239	Sequence 9239, Ap
405	343.5	25.0	460	6	5270178-14	Patent No. 5270178	478	339	24.7	637	4	US-09-949-016-11538	Sequence 11538, A
406	343.5	25.0	460	6	5270178-15	Patent No. 5270178	479	339	24.7	637	4	US-09-949-016-11539	Sequence 11539, A
407	343.5	25.0	460	6	5270178-16	Patent No. 5270178	480	338.5	24.6	230	1	US-08-379-621-2	Sequence 2, Appli
408	343.5	25.0	460	6	5270178-13	Patent No. 5270178	481	338.5	24.6	230	1	US-08-147-000B-2	Sequence 2, Appli
409	343.5	25.0	460	6	5270178-14	Patent No. 5270178	482	338.5	24.6	230	2	US-08-889-078-2	Sequence 2, Appli
410	343.5	25.0	460	6	5270178-15	Patent No. 5270178	483	338.5	24.6	261	6	5270178-5	Patent No. 5270178
411	343.5	25.0	460	6	5270178-16	Patent No. 5270178	484	338.5	24.6	261	6	5270178-5	Patent No. 5270178
412	343	25.0	284	4	US-09-387-375-7	Sequence 7, Appli	485	338.5	24.6	308	3	US-08-705-875A-10	Sequence 10, Appli
413	343	25.0	284	4	US-10-041-400A-7	Sequence 7, Appli	486	338.5	24.6	308	4	US-09-242-999-10	Sequence 10, Appli
414	343	25.0	284	4	US-10-042-091A-7	Sequence 7, Appli	487	338	24.6	250	3	US-08-944-483-51	Sequence 51, Appli
415	342.5	24.9	248	3	US-09-032-215-37	Sequence 37, Appli	488	337.5	24.6	267	4	US-09-949-016-10711	Sequence 10711, A
416	342.5	24.9	249	3	US-09-079-970A-5	Sequence 5, Appli	489	337	24.5	235	3	US-08-944-483-48	Sequence 48, Appli
417	342.5	24.9	273	2	US-08-978-404B-6	Sequence 6, Appli	490	337	24.5	406	4	US-09-851-588-6	Sequence 6, Appli
418	342.5	24.9	546	6	5200340-6	Patent No. 5200340	491	337	24.5	423	4	US-09-607-745-2	Sequence 2, Appli
419	342.5	24.9	546	6	5200340-6	Patent No. 5200340	492	337	24.5	435	4	US-09-607-745-2	Sequence 2, Appli
420	342.5	24.9	713	4	US-09-949-016-9983	Sequence 9983, Ap	493	337	24.5	437	4	US-09-851-588-8	Sequence 8, Appli
421	342.5	24.9	790	1	US-08-469-486-54	Sequence 54, Appli	494	337	24.5	812	1	US-08-248-629A-1	Sequence 1, Appli
422	342.5	24.9	790	1	US-08-469-658-54	Sequence 54, Appli	495	337	24.5	812	1	US-08-451-932-1	Sequence 1, Appli
423	342.5	24.9	791	2	US-09-131-995-1	Sequence 1, Appli	496	337	24.5	812	1	US-08-452-260-1	Sequence 1, Appli
424	342.5	24.9	791	2	US-08-832-087B-1	Sequence 1, Appli	497	337	24.5	812	1	US-08-326-785-1	Sequence 1, Appli
425	342.5	24.9	791	3	US-09-132-154-1	Sequence 1, Appli	498	337	24.5	812	2	US-08-612-788-1	Sequence 1, Appli
426	342.5	24.9	791	4	US-08-991-761A-6	Sequence 6, Appli	499	337	24.5	812	2	US-08-605-598B-1	Sequence 1, Appli
427	342.5	24.9	791	4	US-08-924-287A-1	Sequence 1, Appli	500	337	24.5	812	2	US-08-429-743-1	Sequence 1, Appli
428	342.5	24.9	810	1	US-07-854-603-2	Sequence 2, Appli	501	337	24.5	812	2	US-08-866-735-1	Sequence 1, Appli
429	342.5	24.9	810	1	US-08-147-000B-29	Sequence 29, Appli	502	337	24.5	812	3	US-09-066-028-1	Sequence 1, Appli
430	342.5	24.9	810	3	US-09-086-514-1	Sequence 1, Appli	503	337	24.5	812	4	US-09-192-012-3	Sequence 3, Appli
431	342.5	24.9	810	4	US-09-192-012-5	Sequence 5, Appli	504	337	24.5	812	4	US-09-335-325-1	Sequence 1, Appli
432	342.5	24.9	810	4	US-09-403-736-1	Sequence 1, Appli	505	337	24.5	812	4	US-08-991-761A-12	Sequence 12, Appli
433	342.5	24.9	810	4	US-09-701-265-1	Sequence 1, Appli	506	337	24.5	812	5	PCT-US95-05107-1	Sequence 1, Appli
434	342.5	24.9	810	6	5200340-8	Patent No. 5200340	507	336.5	24.5	435	3	US-09-008-271A-6	Sequence 6, Appli
435	342.5	24.9	810	6	5200340-8	Patent No. 5200340	508	336	24.5	415	2	US-08-073-531B-1	Sequence 1, Appli
436	342	24.9	234	1	US-08-684-862-3	Sequence 3, Appli	509	336	24.5	415	2	US-08-766-288-1	Sequence 1, Appli
437	342	24.9	273	2	US-09-016-366A-19	Sequence 19, Appli	510	336	24.5	790	4	US-08-991-761A-13	Sequence 13, Appli
438	342	24.9	273	2	US-08-978-404B-14	Sequence 14, Appli	511	334.5	24.3	446	4	US-10-177-661-4	Sequence 4, Appli
439	341.5	24.9	156	3	US-09-261-416-6	Sequence 6, Appli	512	334.5	24.3	477	4	US-10-177-661-2	Sequence 2, Appli
440	341.5	24.9	261	6	5270178-19	Patent No. 5270178	513	334.5	24.3	562	4	US-09-879-792-12	Sequence 12, Appli
441	341.5	24.9	261	6	5270178-20	Patent No. 5270178	514	334	24.3	316	4	US-09-387-375-9	Sequence 9, Appli
442	341.5	24.9	261	6	5270178-20	Patent No. 5270178	515	334	24.3	316	4	US-10-041-400A-9	Sequence 9, Appli
443	341.5	24.9	261	6	5270178-20	Patent No. 5270178	516	334	24.3	316	4	US-10-042-091A-9	Sequence 9, Appli
444	341	24.8	261	6	5270178-21	Patent No. 5270178	517	333.5	24.3	290	4	US-09-386-653A-7	Sequence 7, Appli
445	341	24.8	261	6	5270178-21	Patent No. 5270178	518	333.5	24.3	302	3	US-09-220-731-26	Sequence 26, Appli
446	341	24.8	306	4	US-09-386-642-53	Sequence 53, Appli	519	333.5	24.3	302	4	US-09-242-999-22	Sequence 22, Appli
447	341	24.8	415	1	US-09-118-748-2	Sequence 2, Appli	520	333	24.2	415	1	US-08-295-411-2	Sequence 2, Appli
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449	340.5	24.8	230	1	US-08-266-407A-47	Sequence 47, Appli	522	333	24.2	415	5	PCT-US92-10242-2	Sequence 2, Appli
450	340.5	24.8	230	2	US-08-892-544-47	Sequence 47, Appli	523	332.5	24.2	638	2	US-08-681-151-3	Sequence 3, Appli
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453	340.5	24.8	230	3	US-09-296-219-12	Sequence 12, Appli	526	331	24.1	579	1	US-08-295-411-4	Sequence 4, Appli
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456	340.5	24.8	244	4	US-09-601-318-7	Sequence 7, Appli	529	331	24.1	579	5	PCT-US92-10242-4	Sequence 4, Appli
457	340.5	24.8	244	4	US-09-079-970A-6	Sequence 6, Appli	530	331	24.1	615	1	US-07-998-972A-3	Sequence 3, Appli
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459	340.5	24.8	245	3	US-09-601-318-1	Sequence 1, Appli	532	331	24.1	615	1	US-08-462-261-3	Sequence 3, Appli
460	340.5	24.8	267	2	US-09-016-366A-23	Sequence 23, Appli	533	331	24.1	622	3	PCT-US92-11357-3	Sequence 3, Appli
461	340.5	24.8	267	2	US-08-978-404B-18	Sequence 18, Appli	534	331	24.1	622	4	US-08-952-967-8	Sequence 8, Appli
462	340.5	24.8	267	4	US-09-917-254-101	Sequence 101, Appli	535	331	24.1	622	4	US-09-054-272-42	Sequence 42, Appli
463	340.5	24.8	300	3	US-08-705-875A-6	Sequence 6, Appli	536	330.5	24.1	560	4	US-09-949-016-6458	Sequence 6458, Ap
464	340.5	24.8	300	4	US-09-242-999-6	Sequence 6, Appli	537	330.5	24.1	560	4	US-09-912-559-3	Sequence 3, Appli
465	340	24.7	419	4	US-10-182-263-3	Sequence 3, Appli	538	330	24.0	221	3	US-08-944-483-54	Sequence 54, Appli

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540	330	24.0	222	1	US-08-266-407A-46	Sequence 46, Appl	613	321	23.4	315	4	US-09-386-653A-9	Sequence 9, Appl
541	330	24.0	222	2	US-08-892-544-46	Sequence 46, Appl	614	321	23.4	655	1	US-08-148-910-12	Sequence 12, Appl
542	330	24.0	222	6	5223425-6	Patent No. 5223425	615	321	23.4	655	1	US-08-448-937A-12	Sequence 12, Appl
543	330	24.0	222	6	5223425-6	Patent No. 5223425	616	321	23.4	809	4	US-08-991-761A-9	Sequence 9, Appl
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545	329.5	24.0	376	2	US-08-558-269-10	Sequence 10, Appl	618	319.5	23.3	240	1	US-08-483-853-11	Sequence 11, Appl
546	329.5	24.0	376	3	US-09-410-882-10	Sequence 10, Appl	619	319.5	23.3	240	1	US-08-472-173-11	Sequence 11, Appl
547	329	23.9	259	3	US-08-944-483-52	Sequence 52, Appl	620	319.5	23.3	240	2	US-08-487-167-11	Sequence 11, Appl
548	328.5	23.9	238	3	US-08-944-483-64	Sequence 64, Appl	621	319.5	23.3	240	2	US-08-483-816-11	Sequence 11, Appl
549	328.5	23.9	338	4	US-08-991-761A-10	Sequence 10, Appl	622	319.5	23.3	240	2	US-08-296-149-11	Sequence 11, Appl
550	327.5	23.8	151	3	US-09-518-046-21	Sequence 21, Appl	623	319.5	23.3	240	2	US-08-801-493-11	Sequence 11, Appl
551	327.5	23.8	154	3	US-09-261-416-7	Sequence 7, Appl	624	319.5	23.3	240	2	US-08-615-271-11	Sequence 11, Appl
552	327	23.8	241	3	US-08-944-483-60	Sequence 60, Appl	625	319.5	23.3	240	3	US-09-074-660-11	Sequence 11, Appl
553	327	23.8	255	1	US-08-650-129-5	Sequence 5, Appl	626	319.5	23.3	240	3	US-09-074-659-11	Sequence 11, Appl
554	327	23.8	255	3	US-08-984-417-5	Sequence 5, Appl	627	319.5	23.3	240	3	US-09-106-468-11	Sequence 11, Appl
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556	325.5	23.7	261	3	US-08-163-919A-2	Sequence 2, Appl	629	319.5	23.3	240	3	US-09-106-467-11	Sequence 11, Appl
557	325.5	23.7	261	4	US-08-462-515-2	Sequence 2, Appl	630	319.5	23.3	254	3	US-08-944-483-50	Sequence 50, Appl
558	325.5	23.7	261	5	PCT-US94-14073-2	Sequence 2, Appl	631	318	23.1	295	4	US-10-165-442-3	Sequence 3, Appl
559	325	23.7	226	1	US-08-650-129-4	Sequence 4, Appl	632	317.5	23.1	245	3	US-08-944-483-69	Sequence 69, Appl
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562	324.5	23.6	228	1	US-08-483-859-10	Sequence 10, Appl	635	316.5	23.0	226	1	US-07-929-198-2	Sequence 2, Appl
563	324.5	23.6	228	1	US-08-472-173-10	Sequence 10, Appl	636	316.5	23.0	226	1	US-07-929-198-6	Sequence 6, Appl
564	324.5	23.6	228	2	US-08-487-167-10	Sequence 10, Appl	637	316.5	23.0	226	2	US-08-557-146-15	Sequence 15, Appl
565	324.5	23.6	228	2	US-08-482-816-10	Sequence 10, Appl	638	316.5	23.0	226	2	US-09-154-344-15	Sequence 15, Appl
566	324.5	23.6	228	2	US-08-296-149-10	Sequence 10, Appl	639	316.5	23.0	226	3	US-08-944-483-43	Sequence 43, Appl
567	324.5	23.6	228	2	US-08-801-499-10	Sequence 10, Appl	640	316	23.0	246	3	US-08-906-769-127	Sequence 127, App
568	324.5	23.6	228	2	US-08-615-271-10	Sequence 10, Appl	641	316	23.0	246	3	US-08-906-616-127	Sequence 127, App
569	324.5	23.6	228	3	US-09-074-660-10	Sequence 10, Appl	642	316	23.0	246	3	US-08-639-075A-127	Sequence 127, App
570	324.5	23.6	228	3	US-09-074-659-10	Sequence 10, Appl	643	316	23.0	246	3	US-09-012-431-127	Sequence 127, App
571	324.5	23.6	228	3	US-09-106-468-10	Sequence 10, Appl	644	316	23.0	246	3	US-09-012-692-127	Sequence 127, App
572	324.5	23.6	228	3	US-09-106-466A-10	Sequence 10, Appl	645	316	23.0	246	3	US-08-906-613-127	Sequence 127, App
573	324.5	23.6	228	3	US-09-106-467-10	Sequence 10, Appl	646	316	23.0	259	4	US-10-165-442-4	Sequence 4, Appl
574	323.5	23.5	275	2	US-09-016-366A-17	Sequence 17, Appl	647	315.5	23.0	254	3	US-09-578-303-5	Sequence 5, Appl
575	323.5	23.5	275	2	US-08-978-404B-12	Sequence 12, Appl	648	315.5	23.0	292	4	US-09-607-745-9	Sequence 9, Appl
576	323.5	23.5	406	1	US-08-293-778-24	Sequence 24, Appl	649	315.5	23.0	300	3	US-08-705-875A-4	Sequence 4, Appl
577	323.5	23.5	406	1	US-08-955-471-5	Sequence 5, Appl	650	315.5	23.0	300	3	US-09-220-731-21	Sequence 21, Appl
578	323.5	23.5	406	2	US-08-955-471-5	Sequence 5, Appl	651	315.5	23.0	300	4	US-09-243-999-4	Sequence 4, Appl
579	323.5	23.5	406	4	US-09-782-587B-1	Sequence 1, Appl	652	315.5	23.0	487	1	US-08-469-486-53	Sequence 53, Appl
580	323.5	23.5	406	4	US-09-782-587B-3	Sequence 3, Appl	653	315.5	23.0	487	2	US-08-469-658-53	Sequence 53, Appl
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583	323.5	23.5	444	2	US-08-327-690-2	Sequence 2, Appl	656	315	22.9	259	4	US-10-165-442-2	Sequence 2, Appl
584	323.5	23.5	444	2	US-08-660-289-2	Sequence 2, Appl	657	315	22.9	691	4	US-09-949-016-7775	Sequence 7775, Ap
585	323.5	23.5	444	2	US-08-537-807-2	Sequence 2, Appl	658	314.5	22.9	283	4	US-09-244-111-2	Sequence 2, Appl
586	323.5	23.5	444	2	US-08-871-003-2	Sequence 2, Appl	659	314	22.9	855	2	US-09-027-337-2	Sequence 2, Appl
587	323.5	23.5	444	3	US-08-464-233-2	Sequence 2, Appl	660	314	22.9	855	4	US-09-644-600-2	Sequence 2, Appl
588	323.5	23.5	444	3	US-09-189-607-2	Sequence 2, Appl	661	314	22.9	855	4	US-09-654-600A-2	Sequence 2, Appl
589	323.5	23.5	444	3	US-09-378-907-2	Sequence 2, Appl	662	313.5	22.8	226	1	US-07-929-198-4	Sequence 4, Appl
590	323.5	23.5	444	5	PCT-US94-05779-2	Sequence 2, Appl	663	312.5	22.7	242	4	US-09-959-392-34	Sequence 34, Appl
591	323.5	23.5	461	4	US-09-949-016-8839	Sequence 8839, Ap	664	312	22.7	248	3	US-08-944-483-71	Sequence 71, Appl
592	323.5	23.5	466	1	US-07-882-202A-4	Sequence 4, Appl	665	311.5	22.7	251	3	US-08-944-483-47	Sequence 47, Appl
593	323.5	23.5	466	1	US-08-021-615A-4	Sequence 4, Appl	666	311	22.6	383	2	US-08-558-269-6	Sequence 6, Appl
594	323.5	23.5	466	1	US-08-321-777-4	Sequence 4, Appl	667	311	22.6	383	3	US-09-410-882-6	Sequence 6, Appl
595	323.5	23.5	466	3	US-09-009-217-14	Sequence 14, Appl	668	311	22.6	798	1	US-08-200-900A-2	Sequence 2, Appl
596	323.5	23.5	466	3	US-09-009-656-14	Sequence 14, Appl	669	311	22.6	798	4	US-08-794-042-2	Sequence 2, Appl
597	323.5	23.5	466	5	PCT-US93-04493-4	Sequence 4, Appl	670	311	22.6	798	5	PCT-US94-00616-2	Sequence 2, Appl
598	323.5	23.5	483	4	US-09-949-016-9523	Sequence 9523, Ap	671	311	22.6	812	4	US-09-192-012-9	Sequence 2, Appl
599	322.5	23.5	285	4	US-09-023-942A-26	Sequence 26, Appl	672	311	22.6	1042	4	US-09-959-392-2	Sequence 2, Appl
600	322.5	23.5	560	4	US-09-912-559-4	Sequence 4, Appl	673	310.5	22.6	247	2	US-08-978-404B-47	Sequence 47, Appl
601	322	23.4	207	4	US-10-000-489-54	Sequence 54, Appl	674	309.5	22.5	241	4	US-09-657-986B-2	Sequence 2, Appl
602	322	23.4	699	4	US-09-949-016-6138	Sequence 6138, Ap	675	309.5	22.5	492	4	US-09-685-166A-895	Sequence 895, App
603	322	23.4	717	4	US-09-949-016-11182	Sequence 11182, A	676	309.5	22.5	492	4	US-09-879-792-14	Sequence 14, Appl
604	321.5	23.4	255	2	US-09-027-337-7	Sequence 7, Appl	677	309.5	22.5	492	4	US-09-679-426-895	Sequence 895, App
605	321.5	23.4	255	4	US-09-644-600-7	Sequence 7, Appl	678	309.5	22.5	492	4	US-09-759-143-895	Sequence 895, App
606	321.5	23.4	255	4	US-09-654-600A-7	Sequence 7, Appl	679	308.5	22.5	243	3	US-08-944-483-70	Sequence 70, Appl
607	321.5	23.4	418	4	US-10-177-661-6	Sequence 6, Appl	680	308.5	22.5	319	4	US-09-270-767-42672	Sequence 42672, A
608	321	23.4	248	2	US-08-851-974-3	Sequence 3, Appl	681	308	22.4	232	4	US-09-959-392-32	Sequence 32, Appl
609	321	23.4	248	2	US-09-213-390-3	Sequence 3, Appl	682	308	22.4	317	4	US-09-386-629-7	Sequence 7, Appl
610	321	23.4	269	2	US-08-978-404B-10	Sequence 10, Appl	683	308	22.4	317	4	US-09-907-794A-263	Sequence 263, App
611	321	23.4	300	1	US-08-148-910-1	Sequence 1, Appl	684	308	22.4	317	4	US-09-905-125A-263	Sequence 263, App

685	308	22.4	317	4	US-09-902-775A-263	Sequence 263, App	758	304	22.1	562	6	5185259-3	Patent No. 5185259
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687	308	22.4	317	4	US-09-903-603A-263	Sequence 263, App	760	304	22.1	562	6	5244676-5	Patent No. 5244676
688	308	22.4	317	4	US-09-904-920A-263	Sequence 263, App	761	304	22.1	562	6	5344773-2	Patent No. 5344773
689	308	22.4	317	4	US-09-905-064-263	Sequence 263, App	762	304	22.1	562	6	5185259-3	Patent No. 5185259
690	308	22.4	317	4	US-09-905-381A-263	Sequence 263, App	763	304	22.1	562	6	5200340-2	Patent No. 5200340
691	308	22.4	317	4	US-09-906-618-263	Sequence 263, App	764	304	22.1	562	6	5244676-5	Patent No. 5244676
692	308	22.4	317	4	US-08-681-151-1	Sequence 1, Appli	765	304	22.1	562	6	5344773-2	Patent No. 5344773
693	307.5	22.4	376	4	US-09-820-002-2	Sequence 2, Appli	766	304	22.1	587	4	US-09-949-016-11501	Sequence 11501, A
694	307	22.3	268	1	US-08-568-031-2	Sequence 2, Appli	767	303.5	22.1	234	4	US-03-513-999C-7815	Sequence 7815, Ap
695	307	22.3	268	1	US-08-966-319-2	Sequence 2, Appli	768	303.5	22.1	278	4	US-08-332-828C-4	Sequence 4, Appli
696	307	22.3	268	3	US-09-153-304-2	Sequence 2, Appli	769	303.5	22.1	278	3	US-09-330-945-4	Sequence 4, Appli
697	307	22.3	355	2	US-08-811-949-47	Sequence 47, Appl	770	303	22.1	258	3	US-09-949-016-10661	Sequence 10661, A
698	307	22.3	355	2	US-08-811-949-59	Sequence 59, Appl	771	303	22.1	355	2	US-08-811-949-67	Sequence 53, Appl
699	307	22.3	417	4	US-09-820-002-4	Sequence 4, Appli	772	303	22.1	389	2	US-08-811-949-67	Sequence 67, Appl
700	307	22.3	437	2	US-08-811-949-51	Sequence 51, Appl	773	303	22.1	437	2	US-08-811-949-55	Sequence 55, Appl
701	307	22.3	452	4	US-09-949-016-7182	Sequence 7182, Ap	774	303	22.1	527	4	US-09-600-985-1	Sequence 1, Appli
702	307	22.3	527	2	US-08-811-949-39	Sequence 39, Appl	775	302.5	22.0	1113	4	US-09-959-392-4	Sequence 4, Appli
703	306	22.3	256	2	US-09-027-337-3	Sequence 3, Appli	776	302	22.0	389	2	US-08-811-949-65	Sequence 65, Appl
704	306	22.3	256	4	US-09-644-600-3	Sequence 3, Appli	777	302	22.0	477	2	US-08-560-098A-51	Sequence 51, Appl
705	306	22.3	256	4	US-09-654-600A-3	Sequence 3, Appli	778	302	22.0	527	4	US-09-600-985-2	Sequence 2, Appli
706	306	22.3	437	2	US-08-811-949-57	Sequence 57, Appl	779	302	22.0	527	4	US-09-600-985-3	Sequence 3, Appli
707	305.5	22.2	146	4	US-09-618-259-3	Sequence 3, Appli	780	301.5	21.9	226	3	US-08-944-483-41	Sequence 41, Appl
708	305	22.2	247	2	US-08-851-974-1	Sequence 1, Appli	781	301	21.9	255	1	US-08-208-007A-14	Sequence 14, Appl
709	305	22.2	247	2	US-08-851-974-4	Sequence 4, Appli	782	301	21.9	255	3	US-08-915-095A-14	Sequence 14, Appl
710	305	22.2	247	2	US-09-213-390-1	Sequence 1, Appli	783	301	21.9	255	3	US-08-798-096-14	Sequence 14, Appl
711	305	22.2	247	2	US-09-213-390-4	Sequence 4, Appli	784	301	21.9	255	4	US-08-798-096-14	Sequence 14, Appl
712	305	22.2	247	2	US-09-949-016-6457	Sequence 6457, Ap	785	301	21.9	255	4	US-09-953-956-14	Sequence 14, Appl
713	305	22.2	437	2	US-08-811-949-49	Sequence 49, Appl	786	301	21.9	255	4	US-08-553-125A-14	Sequence 14, Appl
714	304.5	22.2	258	3	US-09-004-731-16	Sequence 16, Appl	787	301	21.9	255	4	US-10-114-464-14	Sequence 14, Appl
715	304.5	22.2	258	3	US-09-004-731-19	Sequence 19, Appl	788	301	21.9	257	6	US-09-949-016-10662	Sequence 10662, A
716	304.5	22.2	258	3	US-08-749-699-16	Sequence 16, Appl	789	301	21.9	527	6	5520913-1	Patent No. 5520913
717	304.5	22.2	258	3	US-08-749-699-19	Sequence 19, Appl	790	301	21.9	527	6	5520913-1	Patent No. 5520913
718	304.5	22.2	258	4	US-09-004-723-16	Sequence 16, Appl	791	300	21.8	527	6	5520913-1	Patent No. 5520913
719	304.5	22.2	258	4	US-09-004-723-19	Sequence 19, Appl	792	298	21.7	233	4	US-09-636-382A-24	Sequence 24, Appl
720	304.5	22.2	314	3	US-09-636-382A-2	Sequence 2, Appli	793	297	21.6	347	2	US-08-811-949-1	Sequence 1, Appli
721	304.5	22.2	384	3	US-09-032-215-22	Sequence 22, Appl	794	297	21.6	237	3	US-08-163-919A-3	Sequence 3, Appli
722	304.5	22.2	393	4	US-09-759-143-934	Sequence 934, App	795	297	21.6	237	4	US-08-462-515-3	Sequence 3, Appli
723	304.5	22.2	492	3	US-09-342-749-2	Sequence 2, Appli	796	297	21.6	237	5	PCT-US94-14073-3	Sequence 3, Appli
724	304.5	22.2	492	4	US-09-691-840-2	Sequence 2, Appli	797	297	21.6	252	3	US-08-944-483-72	Sequence 72, Appl
725	304.5	22.2	492	4	US-09-759-143-932	Sequence 932, App	798	297	21.6	253	2	US-09-027-337-8	Sequence 8, Appli
726	304.5	22.2	510	4	US-09-949-016-11074	Sequence 11074, A	799	297	21.6	253	4	US-09-644-600A-8	Sequence 8, Appli
727	304	22.1	232	1	US-07-990-301A-4	Sequence 4, Appli	800	297	21.6	253	4	US-09-654-600A-8	Sequence 8, Appli
728	304	22.1	235	3	US-08-944-483-65	Sequence 65, Appl	801	297	21.6	256	3	US-09-032-215-27	Sequence 27, Appl
729	304	22.1	255	3	US-08-944-483-67	Sequence 67, Appl	802	297	21.6	323	4	US-09-880-503-7	Sequence 7, Appli
730	304	22.1	268	4	US-09-613-822B-2	Sequence 2, Appli	803	297	21.6	354	2	US-08-811-949-61	Sequence 61, Appl
731	304	22.1	327	4	US-09-386-623-8	Sequence 8, Appli	804	297	21.6	411	3	US-09-181-816-1	Sequence 1, Appli
732	304	22.1	355	1	US-08-137-116-1	Sequence 1, Appli	805	297	21.6	521	4	US-09-949-016-11081	Sequence 11081, A
733	304	22.1	355	1	US-08-217-618-1	Sequence 1, Appli	806	297	21.6	521	4	US-09-949-016-11082	Sequence 11082, A
734	304	22.1	355	1	US-08-427-640-2	Sequence 2, Appli	807	296.5	21.6	521	4	US-09-949-016-11083	Sequence 11083, A
735	304	22.1	355	1	US-08-427-640-6	Sequence 6, Appli	808	296.5	21.6	224	1	US-08-278-091-12	Sequence 12, Appl
736	304	22.1	355	1	US-08-217-617A-1	Sequence 1, Appli	809	296.5	21.6	224	1	US-08-483-859-12	Sequence 12, Appl
737	304	22.1	355	1	US-08-217-618-1	Sequence 1, Appli	810	296.5	21.6	224	1	US-08-472-173-12	Sequence 12, Appl
738	304	22.1	355	2	US-08-811-949-45	Sequence 45, Appl	811	296.5	21.6	224	2	US-08-487-167-12	Sequence 12, Appl
739	304	22.1	355	3	US-08-794-528-1	Sequence 1, Appli	812	296.5	21.6	224	2	US-08-483-816-12	Sequence 12, Appl
740	304	22.1	355	6	5223256-1	Patent No. 5223256	813	296.5	21.6	224	2	US-08-296-119-12	Sequence 12, Appl
741	304	22.1	355	6	5223256-1	Patent No. 5223256	814	296.5	21.6	224	2	US-08-801-499-12	Sequence 12, Appl
742	304	22.1	356	1	US-08-427-640-4	Sequence 4, Appli	815	296.5	21.6	224	2	US-08-615-271-12	Sequence 12, Appl
743	304	22.1	356	1	US-08-427-640-8	Sequence 8, Appli	816	296.5	21.6	224	3	US-09-074-660-12	Sequence 12, Appl
744	304	22.1	378	3	US-09-553-498-10	Sequence 10, Appl	817	296.5	21.6	224	3	US-09-074-659-12	Sequence 12, Appl
745	304	22.1	378	4	US-09-618-869-10	Sequence 10, Appl	818	296.5	21.6	224	3	US-09-106-468-12	Sequence 12, Appl
746	304	22.1	433	4	US-09-949-016-8220	Sequence 8220, Ap	819	296.5	21.6	224	3	US-09-106-466A-12	Sequence 12, Appl
747	304	22.1	472	2	US-08-811-949-63	Sequence 63, Appl	820	296.5	21.6	224	3	US-09-106-467-12	Sequence 12, Appl
748	304	22.1	527	1	US-07-609-510B-16	Sequence 16, Appl	821	296.5	21.6	246	4	US-09-205-258-1149	Sequence 1149, Ap
749	304	22.1	527	4	US-09-612-314A-51	Sequence 51, Appl	822	296.5	21.6	254	2	US-08-560-098A-49	Sequence 49, Appl
750	304	22.1	527	5	PCT-US91-01025A-2	Sequence 2, Appli	823	296.5	21.6	276	4	US-09-880-503-5	Sequence 5, Appli
751	304	22.1	527	6	5185259-8	Patent No. 5185259	824	296.5	21.6	306	2	US-08-560-098A-45	Sequence 45, Appl
752	304	22.1	527	6	5185259-8	Patent No. 5185259	825	296.5	21.6	331	2	US-08-560-098A-46	Sequence 46, Appl
753	304	22.1	562	2	US-08-811-949-43	Sequence 43, Appl	826	296.5	21.6	365	1	US-08-560-098A-44	Sequence 44, Appl
754	304	22.1	562	2	US-08-560-098A-50	Sequence 50, Appl	827	296.5	21.6	365	1	US-08-720-012-83	Sequence 83, Appl
755	304	22.1	562	2	US-08-983-795A-38	Sequence 38, Appl	828	296.5	21.6	393	2	US-08-560-098A-44	Sequence 44, Appl
756	304	22.1	562	4	US-09-703-695A-4	Sequence 4, Appli	829	296.5	21.6	393	3	US-08-967-024C-24	Sequence 24, Appl
757	304	22.1	562	4	US-10-443-701-4	Sequence 4, Appli	830	296.5	21.6	403	4	US-09-880-503-6	Sequence 6, Appli

831	296.5	21.6	411	1	US-08-087-163-1	Sequence 1, Appli	904	282	20.5	244	3	US-08-944-483-74	Sequence 74, Appl
832	296.5	21.6	411	1	US-08-286-748B-18	Sequence 18, Appl	905	279	20.3	902	4	US-09-644-600-10	Sequence 10, Appl
833	296.5	21.6	411	1	US-08-153-799-18	Sequence 18, Appl	906	279	20.3	902	4	US-09-654-600A-10	Sequence 10, Appl
834	296.5	21.6	411	2	US-08-560-098A-48	Sequence 48, Appl	907	277.5	20.2	902	4	US-08-944-483-58	Sequence 58, Appl
835	296.5	21.6	411	4	US-09-880-503-3	Sequence 3, Appli	908	277.5	20.2	488	4	US-09-367-777-44	Sequence 44, Appl
836	296.5	21.6	430	6	5219569-2	Patent No. 5219569	909	277	20.2	488	4	US-09-367-791A-27	Sequence 27, Appl
837	296.5	21.6	430	6	5219569-2	Patent No. 5219569	910	276	20.1	306	1	US-08-330-978-1	Sequence 1, Appli
838	296.5	21.6	431	4	US-09-101-272G-1	Sequence 1, Appli	911	276	20.1	306	1	US-08-474-042-1	Sequence 1, Appli
839	296.5	21.6	431	6	5188829-1	Patent No. 5188829	912	276	20.1	306	1	US-08-484-558-1	Sequence 1, Appli
840	296.5	21.6	431	6	5188829-1	Patent No. 5188829	913	276	20.1	306	1	US-08-774-592-1	Sequence 1, Appli
841	296.5	21.6	432	4	US-08-560-098A-47	Sequence 47, Appl	914	276	20.1	437	1	US-08-487-037-2	Sequence 2, Appli
842	296	21.5	269	4	US-09-715-994-2	Sequence 2, Appli	915	276	20.1	448	2	US-08-295-411-3	Sequence 3, Appli
843	295.5	21.5	283	3	US-08-807-151-1	Sequence 1, Appli	916	276	20.1	448	2	US-08-955-471-3	Sequence 3, Appli
844	295.5	21.5	283	3	US-09-478-957-1	Sequence 1, Appli	917	276	20.1	448	5	PCT-US92-10068-1	Sequence 1, Appli
845	295.5	21.5	454	3	US-09-518-046-2	Sequence 2, Appli	918	276	20.1	448	5	PCT-US92-10242-3	Sequence 1, Appli
846	294	21.4	256	3	US-09-032-215-32	Sequence 32, Appl	919	276	20.1	488	1	US-08-487-037-1	Sequence 1, Appli
847	293.5	21.4	239	3	US-08-944-483-61	Sequence 61, Appl	920	276	20.1	496	4	US-09-949-016-9524	Sequence 1, Appli
848	293.5	21.4	411	4	US-09-403-736-2	Sequence 2, Appli	921	274.5	20.0	211	3	US-09-220-731-25	Sequence 25, Appl
849	293.5	21.4	430	1	US-07-942-157A-3	Sequence 3, Appli	922	274.5	20.0	211	4	US-09-242-998-20	Sequence 20, Appl
850	292	21.3	237	3	US-09-004-731-22	Sequence 22, Appl	923	274	19.9	241	1	US-08-330-978-4	Sequence 4, Appli
851	292	21.3	237	3	US-08-749-699-22	Sequence 22, Appl	924	274	19.9	241	1	US-08-474-042-4	Sequence 4, Appli
852	292	21.3	237	4	US-09-004-729-22	Sequence 22, Appl	925	274	19.9	241	1	US-08-484-558-4	Sequence 4, Appli
853	292	21.3	256	3	US-08-906-769-89	Sequence 89, Appl	926	274	19.9	241	1	US-08-774-592-4	Sequence 4, Appli
854	292	21.3	256	3	US-08-906-769-89	Sequence 89, Appl	927	274	19.9	254	1	US-08-330-978-3	Sequence 3, Appli
855	292	21.3	256	3	US-08-906-616-89	Sequence 89, Appl	928	274	19.9	254	1	US-08-474-042-3	Sequence 3, Appli
856	292	21.3	256	3	US-08-817-795-89	Sequence 89, Appl	929	274	19.9	254	1	US-08-484-558-3	Sequence 3, Appli
857	292	21.3	256	3	US-08-639-075A-89	Sequence 89, Appl	930	274	19.9	254	1	US-08-774-592-3	Sequence 3, Appli
858	292	21.3	256	3	US-09-012-431-89	Sequence 89, Appl	931	272	19.8	253	3	US-08-906-769-131	Sequence 131, App
859	292	21.3	256	3	US-09-012-692-89	Sequence 89, Appl	932	272	19.8	253	3	US-08-906-616-131	Sequence 131, App
860	292	21.3	256	5	PCT-US95-14442A-89	Sequence 89, Appl	933	272	19.8	253	3	US-08-639-075A-131	Sequence 131, App
861	292	21.3	414	4	US-09-270-767-46426	Sequence 46426, A	934	272	19.8	253	3	US-09-012-431-131	Sequence 131, App
862	291.5	21.2	242	3	US-08-944-483-57	Sequence 57, Appl	935	272	19.8	253	3	US-09-012-692-131	Sequence 131, App
863	291.5	21.2	253	3	US-08-944-483-73	Sequence 73, Appl	936	272	19.8	253	3	US-08-906-613-131	Sequence 131, App
864	291	21.2	416	2	US-09-000-846-2	Sequence 2, Appli	937	270	19.7	251	3	US-08-944-483-28	Sequence 28, Appl
865	290	21.1	235	2	US-08-557-146-14	Sequence 14, Appl	938	269	19.6	256	4	US-08-395-456C-23	Sequence 23, Appl
866	290	21.1	235	2	US-09-154-344-14	Sequence 14, Appl	939	269	19.6	256	4	US-08-487-453A-23	Sequence 23, Appl
867	290	21.1	235	3	US-08-807-151-3	Sequence 3, Appli	940	268	19.5	256	2	US-08-230-428B-4	Sequence 4, Appli
868	290	21.1	235	3	US-08-944-483-42	Sequence 42, Appl	941	268	19.5	437	1	US-08-007-031-3	Sequence 3, Appli
869	290	21.1	235	3	US-09-478-957-3	Sequence 3, Appli	942	267.5	19.5	266	3	US-09-004-731-24	Sequence 24, Appl
870	289	21.0	223	1	US-07-956-848A-41	Sequence 41, Appl	943	267.5	19.5	266	3	US-08-749-699-24	Sequence 24, Appl
871	289	21.0	223	1	US-08-471-956-41	Sequence 41, Appl	944	267.5	19.5	266	4	US-09-004-729-24	Sequence 24, Appl
872	288.5	21.0	583	4	US-09-576-594-837	Sequence 837, App	945	265.5	19.3	197	1	US-08-456-840-48	Sequence 48, Appl
873	288.5	21.0	255	3	US-08-906-769-91	Sequence 91, Appl	946	265.5	19.3	197	1	US-08-266-407A-48	Sequence 48, Appl
874	288.5	21.0	255	3	US-08-906-616-91	Sequence 91, Appl	947	265.5	19.3	197	2	US-08-892-544-48	Sequence 48, Appl
875	288.5	21.0	255	3	US-08-817-795-91	Sequence 91, Appl	948	264.5	19.3	248	1	US-08-238-130-2	Sequence 2, Appli
876	288.5	21.0	255	3	US-08-639-075A-91	Sequence 91, Appl	949	264.5	19.3	248	1	US-08-921-426-4	Sequence 4, Appli
877	288.5	21.0	255	3	US-09-012-431-91	Sequence 91, Appl	950	264.5	19.3	248	3	US-08-816-915-4	Sequence 4, Appli
878	288.5	21.0	255	3	US-09-012-692-91	Sequence 91, Appl	951	264.5	19.3	248	5	PCT-US95-07743-4	Sequence 4, Appli
879	288.5	21.0	255	3	US-08-906-613-91	Sequence 91, Appl	952	264.5	19.3	249	3	US-09-578-303-2	Sequence 2, Appli
880	288.5	21.0	255	5	PCT-US95-14442A-91	Sequence 91, Appl	953	264	19.2	250	3	US-08-944-483-68	Sequence 68, Appl
881	288	21.0	268	1	US-08-270-584A-2	Sequence 2, Appli	954	264	19.2	256	4	US-09-949-016-6271	Sequence 6271, Ap
882	288	21.0	268	2	US-08-765-192-2	Sequence 2, Appli	955	263.5	19.2	222	2	US-08-491-204A-18	Sequence 18, Appl
883	288	21.0	268	3	US-09-199-793-2	Sequence 2, Appli	956	263.5	19.2	222	4	US-09-949-016-6112	Sequence 6112, Ap
884	287	20.9	227	3	US-08-944-483-40	Sequence 40, Appl	957	263.5	19.2	255	4	US-09-949-018-9690	Sequence 9690, Ap
885	287	20.9	407	3	US-09-734-675-4	Sequence 4, Appli	958	263	19.1	252	3	US-08-906-769-103	Sequence 103, App
886	286.5	20.9	218	3	US-09-578-303-3	Sequence 3, Appli	959	263	19.1	252	3	US-08-906-616-103	Sequence 103, App
887	286.5	20.9	228	3	US-09-004-731-10	Sequence 10, Appl	960	263	19.1	252	3	US-08-817-795-103	Sequence 103, App
888	286.5	20.9	228	3	US-08-749-699-10	Sequence 10, Appl	961	263	19.1	252	3	US-08-639-075A-103	Sequence 103, App
889	286.5	20.9	228	4	US-09-004-729-10	Sequence 10, Appl	962	263	19.1	252	3	US-09-012-431-103	Sequence 103, App
890	286	20.8	228	4	US-09-205-258-1150	Sequence 1150, Ap	963	263	19.1	252	3	US-09-012-692-103	Sequence 103, App
891	284.5	20.7	225	3	US-09-004-731-13	Sequence 13, Appl	964	263	19.1	252	3	US-08-906-613-103	Sequence 103, App
892	284.5	20.7	225	3	US-08-749-699-13	Sequence 13, Appl	965	263	19.1	252	5	PCT-US95-14442A-103	Sequence 103, App
893	284.5	20.7	225	4	US-09-004-729-13	Sequence 13, Appl	966	262.5	19.1	233	3	US-09-004-731-27	Sequence 27, Appl
894	284.5	20.7	255	3	US-08-906-769-83	Sequence 83, Appl	967	262.5	19.1	233	4	US-08-749-699-27	Sequence 27, Appl
895	284.5	20.7	255	3	US-08-906-616-83	Sequence 83, Appl	968	262.5	19.1	233	4	US-09-004-729-27	Sequence 27, Appl
896	284.5	20.7	255	3	US-08-817-795-83	Sequence 83, Appl	969	261.5	19.0	222	1	US-07-969-931-9	Sequence 9, Appli
897	284.5	20.7	255	3	US-08-639-075A-83	Sequence 83, Appl	970	261.5	19.0	222	1	US-07-855-417A-9	Sequence 9, Appli
898	284.5	20.7	255	3	US-09-012-431-83	Sequence 83, Appl	971	261.5	19.0	225	3	US-08-944-483-32	Sequence 32, Appl
899	284.5	20.7	255	3	US-09-012-692-83	Sequence 83, Appl	972	257.5	18.7	267	1	US-08-553-516-2	Sequence 2, Appli
900	284.5	20.7	255	3	US-08-906-613-83	Sequence 83, Appl	973	256	18.6	267	3	US-08-906-769-145	Sequence 145, App
901	284.5	20.7	255	5	PCT-US95-14442A-83	Sequence 83, Appl	974	256	18.6	267	3	US-08-906-616-145	Sequence 145, App
902	283.5	20.6	268	3	US-09-032-215-42	Sequence 42, Appl	975	256	18.6	267	3	US-08-639-075A-145	Sequence 145, App
903	282.5	20.6	144	4	US-09-618-259-4	Sequence 4, Appli	976	256	18.6	267	3	US-09-004-731-67	Sequence 67, Appl

977	256	18.6	267	3	US-09-012-431-145	Sequence 145, App	1050	226	16.4	697	3	US-08-462-040-50	Sequence 50, Appl
978	256	18.6	267	3	US-08-749-699-67	Sequence 67, Appl	1051	226	16.4	723	1	US-07-838-410-1	Sequence 1, Appl
979	256	18.6	267	3	US-09-012-692-145	Sequence 145, App	1052	226	16.4	723	1	US-08-290-937B-1	Sequence 1, Appl
980	256	18.6	267	3	US-08-906-613-145	Sequence 145, App	1053	226	16.4	723	1	US-08-290-937B-2	Sequence 2, Appl
981	256	18.6	267	4	US-09-004-723-67	Sequence 67, Appl	1054	226	16.4	723	1	US-08-290-937B-3	Sequence 3, Appl
982	256	18.6	405	3	US-09-734-675-2	Sequence 2, Appl	1055	226	16.4	723	1	US-08-404-643-1	Sequence 1, Appl
983	254	18.5	242	3	US-09-004-731-41	Sequence 41, Appl	1056	226	16.4	723	3	US-09-194-326-1	Sequence 2, Appl
984	254	18.5	242	3	US-08-749-699-41	Sequence 41, Appl	1057	226	16.4	723	3	US-09-194-326-2	Sequence 2, Appl
985	254	18.5	242	4	US-09-004-729-41	Sequence 41, Appl	1058	226	16.4	723	3	US-09-194-326-3	Sequence 3, Appl
986	254	18.5	255	4	US-09-270-767-43261	Sequence 44361, A	1059	226	16.4	723	3	US-08-700-519J-19	Sequence 19, Appl
987	253	18.4	182	4	US-09-328-925-12	Sequence 12, Appl	1060	226	16.4	723	4	US-09-600-991-18	Sequence 18, Appl
988	253	18.4	231	4	US-08-395-456C-25	Sequence 25, Appl	1061	226	16.4	723	4	US-08-605-221-4	Sequence 4, Appl
989	253	18.4	242	3	US-09-032-215-47	Sequence 47, Appl	1062	226	16.4	723	4	US-09-601-040A-10	Sequence 10, Appl
990	252.5	18.4	221	2	US-08-925-708-1	Sequence 1, Appl	1063	226	16.4	728	4	US-07-815-333A-2	Sequence 2, Appl
991	252.5	18.4	239	3	US-09-004-731-44	Sequence 44, Appl	1064	226	16.4	728	1	US-08-087-783A-22	Sequence 22, Appl
992	252.5	18.4	239	3	US-08-749-699-44	Sequence 44, Appl	1065	226	16.4	728	3	US-08-605-221-2	Sequence 2, Appl
993	252.5	18.4	239	4	US-09-004-723-44	Sequence 44, Appl	1066	223	16.2	723	3	US-08-030-410-3	Sequence 3, Appl
994	252.5	18.4	247	3	US-08-944-483-49	Sequence 49, Appl	1067	222	16.2	213	3	US-08-906-769-149	Sequence 149, App
995	252	18.3	229	4	US-08-395-456C-27	Sequence 27, Appl	1068	222	16.2	213	3	US-08-906-616-149	Sequence 149, App
996	251	18.3	229	2	US-08-394-600B-20	Sequence 20, Appl	1069	222	16.2	213	3	US-08-639-075A-149	Sequence 149, App
997	251	18.3	229	4	US-08-395-456C-20	Sequence 20, Appl	1070	222	16.2	213	3	US-09-012-431-149	Sequence 149, App
998	251	18.3	229	4	US-08-487-453A-20	Sequence 20, Appl	1071	222	16.2	213	3	US-09-012-692-149	Sequence 149, App
999	251	18.3	229	5	PCT-US95-02513-20	Sequence 20, Appl	1072	222	16.2	213	3	US-08-906-613-149	Sequence 149, App
1000	250	18.2	352	4	US-09-902-540-9796	Sequence 9796, Ap	1073	222	16.2	234	3	US-08-944-483-56	Sequence 56, Appl
1001	248.5	18.1	717	4	US-09-601-040A-6	Sequence 6, Appl	1074	220.5	16.0	267	2	US-08-978-404B-46	Sequence 46, Appl
1002	248.5	18.1	717	4	US-09-601-040A-8	Sequence 8, Appl	1075	220	16.0	278	4	US-09-270-767-48024	Sequence 48024, A
1003	247.5	18.0	729	4	US-09-601-040A-4	Sequence 4, Appl	1076	220	16.0	457	4	US-09-270-767-32807	Sequence 32807, A
1004	247.5	18.0	729	4	US-08-944-483-30	Sequence 30, Appl	1077	217.5	15.8	385	4	US-09-163-951-16	Sequence 16, Appl
1005	247	18.0	229	3	US-08-944-483-44	Sequence 44, Appl	1078	217.5	15.8	385	4	US-09-345-881-16	Sequence 16, Appl
1006	245	17.8	226	4	US-09-601-040A-28	Sequence 28, Appl	1079	216	15.7	185	3	US-08-906-769-141	Sequence 141, App
1007	245	17.8	228	2	US-08-766-982-11	Sequence 11, Appl	1080	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1008	245	17.8	228	3	US-08-944-483-55	Sequence 55, Appl	1081	216	15.7	185	3	US-08-639-075A-141	Sequence 141, App
1009	245	17.8	228	3	US-09-296-219-11	Sequence 11, Appl	1082	216	15.7	185	3	US-09-012-431-141	Sequence 141, App
1010	245	17.8	711	1	US-08-184-012C-8	Sequence 8, Appl	1083	216	15.7	185	3	US-09-012-692-141	Sequence 141, App
1011	245	17.8	711	1	US-08-334-177-2	Sequence 2, Appl	1084	216	15.7	185	3	US-08-906-613-141	Sequence 141, App
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1013	245	17.8	711	2	US-08-766-982-2	Sequence 2, Appl	1086	216	15.7	223	1	US-08-483-859-13	Sequence 13, Appl
1014	245	17.8	711	3	US-09-296-219-2	Sequence 2, Appl	1087	216	15.7	223	2	US-08-472-173-13	Sequence 13, Appl
1015	245	17.8	711	4	US-09-600-991-20	Sequence 20, Appl	1088	216	15.7	223	2	US-08-487-167-13	Sequence 13, Appl
1016	245	17.8	711	4	US-09-601-040A-12	Sequence 12, Appl	1089	216	15.7	223	2	US-08-482-816-13	Sequence 13, Appl
1017	245	17.8	711	4	US-09-949-016-6981	Sequence 6981, Ap	1090	216	15.7	223	2	US-08-296-149-13	Sequence 13, Appl
1018	245	17.8	711	5	PCT-US95-13830-2	Sequence 2, Appl	1091	216	15.7	223	2	US-08-801-499-13	Sequence 13, Appl
1019	244.5	17.8	716	3	US-08-766-982-1	Sequence 1, Appl	1092	216	15.7	223	2	US-08-615-271-13	Sequence 13, Appl
1020	244.5	17.8	716	3	US-09-296-219-1	Sequence 1, Appl	1093	216	15.7	223	3	US-09-074-660-13	Sequence 13, Appl
1021	242	17.6	214	6	5180819-3	Patent No. 5180819	1094	216	15.7	223	3	US-09-074-659-13	Sequence 13, Appl
1022	242	17.6	214	6	5180819-3	Patent No. 5180819	1095	216	15.7	223	3	US-09-106-468-13	Sequence 13, Appl
1023	242	17.6	435	3	US-09-261-416-2	Sequence 2, Appl	1096	216	15.7	223	3	US-09-106-468A-13	Sequence 13, Appl
1024	240	17.5	161	3	US-09-261-416-8	Sequence 8, Appl	1097	216	15.7	223	3	US-09-106-467-13	Sequence 13, Appl
1025	234	17.0	158	3	US-09-518-046-22	Sequence 22, Appl	1098	211	15.4	223	1	US-08-485-455D-17	Sequence 17, Appl
1026	232.5	16.9	185	3	US-08-705-875A-5	Sequence 5, Appl	1099	211	15.4	223	1	US-08-482-130C-17	Sequence 17, Appl
1027	232.5	16.9	185	3	US-09-220-731-22	Sequence 22, Appl	1100	211	15.4	223	2	US-08-484-211C-17	Sequence 17, Appl
1028	232.5	16.9	185	4	US-09-242-999-5	Sequence 5, Appl	1101	211	15.4	223	2	US-08-817-795-17	Sequence 17, Appl
1029	231.5	16.8	219	2	US-08-925-708-2	Sequence 2, Appl	1102	211	15.4	223	3	US-08-485-443B-17	Sequence 17, Appl
1030	231	16.8	242	3	US-08-944-483-29	Sequence 29, Appl	1103	211	15.4	223	5	PCT-US95-1442A-17	Sequence 17, Appl
1031	230.5	16.8	307	4	US-09-088-651-2	Sequence 2, Appl	1104	211	15.4	224	3	US-08-906-769-17	Sequence 17, Appl
1032	228.5	16.6	284	4	US-09-270-767-33263	Sequence 33263, A	1105	211	15.4	224	3	US-08-906-616-17	Sequence 17, Appl
1033	228.5	16.6	287	4	US-09-270-767-48480	Sequence 48480, A	1106	211	15.4	224	3	US-08-639-075A-17	Sequence 17, Appl
1034	227	16.5	258	4	US-09-023-942A-8	Sequence 8, Appl	1107	211	15.4	224	3	US-09-012-431-17	Sequence 17, Appl
1035	227	16.5	258	3	US-08-906-769-190	Sequence 190, App	1108	211	15.4	224	3	US-09-012-692-17	Sequence 17, Appl
1036	227	16.5	259	3	US-08-906-616-190	Sequence 190, App	1109	211	15.4	224	3	US-08-906-613-17	Sequence 17, Appl
1037	227	16.5	259	3	US-08-639-075A-190	Sequence 190, App	1110	211	15.4	224	3	US-08-906-613-17	Sequence 17, Appl
1038	227	16.5	259	3	US-09-004-731-85	Sequence 85, Appl	1111	210.5	15.3	222	4	US-09-270-767-62005	Sequence 62005, A
1039	227	16.5	259	3	US-09-012-431-190	Sequence 190, App	1112	210.5	15.3	238	3	US-08-944-483-31	Sequence 31, Appl
1040	227	16.5	259	3	US-08-749-699-85	Sequence 85, Appl	1113	210.5	15.3	238	6	5180819-4	Patent No. 5180819
1041	227	16.5	259	3	US-09-012-692-190	Sequence 190, App	1114	210.5	15.3	238	6	5180819-4	Patent No. 5180819
1042	227	16.5	259	3	US-08-906-613-190	Sequence 190, App	1115	206	15.0	164	3	US-09-518-046-25	Sequence 25, Appl
1043	227	16.5	259	4	US-08-700-519J-18	Sequence 18, Appl	1116	206	15.0	250	4	US-09-270-767-33709	Sequence 33709, A
1044	227	16.5	723	3	US-08-700-519J-18	Sequence 18, Appl	1117	204.5	14.9	157	3	US-09-518-046-23	Sequence 23, Appl
1045	226.5	16.5	215	6	5180819-2	Patent No. 5180819	1118	204.5	14.9	178	3	US-08-906-769-107	Sequence 107, App
1046	226.5	16.5	215	6	5180819-2	Patent No. 5180819	1119	204.5	14.9	178	3	US-08-906-616-107	Sequence 107, App
1047	226	16.4	697	2	US-08-460-890A-50	Sequence 50, Appl	1120	204.5	14.9	178	3	US-08-817-795-107	Sequence 107, App
1048	226	16.4	697	3	US-08-167-641C-50	Sequence 50, Appl	1121	204.5	14.9	178	3	US-08-639-075A-107	Sequence 107, App
1049	226	16.4	697	3	US-08-460-971A-50	Sequence 50, Appl	1122	204.5	14.9	178	3	US-09-012-431-107	Sequence 107, App

1123	204.5	14.9	178	3	US-09-012-692-107	Sequence 107, App	1196	160.5	11.7	178	3	US-09-220-731-24	Sequence 24, Appl
1124	204.5	14.9	178	3	US-08-906-613-107	Sequence 107, App	1197	160.5	11.7	178	3	US-09-242-999-24	Sequence 24, Appl
1125	204.5	14.9	178	5	PCT-US95-14442A-107	Sequence 107, App	1198	160	11.6	97	4	US-09-270-767-31931	Sequence 31931, A
1126	200.5	14.6	159	3	US-09-518-046-24	Sequence 24, Appl	1199	160	11.6	97	4	US-09-270-767-47148	Sequence 47148, A
1127	200	14.6	223	4	US-09-270-767-45768	Sequence 45768, A	1200	159	11.6	190	2	US-08-845-998-6	Sequence 6, Appl1
1128	198.5	14.4	254	3	US-08-906-769-139	Sequence 129, App	1201	159	11.6	190	3	US-09-206-537-6	Sequence 6, Appl1
1129	198.5	14.4	254	3	US-08-906-616-129	Sequence 129, App	1202	159	11.6	190	3	US-09-430-854-6	Sequence 6, Appl1
1130	198.5	14.4	254	3	US-08-639-075A-129	Sequence 129, App	1203	158	11.5	357	4	US-09-270-767-43564	Sequence 43564, A
1131	198.5	14.4	254	3	US-09-012-431-129	Sequence 129, App	1204	158	11.5	357	4	US-09-270-767-58936	Sequence 58936, A
1132	198.5	14.4	254	3	US-09-012-692-129	Sequence 129, App	1205	157.5	11.5	764	2	US-08-177-109A-2	Sequence 2, Appl1
1133	198.5	14.4	254	3	US-08-906-613-129	Sequence 129, App	1206	157.5	11.5	764	2	US-08-687-706-2	Sequence 2, Appl1
1134	196.5	14.3	141	4	US-09-949-016-7265	Sequence 7265, App	1207	157.5	11.5	798	4	US-09-949-016-11021	Sequence 11021, A
1135	195	14.2	326	3	US-09-411-977-3	Sequence 3, Appl1	1208	157	11.4	141	4	US-09-513-999C-4215	Sequence 4215, App
1136	195	14.2	326	4	US-10-057-951-3	Sequence 3, Appl1	1209	156.5	11.4	163	4	US-09-270-767-60652	Sequence 60652, A
1137	192.5	14.0	260	3	US-08-906-769-139	Sequence 139, App	1210	156.5	11.4	286	4	US-09-270-767-45162	Sequence 45162, A
1138	192.5	14.0	260	3	US-08-906-616-139	Sequence 139, App	1211	156	11.4	112	4	US-09-270-767-33319	Sequence 33319, A
1139	192.5	14.0	260	3	US-08-639-075A-139	Sequence 139, App	1212	156	11.4	112	4	US-09-270-767-48536	Sequence 48536, A
1140	192.5	14.0	260	3	US-09-012-431-139	Sequence 139, App	1213	154.5	11.2	204	3	US-08-906-769-147	Sequence 147, App
1141	192.5	14.0	260	3	US-09-012-692-139	Sequence 139, App	1214	154.5	11.2	204	3	US-08-639-075A-147	Sequence 147, App
1142	192.5	14.0	260	3	US-08-906-613-139	Sequence 139, App	1215	154.5	11.2	204	3	US-09-012-431-147	Sequence 147, App
1143	191	13.9	74	4	US-09-205-258-1151	Patent No. 5200340-4	1216	154.5	11.2	204	3	US-09-012-692-147	Sequence 147, App
1144	191	13.9	138	6	5200340-4	Patent No. 5200340-4	1217	154.5	11.2	204	3	US-09-012-692-147	Sequence 147, App
1145	191	13.9	138	6	5200340-4	Patent No. 5200340-4	1218	154.5	11.2	204	3	US-08-906-613-147	Sequence 147, App
1146	190	13.8	90	4	US-09-270-767-57991	Sequence 57991, A	1219	153.5	11.2	151	4	US-09-270-767-33178	Sequence 33178, A
1147	187	13.6	312	4	US-09-636-382A-15	Sequence 15, Appl	1220	153.5	11.2	151	4	US-09-270-767-48395	Sequence 48395, A
1148	186.5	13.6	570	4	US-10-067-422-9	Sequence 9, Appl1	1221	152.5	11.1	139	4	US-09-270-767-33648	Sequence 33648, A
1149	186	13.5	159	4	US-09-618-259-5	Sequence 5, Appl1	1222	150.5	11.0	79	4	US-09-270-767-33666	Sequence 33666, A
1150	183	13.3	313	4	US-09-270-767-44375	Sequence 44375, A	1223	150.5	11.0	79	4	US-09-270-767-48883	Sequence 48883, A
1151	182	13.2	145	3	US-08-906-769-123	Sequence 123, App	1224	149	10.8	77	3	US-09-439-313-329	Sequence 329, App
1152	182	13.2	145	3	US-08-906-616-123	Sequence 123, App	1225	149	10.8	77	3	US-09-352-616A-329	Sequence 329, App
1153	182	13.2	145	3	US-08-639-075A-123	Sequence 123, App	1226	149	10.8	77	4	US-09-232-149A-329	Sequence 329, App
1154	182	13.2	145	3	US-09-012-692-123	Sequence 123, App	1227	149	10.8	77	4	US-09-636-215-329	Sequence 329, App
1155	182	13.2	145	3	US-08-906-613-123	Sequence 123, App	1228	149	10.8	77	4	US-09-685-166A-329	Sequence 329, App
1156	181	13.2	118	4	US-09-621-976-5522	Sequence 5522, App	1229	149	10.8	77	4	US-09-688-489-329	Sequence 329, App
1157	181	13.2	133	4	US-09-949-016-7471	Sequence 7471, App	1230	149	10.8	77	4	US-09-679-426-329	Sequence 329, App
1158	180	13.1	144	3	US-09-012-431-123	Sequence 123, App	1231	149	10.8	77	4	US-09-753-143-329	Sequence 329, App
1159	178.5	13.0	164	3	US-09-020-956-178	Sequence 178, App	1232	149	10.8	77	4	US-09-651-236-329	Sequence 329, App
1160	178.5	13.0	164	3	US-09-030-607-178	Sequence 178, App	1233	148.5	10.8	276	4	US-09-270-767-32048	Sequence 32048, A
1161	178.5	13.0	164	3	US-09-439-313-178	Sequence 178, App	1234	148.5	10.8	276	4	US-09-270-767-47265	Sequence 47265, A
1162	178.5	13.0	164	3	US-09-352-616A-178	Sequence 178, App	1235	143.5	10.4	72	3	US-08-906-769-87	Sequence 87, Appl
1163	178.5	13.0	164	4	US-09-232-149A-178	Sequence 178, App	1236	143.5	10.4	72	3	US-08-616-87	Sequence 87, Appl
1164	178.5	13.0	164	4	US-09-559-812-178	Sequence 178, App	1237	143.5	10.4	72	3	US-08-817-795-87	Sequence 87, Appl
1165	178.5	13.0	164	4	US-09-636-215-178	Sequence 178, App	1238	143.5	10.4	72	3	US-08-639-075A-87	Sequence 87, Appl
1166	178.5	13.0	164	4	US-09-685-166A-178	Sequence 178, App	1239	143.5	10.4	72	3	US-09-012-431-87	Sequence 87, Appl
1167	178.5	13.0	164	4	US-09-115-453-178	Sequence 178, App	1240	143.5	10.4	72	3	US-09-012-692-87	Sequence 87, Appl
1168	178.5	13.0	164	4	US-09-688-489-178	Sequence 178, App	1241	143.5	10.4	72	3	US-08-906-613-87	Sequence 87, Appl
1169	178.5	13.0	164	4	US-09-679-426-178	Sequence 178, App	1242	143.5	10.4	72	5	PCT-US95-14442A-87	Sequence 87, Appl
1170	178.5	13.0	164	4	US-09-759-143-178	Sequence 178, App	1243	142.5	10.4	208	3	US-08-906-769-151	Sequence 151, App
1171	178.5	13.0	164	4	US-09-651-236-178	Sequence 178, App	1244	142.5	10.4	208	3	US-08-906-616-151	Sequence 151, App
1172	178	13.0	346	4	US-09-949-016-9000	Sequence 9000, App	1245	142.5	10.4	208	3	US-08-639-075A-151	Sequence 151, App
1173	176	12.8	348	4	US-09-949-016-6979	Sequence 6979, App	1246	142.5	10.4	208	3	US-09-012-431-151	Sequence 151, App
1174	174.5	12.7	271	3	US-09-578-303-6	Sequence 6, Appl1	1247	142.5	10.4	208	3	US-09-012-692-151	Sequence 151, App
1175	171.5	12.5	218	4	US-09-270-767-44299	Sequence 44299, A	1248	142.5	10.4	208	3	US-08-906-613-151	Sequence 151, App
1176	168	12.2	141	3	US-08-906-769-135	Sequence 135, App	1249	141.5	10.3	85	4	US-09-270-767-32321	Sequence 32321, A
1177	168	12.2	141	3	US-08-906-616-135	Sequence 135, App	1250	141.5	10.3	85	4	US-09-270-767-48448	Sequence 48448, A
1178	168	12.2	141	3	US-08-639-075A-135	Sequence 135, App	1251	139	10.1	87	3	US-08-906-769-161	Sequence 161, App
1179	168	12.2	141	3	US-09-012-431-135	Sequence 135, App	1252	139	10.1	87	3	US-08-906-616-161	Sequence 161, App
1180	168	12.2	141	3	US-09-012-692-135	Sequence 135, App	1253	139	10.1	87	3	US-08-639-075A-161	Sequence 161, App
1181	168	12.2	141	3	US-08-906-613-135	Sequence 135, App	1254	139	10.1	87	3	US-09-012-431-161	Sequence 161, App
1182	166.5	12.1	178	3	US-08-705-875A-8	Sequence 8, Appl1	1255	139	10.1	87	3	US-09-012-692-161	Sequence 161, App
1183	166.5	12.1	178	3	US-09-220-731-23	Sequence 23, Appl	1256	139	10.1	87	3	US-08-906-613-161	Sequence 161, App
1184	166.5	12.1	178	3	US-09-242-999-8	Sequence 8, Appl1	1257	139	10.1	89	3	US-08-906-769-165	Sequence 165, App
1185	166	12.1	243	4	US-09-270-767-44348	Sequence 44348, A	1258	139	10.1	89	3	US-08-906-616-165	Sequence 165, App
1186	166	12.1	769	4	US-09-949-016-11019	Sequence 11019, A	1259	139	10.1	89	3	US-08-639-075A-165	Sequence 165, App
1187	165	12.0	198	3	US-08-906-769-133	Sequence 133, App	1260	139	10.1	89	3	US-09-012-431-165	Sequence 165, App
1188	165	12.0	198	3	US-08-906-616-133	Sequence 133, App	1261	139	10.1	89	3	US-09-012-692-165	Sequence 165, App
1189	165	12.0	198	3	US-08-639-075A-133	Sequence 133, App	1262	139	10.1	89	3	US-08-906-613-165	Sequence 165, App
1190	165	12.0	198	3	US-09-012-431-133	Sequence 133, App	1263	138	10.0	278	4	US-09-602-777A-76	Sequence 76, Appl
1191	165	12.0	198	3	US-09-012-692-133	Sequence 133, App	1264	134	9.8	203	4	US-09-270-767-32531	Sequence 32531, A
1192	165	12.0	198	3	US-08-906-613-133	Sequence 133, App	1265	134	9.8	203	4	US-09-270-767-47748	Sequence 47748, A
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ALIGNMENTS

RESULT 1

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US-09-949-016-8151
; Sequence 8151, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE OF INVENTION: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8151
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8151
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Best Local Similarity 99.6%; Pred. No. 3.1e-124;

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RESULT 2

US-09-949-016-6948

; Sequence 6948, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
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US-09-949-016-6948

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QY 121 TSSVQPLPLPNDCATAGTECHVSGWGI TNHPRNPFPDLLQCLNLSIVSHATCHGVYVPGRI 180
DB 121 TSSVQPLPLPNDCATAGTECHVSGWGI TNHPRNPFPDLLQCLNLSIVSHATCHGVYVPGRI 180

QY 181 TSNMVCAGVPGQDACQDGGPLVCGGVLOGLVSWGSGVPCQDGI PGVYTYICKYVDW 235
DB 181 TSNMVCAGVPGQDACQDGGPLVCGGVLOGLVSWGSGVPCQDGI PGVYTYICKYVDW 235

RESULT 3
US-09-244-111-6
Sequence 6, Application US/09244111
Patent No. 6566498
GENERAL INFORMATION:
APPLICANT: NI, et al.
TITLE OF INVENTION: Human Serine Protease and Serpin Polypeptides
FILE REFERENCE: PF391
CURRENT APPLICATION NUMBER: US/09/244,111
CURRENT FILING DATE: 1999-02-04
EARLIER APPLICATION NUMBER: 60/073,961
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 6
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-09-244-111-6

Query Match 59.0%; Score 811; DB 4; Length 162;
Best Local Similarity 64.1%; Pred. No. 3.8e-71;
Matches 159; Conservative 0; Mismatches 3; Indels 86; Gaps 3;

QY 1 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSRCCGVLIDHRWLTA 60
DB 1 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSRCCGVLIDHRWLTA 60

QY 61 AHCSGRYVWRLGEHSLDQTEQIRHSGFVTHPGYLGASTSHEHDLRLRLPVRV 120
DB 61 AH-----WQRO-----THS----- 69

QY 121 TSSVQPLPLPNDCATAGTECHVSGWGI TNHPRNPFPDLLQCLNLSIVSHATCHGVYVPGRI 180
DB 70 -----PDLQLCLNLSIVSHATCHGVYVPGRI 94

QY 181 TSNMVCAGVPGQDACQDGGPLVCGGVLOGLVSWGSGVPCQDGI PGVYTYICKYVDW 240
DB 95 TSNMVCAGVPGQDACQDGGPLVCGGVLOGLVSWGSGVPCQDGI PGVYTYICKYVDW 154

QY 241 IRMIMRN 248
DB 155 IRMIMRN 162

RESULT 4
US-09-618-259-7
Sequence 7, Application US/09618259
Patent No. 6642013
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
FILE REFERENCE: D6020CIP2
CURRENT APPLICATION NUMBER: US/09/618,259
CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: US 09/127,444
PRIOR FILING DATE: 1998-08-21
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 7
LENGTH: 260
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Amino acid sequence of TADG-14 protein
US-09-618-259-7

Query Match 45.9%; Score 630.5; DB 4; Length 260;
Best Local Similarity 50.2%; Pred. No. 2.5e-53;
Matches 123; Conservative 24; Mismatches 93; Indels 5; Gaps 3;

QY 5 IFLLL---CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSRCCGVLIDHRWLTA 61
DB 13 MFLLLGGAWAGHSEAQEDKVLGGHECQPHSQPWAALFQGGQLCGVLVGNWLTA 72

QY 62 HCSGRYVWRLGEHSLDQTEQIRHSGFVTHPGYLGAST-SHEHDLRLRLPVRV 120
DB 73 HCKPKYTVRLGDHSLQNKDQPEQI PVVQSTPHPCYNSSDVEDHNDLMLQLRDOASL 132

QY 121 TSSVQPLPLPNDCATAGTECHVSGWGI TNHPRNPFPDLLQCLNLSIVSHATCHGVYVPGRI 180
DB 133 GSKVKPISLADHCTQPGQKCTVSGWGTVPSTRENFPDTLNCAEVKIFPKKCEDAYPGQI 192

QY 181 TSNMVCAGVPGQDACQDGGPLVCGGVLOGLVSWGSGVPCQDGI PGVYTYICKYVDW 240
DB 193 TGMVCAGSSKGADTCQDGGPLVCDGALQGITSWGSDPCGRSDKFGVYTNICRYLDW 251

QY 241 IRMIM 245
DB 252 IKKII 256

RESULT 5
US-09-070-526-2
Sequence 2, Application US/09070526
Patent No. 6100059
GENERAL INFORMATION:
APPLICANT: SOUTHAN, CHRISTOPHER
APPLICANT: CLINKENBEARD, HELEN
APPLICANT: BURGESS, NICOLA
TITLE OF INVENTION: No. 6100059el Compounds
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P. O. BOX 980

;
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/070/070,526
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711952.3
; FILING DATE: 9-JUN-1997
; APPLICATION NUMBER: EP 97309646.4
; FILING DATE: 1-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-30353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-070-526-2

Query Match 45.6%; Score 626.5; DB 3; Length 260;
Best Local Similarity 50.4%; Pred. No. 6.2e-53;
Matches 122; Conservative 23; Mismatches 92; Indels 5; Gaps 3;

QY 5 IFLLV---CVLGLSQAATPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIIDHRWLTAA 61
DB 13 MFLLLGGAWGHSRAQEDKVIHGECQPHSQPWAALFQGGQLLCGGVILVGNWLTAA 72

QY 62 HCSGRYVRLGEHSLQSLDWTETQIRHSGFVTHPGYLGAST-SHEHDLRLRLRLPVRV 120
DB 73 HCKKPKYTVRLGDHSLQNGDPEQEI PVVQSI PHPCYNSSDVEDHNDLMLQLRQASL 132

QY 121 TSSVQPLPLPNDCATAGTCHVSGWGITNHPNPDPDLLOCLNLSIVSHATCHGVYPGRI 180
DB 133 GSKVRPISLADHCTOPGQKCTVSGMGVTSPRENFPDTLNCFAEVKIFPOKKCEDAYPGQI 192

QY 181 TSNMVCAGVPQDADCGDGGPLVCGGVLCGLVSGVSGPCQDGI PGVYTVICKYVDW 240
DB 193 TGMVCAKSGKADTCQDGGSGPLVCDGALQGITSWGSDPCGRSDKPKGVYTNICRYLDW 251

QY 241 IR 242
DB 252 IK 253

RESULT 6
US-09-025-059-3
; Sequence 3, Application US/09025059
; Patent No. 6075136
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.

;
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,059
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0481 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1020091
; US-09-025-059-3

Query Match 45.3%; Score 622.5; DB 3; Length 260;
Best Local Similarity 49.0%; Pred. No. 1.5e-52;
Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;

QY 5 IFLLV---LGLSQAATPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIIDHRWLTAA 61
DB 13 ILLLLFMGAWAGTQAQSKILEGECIPHSPQWAALFQGERLIGGVLVGDRWLTAA 72

QY 62 HCSGRYVRLGEHSLQSLDWTETQIRHSGFVTHPGYLGAS-TSHEHDLRLRLRLPVRV 120
DB 73 HCKKPKYTVRLGDHSLQSDQPEQEI QVAQSI QHPCYNNSNPEDHSHDMLIRLONSANL 132

QY 121 TSSVQPLPLPNDCATAGTCHVSGWGITNHPNPDPDLLOCLNLSIVSHATCHGVYPGRI 180
DB 133 GSKVRPVQLANLCPKVQKCIISGMGTVTSPOENFPNTLNCFAEVKIYQNKCEAYPGKI 192

QY 181 TSNMVCAGVPQDADCGDGGPLVCGGVLCGLVSGVSGPCQDGI PGVYTVICKYVDW 240
DB 193 TGMVCAKSGKADTCQDGGSGPLVCDGMLQGITSWGSDPCGKPKPKGVYTKICRYTTW 251

QY 241 IRMINRN 247
DB 252 IKKTMND 258

RESULT 7
US-09-008-271A-7
; Sequence 7, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES

```
/
/ NUMBER OF SEQUENCES: 24
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Dr.
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/008,271A
/ FILING DATE: 16-Jan-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: <Unknown>
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mohan-Peterson, Sheela
/ REGISTRATION NUMBER: 41,201
/ REFERENCE/DOCKET NUMBER: PF-0458 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 260 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: COLANOT27
/ CLONE: 1798496
/ SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
US-09-008-271A-7

Query Match 45.3%; Score 622.5; DB 3; Length 260;
Best Local Similarity 49.8%; Pred. No. 1.5e-52;
Matches 122; Conservative 24; Mismatches 94; Indels 5; Gaps 3;

QY 5 IFLLV---CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA 61
DB 13 MFLLLGGAWAGHRAQEDKVLGGHECPHSPQWQAALSGQQLLCGGVLGVGNVLTAA 72
QY 62 HCSGRYVRLGEHSLQSDWTEQIRHSGFSTVTHPGYLGAST-SHEHDLRLRLPLVRV 120
DB 73 HCKPKYTVRLGDHSLQSDWTEQIRHSGFSTVTHPGYLGAST-SHEHDLRLRLPLVRV 132
QY 121 TSSVQPLPLPNDCAATAGTECHVSGWGITNHPNPPDQLLQCLNLSIVSHATGCHVYVPGRI 180
DB 133 GSKVAPISLADHCTQPGKCTVSGWGTVPSPNPPDNLNCAEVKIFPKKCEDAYPGQI 192
QY 181 TSNMVCAGVPGQDQACQDGGPLVCGVGLQGLVSGVSGPGQDGIPIGVYTIICKYVDW 240
DB 193 TDGMVCASSKGAADTCQDGGPLVCDGALQGITSWGSD-PCGRSKPKGVYTIICKYLDW 251
QY 241 IRMIM 245
DB 252 IKKII 256

RESULT 8
US-09-618-259-8
/ Sequence 8, Application US/09618259
/ Patent No. 6642013
/ GENERAL INFORMATION:
/ APPLICANT: O'Brien, Timothy J.
/ TITLE OF INVENTION: No. 6642013a1 Extracellular Serine Protease
/ FILE REFERENCE: D6020CIP2
/ CURRENT APPLICATION NUMBER: US/09/618,259
```

```
/
/ CURRENT FILING DATE: 2000-07-18
/ PRIOR APPLICATION NUMBER: US 09/127,444
/ FILING DATE: 1998-08-21
/ NUMBER OF SEQ ID NOS: 72
/ SEQ ID NO 8
/ LENGTH: 260
/ TYPE: PRT
/ ORGANISM: Mus sp.
/ FEATURE:
/ OTHER INFORMATION: Amino acid sequence of mouse neuropsin homologous
/ OTHER INFORMATION: to TADG-14; accession no. D30785
US-09-618-259-8

Query Match 45.3%; Score 622.5; DB 4; Length 260;
Best Local Similarity 49.0%; Pred. No. 1.5e-52;
Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;

QY 5 IFLLV---LGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA 61
DB 13 ILLLLFMGAWAGLTRAQSKILEGECIPHSQWQAALFQGBRLICGGVLVGDRLVLTAA 72
QY 62 HCSGRYVRLGEHSLQSDWTEQIRHSGFSTVTHPGYLGAS-TSHEHDLRLRLPLVRV 120
DB 73 HCKQKYSVRLGDHSLQSDWTEQIRHSGFSTVTHPGYLGAS-TSHEHDLRLRLPLVRV 132
QY 121 TSSVQPLPLPNDCAATAGTECHVSGWGITNHPNPPDQLLQCLNLSIVSHATGCHVYVPGRI 180
DB 133 GSKVAPISLADHCTQPGKCTVSGWGTVPSPNPPDNLNCAEVKIFPKKCEDAYPGQI 192
QY 181 TSNMVCAGVPGQDQACQDGGPLVCGVGLQGLVSGVSGPGQDGIPIGVYTIICKYVDW 240
DB 193 TDGMVCASSKGAADTCQDGGPLVCDGMLQGITSWGSD-PCGKPKGVYTIICKYTTW 251
QY 241 IRMIM 247
DB 252 IKKTM 258

RESULT 9
US-09-205-258-427
/ Sequence 427, Application US/09205258
/ Patent No. 6525174
/ GENERAL INFORMATION:
/ APPLICANT: Young et al.
/ TITLE OF INVENTION: 207 Human Secreted Proteins
/ FILE REFERENCE: PZ007P1
/ CURRENT APPLICATION NUMBER: US/09/205,258
/ CURRENT FILING DATE: 1998-12-04
/ EARLIER APPLICATION NUMBER: PCT/US98/11422
/ EARLIER FILING DATE: 1998-06-04
/ EARLIER APPLICATION NUMBER: 60/048,885
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,375
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,881
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,880
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,896
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,020
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,876
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,895
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,884
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,894
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,971
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,964
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Db 95 CLKPRYIVHLOHNLQKEEGCEQTRTATESPPHGFNNNSLPNKHNRNDIMLVKMASPVSI 154
QY 121 TSSVOPPLPNDCATAGTECHVSGWGTTHNRPDPDLLOCLNLSIVSHATCHGVYPGRI 180
Db 155 TWAVRPLTLSSKCVTAGTSCLSISGWSTSPQLRPLHTLRCANITIIIEHQKCNAYPGNI 214
QY 181 TSNMVCAG-GVPGQACQDSGGLVCGGVLLQGLVSWGSGVPGCGDGPVGYTYICKYVD 239
Db 215 TDTMVCASVQEGGKDCQCGSDGGLVVCNQLGIIISWQ-DPCATRKPGVYTKVCKYVD 273
QY 240 WIRMTNRN 248
Db 274 WIQETMKN 282

RESULT 11

US-09-386-642-13
; Sequence 13, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Q1, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-13

Query Match 43.9%; Score 602.5; DB 4; Length 288;
Best Local Similarity 51.1%; Pred. No. 1.5e-50;
Matches 116; Conservative 21; Mismatches 87; Indels 3; Gaps 3;
QY 21 KIFNGTEC-GRNSOPWQVGLFEGTSLRCGGVLIDHRVLTAAHCSGSRYWVRLGSHLSQ 79
Db 51 KIVGGYNCLPHEPSQWQAALFQGLCGVVGNGVLTAAHCKPKYTVRLGSHLSQ 110
QY 80 LDWTEQIRHSGFVTHPGYLGA--STSHEDLRLRLPVRVTSSVQPLPNDCATAGT 138
Db 111 KDGPEQEIPIVQSIHPHCYNSSDVEDHNDMLLQLRDQASLGSKVKPISLADHCTQPGQ 170
QY 139 ECHVSGWGTTHNRPDPDLLOCLNLSIVSHATCHGVYPGRTISNMVCAGGVPGQACQG 198
Db 171 KCTVSGWGTVSPRENFPDITLCAEVKIFPQKKCEDAIPGQITDGMVCAGSGKADTCQG 230
QY 199 DSGGLVCGGLVQGLVSWGSGVPGCGDGPVGYTYICKYVDMIRMIM 245
Db 231 DSGGLVCDGALQGITWSGS-DPCGRSDKPGVYTNICRYLDWIKKII 276

RESULT 12

US-09-386-642-14
; Sequence 14, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Q1, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 14
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-14
Query Match 43.6%; Score 598.5; DB 4; Length 289;
Best Local Similarity 49.1%; Pred. No. 3.8e-50;
Matches 114; Conservative 34; Mismatches 79; Indels 5; Gaps 4;
QY 21 KIFNGTEC-GRNSOPWQVGLFEGTSLRCGGVLIDHRVLTAAHCSGSRYWVRLGSHLSQ 79
Db 51 KIVGGYNCLPHEPSQWQAALFQGLCGVVGNGVLTAAHCKPKYTVRLGSHLSQ 110
QY 80 LDWTEQIRHSGFVTHPGYLGA--STSHEDLRLRLPVRVTSSVQPLPNDCATAG 137
Db 111 BEGCEQTRTATESPPHGFNNNSLPNKHNRNDIMLVKMASPVSIWAVRPLTLSSKCVTAG 170
QY 138 TECHVSGWGTTHNRPDPDLLOCLNLSIVSHATCHGVYPGRTISNMVCAG-GVPGQAC 196
Db 171 TSLISGWSTSPQLRPLHTLRCANITIIIEHQKCNAYPGNITDTMVCASVQEGGKDC 230
QY 197 QDGGGLVCGGLVQGLVSWGSGVPGCGDGPVGYTYICKYVDMIRMIRN 248
Db 231 QDGGGLVVCNQLGIIISWQ-DPCATRKPGVYTKVCKYVDMIQETMKN 281

RESULT 13

US-08-944-483-24
; Sequence 24, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; TITLE OF INVENTION: OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623


```
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
; US-08-944-483-24

Query Match
Best Local Similarity 43.5%; Score 597.5; DB 3; Length 248;
Matches 119; Conservative 36; Mismatches 87; Indels 7; Gaps 6;

QY 3 LSIPIILLCVLGLSQAATPKIFNGTECGRNSQWQVGLFEGTSLRCGGVLIDHRWVLTAAH 62
Db 4 LQILLALATLGGGT-RIKGFEC-PHSQWQAALFK-TRLLCGATLIAFRWLTAAH 60
QY 63 CSGSRYWVRLGSHLSOLDWTEQIRHSGFSVTHPGYLGA--STSHEDLRLRLRPVTV 120
Db 61 CLKPRYIVHLGQHNQLKEGCGEQTRTATESFFHPGFNNSLPNKDRNDIMLVKMASPVSI 120
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRPFPDLLQCLNLSIVSHATCHGVYVGR 180
Db 121 TWAVRPLTLSSRCVTAGTSCLSGWSGTSPPQLRPLHTLRKANITIIIEHKCNAYPGNI 180
QY 181 TSNMVCAG-GVPGQDACQDGGPLVCGGVLOGLVSWGSGVPGCGQDGIPIGVYTYICKYVD 239
Db 181 TDTMVCASVQEGGKDSQCGDSGGPLVCNQLGIIISWGQ-DFCAITRKPGVTVTKCKYVD 239
QY 240 WIRIMRN 248
Db 240 WIQETMKN 248

RESULT 14
US-08-956-267A-2
; Sequence 2, Application US/08956267A
; Patent No. 5945328
; GENERAL INFORMATION:
; APPLICANT: WOLDIKE, Helle Fabricius
; APPLICANT: KJELSEN, Thomas Borglum
; TITLE OF INVENTION: A Process For Producing Trypsin
; TITLE OF INVENTION: (Trypsinogen)
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 5945328o No. 5945328disk of No. 5945328th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,267A
; FILING DATE: 22-OCT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 4500.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
; US-08-956-267A-2

Query Match
Best Local Similarity 41.7%; Score 573; DB 2; Length 247;
Matches 113; Conservative 42; Mismatches 83; Indels 10; Gaps 5;

QY 6 FLLLCVLGLSQA-----ATPKIFNGTECGRNSQWQVGLFEGTSLRCGGVLIDHRWVLTAA 61
Db 5 FVLLALLGAAPFTDDDDKIVGGYTCAANSIPYQVSLNSGSHF-CGGSLLNSQWVVSAA 63
QY 62 HCSGSRYWVRLGSHLSOLDWTEQIRHSGFSVTHPGYLCASTSHEHDLRLRLRPVTV 121
Db 64 HCYSRIQVRLGSHLSOLDWTEQIRHSGFSVTHPGYLCASTSHEHDLRLRLRPVTV 121
QY 122 SSVQPLPLPNDCATAGTECHVSGWGITNHPRPFPDLLQCLNLSIVSHATCHGVYVGRIT 181
Db 122 SRVATVSLPRSCAAAGTECLISGWNKTSKSSGYSLSLQCLKAPVLSDSCKSSYPGQIT 181
QY 182 SNMVCAGVP-GQDACQDGGPLVCGGVLOGLVSWGSGVPGCGQDGIPIGVYTYICKYVD 240
Db 182 GNMICVGFLEGGKDSQCGDSGGPVVCGQLQGVISWGY--GCAQKNKPGVTVKVCNVNV 239
QY 241 IRMIMRN 248
Db 240 IQOTIAAN 247

RESULT 15
US-09-949-016-8166
; Sequence 8166, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8166
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-8166

Query Match
Best Local Similarity 41.3%; Score 567; DB 4; Length 290;
Matches 116; Conservative 36; Mismatches 80; Indels 16; Gaps 6;

QY 13 GLSQAATPKIFN-----GTECGRNSQWQVGLFEGTSLRCGGVLIDHRWVLTAAH 62
Db 31 GVSQESS-KVLTNTGTSGLPGGYTCFFPHSQWQAALLVQGRLLCGGLVHPKWLTAH 89
QY 63 CSGSRYWVRLGSHLSOLDWTEQIRHSGFSVTHPGYLGA--SHEHDLRLRLRPVTV 120
Db 90 CLKELKVLKHALGRVEAGEQVEVHSHIPPEYRRSPTHLNHDHIMLELQSPVL 149
QY 121 TSSVQPLPLP-NDCATAGTECHVSGWGITNHPRPFPDLLQCLNLSIVSHATCHGVYVGR 179
Db 150 TGYIQTPLSHNNRLTPGTTCRVSGWGTTSQVNVYKTLQCANIQLRDEECRVYPGK 209
QY 180 ITSNNVCAGVP-GQDACQDGGPLVCGGVLOGLVSWGSGVPGCGQDGIPIGVYTYICKYV 238
Db 210 ITDNMLCAGTKEGGKDSCEGSGGGLVNCNRTLYGIVSWGDF-PCGQDPGPGVTVTRSV 268
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QY 239 DWIRIMR 246
||| :
Db 269 LWIRETIR 276

Search completed: March 5, 2005, 20:45:52
Job time : 51 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 5, 2005, 20:36:50 ; Search time 41 Seconds
(without alignments)
581.994 Million cell updates/sec

Title: US-10-015-385a-194

Perfect score: 1374

Sequence: 1 MGLSIFLLCVLGLSQAATP.....GVYTVICKYDWMRMNRN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 79:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	622.5	45.3	260	I56559	neuropsin - mouse
2	569.5	41.4	248	S55066	trypsin (EC 3.4.21
3	567	41.3	248	S55067	trypsin (EC 3.4.21
4	561	40.8	231	TRPOTR	trypsin (EC 3.4.21
5	555	40.4	243	A35871	serine proteinase
6	555	40.4	253	A53968	trypsin (EC 3.4.21
7	553	40.2	246	B25528	trypsin (EC 3.4.21
8	552	40.2	229	TRBOTR	trypsin (EC 3.4.21
9	550	40.0	247	I13813	trypsin (EC 3.4.21
10	546	39.7	247	TRDG	trypsin (EC 3.4.21
11	545	39.7	246	TRDGC	trypsin (EC 3.4.21
12	544.5	39.6	247	A27547	trypsin (EC 3.4.21
13	543	39.5	246	TRRT1	trypsin (EC 3.4.21
14	540	39.3	238	S31779	trypsin (EC 3.4.21
15	533.5	38.8	247	S05494	trypsin (EC 3.4.21
16	532	38.7	246	TRRT2	trypsin (EC 3.4.21
17	527.5	38.4	261	A31136	tissue kallikrein
18	524	38.1	232	KQPG	tissue kallikrein
19	520.5	37.9	261	A25606	tissue kallikrein
20	519	37.8	246	JQ1471	trypsin (EC 3.4.21
21	518	37.7	246	JQ1472	trypsin (EC 3.4.21
22	518	37.7	261	A34079	tissue kallikrein
23	513.5	37.4	231	S31778	trypsin (EC 3.4.21
24	513.5	37.4	239	A27207	tissue kallikrein
25	511.5	37.2	261	S45303	tissue kallikrein
26	510.5	37.2	261	1 NGMSG	7S nerve growth fa
27	508	37.0	242	S31776	trypsin (EC 3.4.21
28	508	37.0	242	S31775	trypsin (EC 3.4.21
29	503	36.6	260	A37938	tissue kallikrein

30	503	36.6	263	2	S15686	tissue kallikrein
31	502	36.5	259	2	B31136	tissue kallikrein
32	501	36.5	247	1	B25852	trypsin (EC 3.4.21
33	499.5	36.4	241	2	S39048	trypsin (EC 3.4.21
34	496.5	36.1	261	1	TRMSM5	tissue kallikrein
35	496	36.1	242	2	S49489	trypsin (EC 3.4.21
36	495.5	36.1	257	2	S33772	tissue kallikrein
37	495.5	36.1	261	2	S01971	tissue kallikrein
38	494.5	36.0	247	1	A25852	trypsin (EC 3.4.21
39	493	35.9	262	1	KQHU	tissue kallikrein
40	491.5	35.8	240	2	S39047	trypsin (EC 3.4.21
41	491	35.7	256	1	NGMSA	7S nerve growth fa
42	490.5	35.7	229	1	TRDFS	trypsin (EC 3.4.21
43	490.5	35.7	261	2	A41020	tissue kallikrein
44	489	35.6	244	2	A44284	tissue kallikrein
45	485.5	35.3	261	2	JB0236	tissue kallikrein
46	484.5	35.3	259	2	A29746	tissue kallikrein
47	484.5	35.3	304	2	S33496	trypsin (EC 3.4.21
48	483.5	35.2	265	1	KQRTF	tissue kallikrein
49	481.5	35.0	250	2	T01779	trypsin (EC 3.4.21
50	481.5	35.0	261	2	A29745	tissue kallikrein
51	479	34.9	261	1	S35711	seminogelase (EC 3
52	477.5	34.8	261	1	KQMS1	trypsin (EC 3.4.21
53	476	34.6	259	2	I38363	trypsin (EC 3.4.21
54	470.5	34.2	261	1	A32297	seminogelase (EC 3
55	469.5	34.2	261	2	A24378	tissue kallikrein
56	468	34.1	259	1	KQRTTN	tonin (EC 3.4.21.-
57	467.5	34.0	261	1	EGMSB	tissue kallikrein
58	467	34.0	247	2	S12764	trypsin (EC 3.4.21
59	461.5	33.6	259	2	D23863	tissue kallikrein
60	458.5	33.4	250	2	S31384	trypsin (EC 3.4.21
61	458.5	33.4	261	2	A29586	tissue kallikrein
62	449	32.7	258	2	A57290	venom plasminogen
63	436.5	31.8	250	2	S15685	kallikrein, glandu
64	436.5	31.8	257	1	JC2479	venombin B (EC 3.4
65	432	31.4	236	1	A32121	snake venom factor
66	431.5	31.4	261	2	A28062	gamma-amin (EC 3.
67	431	31.4	262	1	JC4803	venombin A (EC 3.4
68	422.5	30.7	233	1	JG0169	venombin A (EC 3.4
69	417	30.3	236	1	B32121	snake venom factor
70	411.5	29.9	228	1	S35689	venombin A (EC 3.4
71	408	28.7	235	1	S65621	venombin AB (EC 3.
72	406.5	29.6	231	2	A60468	venombin A (EC 3.4
73	402	29.3	255	1	A28169	venombin A (EC 3.4
74	394	28.7	236	1	A41456	pancreatic elastase
75	388	28.2	269	2	A26823	pancreatic elastase
76	386	28.1	232	1	A54361	venombin A (EC 3.4
77	385.5	28.1	188	2	B32340	tissue kallikrein
78	385.5	28.1	264	2	I38136	chymotrypsin-like
79	382.5	27.8	1524	2	T30337	polypeptide - Afri
80	382	27.8	246	1	DBHU	complement factor
81	381	27.7	263	1	I55608	complement factor
82	377	27.4	225	1	S45356	complement factor
83	374.5	27.3	259	1	WMS28	complement factor
84	371	27.0	271	1	ELRT2	pancreatic elastase
85	370.5	27.0	263	2	A21195	chymotrypsin (EC 3
86	370	26.9	234	1	S20407	venombin A (EC 3.4
87	368.5	26.8	343	1	A57014	proctasin (EC 3.4.
88	367.5	26.7	638	1	KQHUP	plasma kallikrein
89	366	26.6	258	1	S36783	venombin A (EC 3.4
90	364	26.5	156	2	B23863	tissue kallikrein
91	362.5	26.4	246	2	S64707	chymase (EC 3.4.21
92	359.5	26.2	277	2	S35340	trypsin (EC 3.4.21
93	359	26.1	443	2	I46932	coagulation factor
94	358	26.1	812	1	PLBO	plasmin (EC 3.4.21
95	357	26.0	262	1	A31372	granzyme A (EC 3.4
96	357	26.0	263	2	A31299	chymotrypsin (EC 3
97	357	26.0	271	2	S29239	chymotrypsin (EC 3
98	357	26.0	1019	2	A38738	coagulation factor
99	355.5	25.9	276	2	A38654	mast cell proteina
100	354	25.8	271	2	A25528	pancreatic elastase
101	353.5	25.7	263	2	S47537	chymotrypsin (EC 3
102	353.5	25.7	270	2	S56160	mast cell tryptase

103	353	25.7	274	2	JC4171	trypsin (EC 3.4.21)	176	320.5	23.3	247	1	PRMSCL	granzyme B (EC 3.4
104	352	25.6	260	1	A45061	granzyme A (EC 3.4	177	319.5	23.3	559	1	A29941	t-plasminogen acti
105	352	25.6	461	1	JX0210	protein C (activat	178	319	23.2	1034	1	A53663	enteropeptidase (E
106	351	25.5	456	1	KX80	protein C (activat	179	318.5	23.2	460	2	B61545	plasmin (EC 3.4.21
107	349.5	25.4	269	2	B26823	pancreatic elastase	180	318	23.1	265	2	T10495	chymotrypsin (EC 3
108	348	25.3	267	2	S40006	trypsin (EC 3.4.21	181	318	23.1	271	2	I46580	factor IX - pig (f
109	347	25.3	461	1	KXHU	protein C (activat	182	318	23.1	274	2	I47078	coagulation factor
110	346.5	25.2	244	2	S26042	chymase (EC 3.4.21	183	318	23.1	618	2	A35827	thrombin (EC 3.4.2
111	346.5	25.2	461	1	S18994	protein C (activat	184	317.5	23.1	245	1	KYBOB	chymotrypsin (EC 3
112	344	25.0	275	2	B35863	trypsin (EC 3.4.2	185	317.5	23.1	246	2	A32692	cytotoxic T-lympho
113	343.5	25.0	273	2	A47246	trypsin (EC 3.4.2	186	317	23.1	249	2	A56634	granzyme M (EC 3.4
114	343.5	25.0	274	2	S33339	trypsin (EC 3.4.21	187	316.5	23.0	246	1	A46504	chymase (EC 3.4.21
115	343	25.0	275	2	A32410	trypsin (EC 3.4.2	188	315.5	23.0	254	1	TRWV3Y	trypsin-like prote
116	342.5	24.9	558	2	JC5878	plasma hyaluronan-	189	315.5	23.0	266	1	ELRT1	pancreatic elastase
117	342.5	24.9	810	1	PLHU	plasmin (EC 3.4.21	190	315.5	23.0	392	1	A30100	serine proteinase
118	342	24.9	275	2	C35863	trypsin (EC 3.4.2	191	315.5	23.0	492	1	EXBO	coagulation factor
119	341.5	24.9	275	2	A35863	trypsin (EC 3.4.2	192	315	22.9	248	2	S43259	granzyme-like prot
120	341.5	24.9	258	2	I56220	trypsin (EC 3.4.2	193	315	22.9	617	2	S10511	thrombin (EC 3.4.2
121	340.5	24.8	246	2	B38678	serine proteinase	194	315	22.9	686	1	A59271	Ra-reactive factor
122	339.5	24.7	258	2	A45161	probable pancreati	195	314	22.9	275	2	S40005	trypsin (EC 3.4.21
123	339.5	24.7	267	4	A56615	granzyme A (EC 3.4	196	313	22.8	613	2	S15468	complement C3b/C4b
124	339	24.7	257	2	B45061	coagulation factor	197	313	22.8	855	2	JC7731	membrane-bound arg
125	339	24.7	461	1	KFHU1	coagulation factor	198	312.5	22.7	274	2	S40004	trypsin-related pr
126	339	24.7	625	1	KFHU1	coagulation factor	199	312.5	22.7	615	1	KFHU12	coagulation factor
127	338	24.6	625	1	TBBO	thrombin (EC 3.4.2	200	311.5	22.7	761	2	JC5759	brain-specific ser
128	337.5	24.6	238	1	TRWV5Y	trypsin-like prote	201	311	22.6	261	2	S40162	cathepsin G (EC 3.
129	337.5	24.6	264	2	S65663	granzyme 3 (EC 3.4	202	311	22.6	431	2	S47538	acrosin (EC 3.4.21
130	337	24.5	434	1	A35005	u-plasminogen acti	203	311	22.6	433	1	JN0560	u-plasminogen acti
131	337	24.5	812	1	PLMS	plasmin (EC 3.4.21	204	311	22.6	1035	1	A43090	enteropeptidase (E
132	336.5	24.5	251	2	T10262	mast cell serine p	205	310.5	22.6	247	1	PRRTG	mast cell proteina
133	336.5	24.5	251	2	PC1235	29K serine protein	206	310.5	22.6	559	1	A35029	t-plasminogen acti
134	336.5	24.5	638	1	KOMSP	plasma kallikrein	207	310	22.6	275	2	I46712	factor IX - rabbit
135	336	24.5	416	1	KFBO	coagulation factor	208	309.5	22.5	482	1	EXRT	coagulation factor
136	336	24.5	790	1	PLFG	plasmin (EC 3.4.21	209	307	22.3	250	2	S55493	serine proteinase
137	335.5	24.4	258	4	S70439	pancreatic elastase	210	307	22.3	259	1	S49129	chymotrypsin (EC 3
138	333	24.2	245	1	KYBOA	chymotrypsin (EC 3	211	307	22.3	417	1	S00845	hepsin (EC 3.4.21.
139	333	24.2	285	2	I48144	coagulation factor	212	306.5	22.3	375	1	A23689	limulus clotting e
140	332.5	24.2	638	1	KORTPL	plasma kallikrein	213	305.5	22.2	236	2	I42696	thrombin (EC 3.4.2
141	332.5	24.2	810	2	I46260	plasmin (EC 3.4.21	214	305	22.2	281	1	A61021	granzyme B (EC 3.4
142	332.5	24.2	810	2	B30848	plasmin (EC 3.4.21	215	304	22.1	149	1	KOMSM	tissue kallikrein
143	331.5	24.1	256	1	TRFP	trypsin (EC 3.4.21	216	304	22.1	236	2	C42696	thrombin (EC 3.4.2
144	331.5	24.1	275	2	S40007	trypsin (EC 3.4.21	217	304	22.1	268	2	S68825	pancreatic elastase
145	331	24.1	263	1	KYRTB	chymotrypsin (EC 3	218	304	22.1	562	1	UKHT	t-plasminogen acti
146	331	24.1	622	1	TBHU	thrombin (EC 3.4.2	219	303.5	22.1	244	2	A46721	chymase (EC 3.4.21
147	330.5	24.1	247	1	KYHUCM	chymase (EC 3.4.21	220	303.5	22.1	309	2	B49878	coagulation factor
148	330.5	24.1	560	1	JC4795	plasma hyaluronan-	221	303	22.1	196	2	T08808	hypothetical prote
149	330	24.0	282	2	I84621	coagulation factor	222	302.5	22.0	244	2	A34910	mast cell proteina
150	330	24.0	4548	1	S00657	apoprotein(a) (EC	223	302.5	22.0	273	2	S40003	trypsin-related pr
151	329.5	24.0	226	2	JEO151	myonase (EC 3.4.-	224	302.5	22.0	1004	2	T30338	oviductin (EC 3.4.
152	329.5	24.0	237	2	S68702	trypsin (EC 3.4.2	225	302.5	22.0	1113	2	JEO315	low-density lipopr
153	329.5	24.0	269	2	C26823	pancreatic elastase	226	302	22.0	268	2	S68826	pancreatic elastase
154	329.5	24.0	1420	2	A32869	apolipoprotein(a)	227	302	22.0	394	2	J06060	t-plasminogen acti
155	328.5	23.9	455	2	A61545	plasmin (EC 3.4.21	228	302	22.0	477	1	A34369	t-plasminogen acti
156	328.5	23.9	786	1	A47547	serine proteinase	229	302	22.0	477	2	J05058	t-plasminogen acti
157	328	23.8	452	1	A30351	coagulation factor	230	301	21.9	255	2	A27122	cathepsin G (EC 3.
158	327.5	23.8	266	2	S54146	trypsin (EC 3.4.21	231	301	21.9	431	2	J05059	t-plasminogen acti
159	327	23.8	244	2	S72219	chymotrypsin B - A	232	300.5	21.9	442	1	UKPG	u-plasminogen acti
160	327	23.8	259	2	S68424	allergen der f III	233	300	21.8	245	2	A48598	kallikrein-like se
161	326.5	23.8	248	1	PRMSC2	granzyme C (EC 3.4	234	299.5	21.8	235	2	E42696	thrombin (EC 3.4.2
162	326.5	23.8	266	1	ELFG	pancreatic elastase	235	299.5	21.8	246	2	A38678	mast cell proteina
163	326	23.7	248	2	S33755	granzyme-like prot	236	299.5	21.8	258	1	S44184	chymotrypsin (EC 3
164	324	23.6	274	2	A45754	trypsin (EC 3.4.2	237	299.5	21.8	436	2	JX0172	acrosin (EC 3.4.21
165	324	23.6	459	2	JQ0419	coagulation factor	238	299	21.8	437	2	S18407	acrosin (EC 3.4.21
166	324	23.6	1019	1	A56318	enteropeptidase (E	239	298.5	21.7	191	2	S54115	complement factor
167	323.5	23.5	466	1	KFHU7	coagulation factor	240	298.5	21.7	249	1	A35842	chymase (EC 3.4.21
168	323	23.4	699	1	I54763	Ra-reactive factor	241	298.5	21.7	270	2	B29934	pancreatic elastase
169	321.5	23.4	251	2	JC2125	chymase (EC 3.4.21	242	298.5	21.7	407	1	KFBO7	coagulation factor
170	321	23.4	226	1	KCUF	bradykinin (EC 3.4	243	297	21.6	237	1	TRCY1	trypsin (EC 3.4.21
171	321	23.4	226	2	S69370	duodenase - bovine	244	297	21.6	260	2	S26043	chymase (EC 3.4.21
172	321	23.4	247	2	S64708	chymase (EC 3.4.21	245	297	21.6	418	2	A37344	acrosin (EC 3.4.21
173	321	23.4	248	2	A43520	natural killer cel	246	297	21.6	477	2	J05057	t-plasminogen acti
174	321	23.4	269	2	B32410	mastocytoma protei	247	296.5	21.6	248	1	S01007	granzyme F (EC 3.4
175	321	23.4	655	1	A46688	hepatocyte growth	248	296	21.5	281	2	T13596	trypsin homolog -

249	295.5	21.5	239	2	G42696	thrombin (EC 3.4.2	322	220.5	16.0	267	1	ELHUL	leukocyte elastase
250	295.5	21.5	433	1	UKMS	u-plasminogen acti	323	217.5	15.8	710	1	I51283	hepatocyte growth
251	294	21.4	247	2	S23504	chymase (EC 3.4.21	324	216	15.7	728	1	A35644	hepatocyte growth
252	294	21.4	303	2	T13598	trypsin homolog -	325	216	15.7	728	1	A60185	chymase (EC 3.4.21
253	293.5	21.4	431	1	UKHU	u-plasminogen acti	326	204.5	14.9	177	2	S23505	fibrinolytic prote
254	293	21.3	234	2	F42696	thrombin (EC 3.4.2	327	201	14.6	214	2	S17680	chymase (EC 3.4.21
255	293	21.3	247	2	S59135	mast cell proteina	328	197.5	14.4	213	2	S17537	chymotrypsin (EC 3
256	293	21.3	265	2	A38894	serine proteinase	329	196	14.3	248	2	S49323	chymotrypsin (EC 3
257	293	21.3	265	2	JS0260	serine proteinase	330	192.5	14.0	763	2	I50807	complement factor
258	293	21.3	433	1	UKBAY	u-plasminogen acti	331	189.5	13.8	94	2	PC2013	tissue kallikrein
259	292.5	21.3	236	2	A28566	T-cell suppressor	332	182	13.2	104	2	S15395	tissue kallikrein-
260	291.5	21.2	216	1	KYVH20	chymotrypsin (EC 3	333	180	13.1	258	2	G02959	haptoglobin - rhes
261	291	21.2	271	2	S41308	serine proteinase	334	179.5	13.1	149	2	S35208	serine proteinase
262	289.5	21.1	248	2	A33412	cytotoxic T-lympho	335	178	13.0	348	1	HPHUR	haptoglobin-relate
263	289	21.0	583	2	A29154	complement factor	336	177	12.9	347	1	HPHU1	haptoglobin precu
264	288.5	21.0	270	2	A29934	pancreatic elastas	337	177	12.9	406	1	HPHU2	haptoglobin precu
265	288.5	21.0	1047	2	A55617	masquerade precurs	338	176.5	12.8	760	1	C2MS	classical-compleme
266	288	21.0	268	2	JQ1473	pancreatic elastas	339	176	12.8	735	2	T35778	probable fusidic a
267	288	21.0	421	2	S29599	thrombin (EC 3.4.21	340	174.5	12.7	377	2	C88710	protein C43G2.5 [1
268	287.5	20.9	235	2	H42696	thrombin (EC 3.4.2	341	174	12.7	161	2	I48158	coagulation factor
269	287.5	20.9	618	2	S28941	u-plasminogen acti	342	174	12.7	330	2	B82415	probable serine pr
270	286.5	20.9	203	1	KYVH2C	chymotrypsin (EC 3	343	172	12.5	346	2	I36942	haptoglobin - chim
271	286	20.8	254	2	S35585	chymotrypsin-like	344	171	12.4	159	2	S35202	proteinase 2 - buf
272	285.5	20.8	235	2	D42696	thrombin (EC 3.4.2	345	171	12.4	258	2	I36945	haptoglobin Hp - c
273	282.5	20.6	331	2	T27906	hypothetical prote	346	171	12.4	345	2	I36941	haptoglobin - chim
274	282	20.5	416	1	S33777	hepsin (EC 3.4.21	347	170	12.4	347	2	GP0006	haptoglobin precu
275	280	20.4	254	2	S65465	trypsin-like prote	348	169	12.3	329	1	HPDG	haptoglobin precu
276	278.5	20.3	593	2	S45281	coagulation factor	349	168	12.2	66	2	I52972	kallikrein - mouse
277	277.5	20.2	266	2	JC4850	trypsin-like prote	350	168	12.2	154	2	S35207	proteinase 7 - buf
278	276	20.1	430	1	A24702	serine proteinase	351	166	12.1	258	2	I36947	haptoglobin Hpp -
279	276	20.1	488	1	EXHU	coagulation factor	352	166	12.1	349	2	I36944	haptoglobin - chim
280	275.5	20.1	240	1	CPBOA3	procarboxypeptidas	353	166	12.1	752	1	C2HU	complement C2 prec
281	275	20.0	237	2	S55378	serine proteinase	354	165	12.0	161	2	I62744	coagulation factor
282	274.5	20.0	695	1	S05008	complement subcomp	355	165	12.0	347	1	HPMS	serine proteinase
283	273	19.9	247	2	S45113	granzyme-like prot	356	159.5	11.6	152	2	S35209	chymotrypsin-like
284	273	19.9	265	2	T15451	hypothetical prote	357	159	11.6	126	2	A23473	pancreatic elastas
285	272.5	19.8	432	1	S18932	u-plasminogen acti	358	158.5	11.5	264	2	A28942	complement factor
286	272	19.8	475	1	EXCH	coagulation factor	359	157.5	11.5	764	1	BBHU	complement factor
287	272	19.8	688	1	CHUS	complement subcomp	360	154.5	11.2	747	2	I51579	complement factor
288	271	19.7	2616	2	A57096	nudel protein prec	361	153.5	11.2	761	1	BMMS	complement factor
289	270	19.7	694	2	JC6554	complement subcomp	362	152.5	11.1	159	2	I48615	coagulation factor
290	269.5	19.6	248	2	S33756	granzyme-like prot	363	152	11.1	181	2	T08805	hypothetical prote
291	269	19.6	256	1	PRHU3	proteinase 3 (EC 3	364	151.5	11.0	152	2	S35203	serine proteinase
292	268.5	19.5	420	2	A55283	acrosin (EC 3.4.21	365	148	10.8	81	2	A18966	tissue kallikrein
293	265	19.3	415	1	A34170	acrosin (EC 3.4.21	366	145.5	10.6	82	2	T46510	hypothetical prote
294	264.5	19.3	256	2	T10109	trypsin (EC 3.4.21	367	138.5	10.1	158	2	S35201	serine proteinase
295	264.5	19.3	264	2	S32794	trypsin-like prote	368	138	10.0	153	2	S35204	proteinase 4 buf
296	263.5	19.2	251	1	TRHUAZ	azurocidin precurs	369	137	10.0	743	2	T34853	probable fusidic a
297	261.5	19.0	366	2	JE0105	testicular serine	370	136.5	9.9	152	2	S35206	serine proteinase
298	261.5	19.0	421	1	S11674	acrosin (EC 3.4.21	371	135.5	9.9	46	2	I49416	glandular kallikre
299	259	18.9	248	2	S01006	cytotoxic T-lympho	372	132	9.6	347	1	HPRT	haptoglobin precu
300	258.5	18.8	252	2	A36172	procytotoxic T-lym	373	129.5	9.4	396	1	KYBOZ	plasma protein 2 -
301	258.5	18.8	285	2	T35195	probable serine pr	374	127.5	9.3	69	2	S28195	tissue kallikrein
302	257.5	18.7	254	2	S49329	trypsin-like prote	375	127.5	9.3	72	2	S28196	tissue kallikrein
303	256	18.6	403	2	C82228	probable trypsin V	376	126	9.2	80	2	A05324	gamma- α -renin (EC 3
304	252	18.3	400	1	A48050	coagulation factor	377	123.5	9.0	137	2	S53364	serine proteinase
305	248	18.0	367	2	JE0104	testicular serine	378	123.5	9.0	151	2	S35205	proteinase 5 - buf
306	247	18.0	243	2	A56338	venom proteinase (379	122.5	8.9	75	2	A37002	catroboxobin I (EC 3
307	245	17.8	711	1	A47136	macrophage-stimula	380	115.5	8.4	422	1	KXHUZ	plasma protein 2 p
308	244.5	17.8	716	1	A40332	macrophage-stimula	381	114.5	8.3	85	2	S44461	elastase (EC 3.4.2
309	239.5	17.4	265	2	I48679	neutrophil elastas	382	109.5	8.0	61	2	PS0049	serine proteinase
310	237.5	17.3	198	2	S32398	serine proteinase	383	108	7.9	333	2	T15257	hypothetical prote
311	235.5	17.1	232	2	S06176	cytotoxic T-lympho	384	104.5	7.6	256	2	A56593	trypsin-related pr
312	235.5	17.1	716	1	JC5061	macrophage-stimula	385	104	7.6	49	2	B24696	tissue kallikrein
313	235	17.1	96	2	A05308	tissue kallikrein	386	103.5	7.5	64	2	A30981	prostatic arginine
314	235	17.1	230	2	A27802	hypodermin_C (EC 3	387	99.5	7.2	340	2	T34423	hypothetical prote
315	234.5	17.1	219	1	TRFGAZ	azurocidin α -pig	388	97	7.1	388	2	S34672	alkaline serine pr
316	233	17.0	705	1	CHURB	complement subcomp	389	96.5	7.0	416	2	AH2387	hypothetical prote
317	231.5	16.8	230	2	I48685	mast cell proteina	390	94.5	6.9	416	2	G71965	glycine hydroxymet
318	227.5	16.6	272	2	JC4170	trypsin-like prote	391	93.5	6.8	73	2	S44462	elastase (EC 3.4.2
319	227	16.5	259	1	TRSMG	trypsin (EC 3.4.21	392	93.5	6.8	299	1	PRSMBG	streptoglycin B (E
320	226	16.4	728	1	JH0579	hepatocyte growth	393	92.5	6.7	416	2	G64542	glycine hydroxymet
321	225	16.4	548	2	D82175	probable trypsin V	394	91	6.6	31	2	A18671	tissue kallikrein

395	90.5	6.6	48	2	A61331	trypsin (EC 3.4.21	468	78	5.7	4006	2	T09070	probable tenascin
396	90	6.6	1746	1	S19694	tenascin precursor	469	77.5	5.6	438	2	S53787	collagen alpha 1(I)
397	90	6.6	2825	2	T14271	Dc4 protein, stre	470	77.5	5.6	921	2	S42617	collagen alpha 1(I)
398	89	6.5	457	2	A53669	streptogrisin C (E	471	77.5	5.6	1669	1	CGMS4B	collagen alpha 1(I)
399	89	6.5	1737	2	T00209	MEGF8 protein - hu	472	77.5	5.6	1691	1	CGH06B	collagen alpha 6(I)
400	88.5	6.4	2205	1	MNWRN	nonstructural poly	473	77.5	5.6	2907	2	A57278	fibrillin-2 precur
401	88.5	6.4	3002	2	A47221	fibrillin 1 precur	474	77	5.6	517	2	T71134	hypothetical prote
402	87.5	6.4	278	2	AH0282	probable pepetidas	475	77	5.6	553	2	F75407	probable transport
403	87.5	6.4	1582	2	T15308	hypothetical prote	476	77	5.6	668	2	A41234	melanocyte-specifi
404	86.5	6.3	34	2	I49417	nerve growth facto	477	77	5.6	710	2	T31502	hypothetical prote
405	86.5	6.3	38	2	I70029	kallikrein, exon 2	478	77	5.6	1104	2	I38869	transcription fact
406	86.5	6.3	38	2	I70016	kallikrein - mouse	479	77	5.6	3566	1	A40701	tenascin-X precurs
407	86.5	6.3	38	2	I70036	kallikrein - mouse	480	76.5	5.6	295	2	A44984	collagen - nematod
408	86	6.3	70	2	A56784	kallikrein-like se	481	76.5	5.6	315	2	H83096	probable pyrophosp
409	86	6.3	502	2	A48679	differentiated ker	482	76.5	5.6	348	2	A34705	collagen - Caenorh
410	86	6.3	2704	2	S09118	G surface protein	483	76.5	5.6	382	2	PC2053	alkaline proteinas
411	85	6.2	398	2	B75254	acetate kinase - D	484	76.5	5.6	469	1	S29126	properdin precursor
412	85	6.2	411	2	T34585	probable secreted	485	76.5	5.6	1042	1	CGH1S	collagen alpha 1(I)
413	85	6.2	2718	2	A23475	G surface protein	486	76.5	5.6	1453	2	S21626	collagen alpha 1(I)
414	84.5	6.1	287	2	T22637	hypothetical prote	487	76.5	5.6	1532	2	A61262	collagen alpha 1(X
415	84.5	6.1	1023	2	T30257	IGG Fc binding pro	488	76	5.5	257	2	T52298	squamosa promoter
416	84.5	6.1	2871	2	A55567	fibrillin 1 - bovi	489	76	5.5	301	2	C84474	hypothetical prote
417	84	6.1	273	2	E85765	hypothetical prote	490	76	5.5	361	2	S30325	hypothetical prote
418	84	6.1	305	2	A44767	C2954.1 protein -	491	76	5.5	465	2	AF2949	ornithine decarbox
419	84	6.1	458	2	T36442	probable serine pr	492	76	5.5	512	2	E98333	probable ornithine
420	84	6.1	725	2	E96596	hypothetical prote	493	76	5.5	608	2	T05442	glycine-rich prote
421	83.5	6.1	133	2	T17300	hypothetical prote	494	76	5.5	677	2	S23296	collagen alpha 2(I
422	83.5	6.1	788	2	A37057	integrin beta-6 ch	495	76	5.5	920	2	B34493	collagen alpha 1(I
423	83.5	6.1	1433	2	A46053	bullous pemphigoid	496	76	5.5	986	1	OXURGA	speract receptor p
424	83	6.0	266	2	T21597	hypothetical prote	497	76	5.5	3396	1	A42551	genome polyprotein
425	83	6.0	273	2	H64915	Putative protease	498	75.5	5.5	396	2	S22909	interleukin-3 rece
426	82.5	6.0	522	2	T29767	hypothetical prote	499	75.5	5.5	481	2	A35628	loricrin - mouse
427	82.5	6.0	644	2	C75457	alpha-amylyase - De	500	75.5	5.5	596	2	T26950	hypothetical prote
428	82.5	6.0	4936	2	AH2515	hypothetical prote	501	75.5	5.5	621	2	T50024	amyloid precursor-
429	82	6.0	90	2	JE0210	proteinase (EC 3.4	502	75.5	5.5	653	2	A46362	collagen alpha 2(I
430	82	6.0	357	2	T21152	hypothetical prote	503	75.5	5.5	677	2	T37310	collagen alpha 2(I
431	82	6.0	418	2	A46076	staphylyolytic prot	504	75.5	5.5	688	2	A53330	hypothetical prote
432	82	6.0	418	2	F83411	LaaA proteinase pr	505	75.5	5.5	697	2	T18681	collagen alpha 1(X
433	81.5	5.9	244	2	JC4708	gelatin-binding 28	506	75.5	5.5	1142	2	JX0369	hypothetical prote
434	81.5	5.9	323	2	T27450	hypothetical prote	507	75	5.5	291	2	T20083	hypothetical prote
435	81.5	5.9	779	1	CG8018	collagen alpha 1(I	508	75	5.5	291	2	T26576	hypothetical prote
436	81.5	5.9	2229	2	T16199	hypothetical prote	509	75	5.5	310	2	I50696	collagen alpha 1(I
437	81	5.9	247	2	T26688	hypothetical prote	510	75	5.5	437	2	I50478	properdin - mouse
438	81	5.9	428	2	T24769	hypothetical prote	511	75	5.5	809	1	IJBODD	desmocollin 2b pre
439	80.5	5.9	283	2	T29837	hypothetical prote	512	75	5.5	863	1	IJBODC	desmocollin 2a pre
440	80.5	5.9	290	2	T46470	hypothetical prote	513	75	5.5	864	1	EART	elastin precursor
441	80.5	5.9	294	2	T23839	hypothetical prote	514	75	5.5	902	2	T26775	hypothetical prote
442	80.5	5.9	812	2	S31521	collagen ColFI - f	515	75	5.5	1140	2	AS0180	probable membrane
443	80.5	5.9	1464	1	CGH1S	collagen alpha 1(I	516	75	5.5	1236	1	VHWVWE	structural polypro
444	80.5	5.9	2871	2	A55624	fibrillin-1 precur	517	75	5.5	1514	2	T52080	multi resistance p
445	80	5.8	248	2	A48853	pulmonary surfacta	518	75	5.5	1752	2	A45407	collagen alpha 3(I
446	80	5.8	333	2	T23618	hypothetical prote	519	74.5	5.4	177	2	AB3269	outer membrane lip
447	79.5	5.8	550	2	E90723	probable fumarate	520	74.5	5.4	246	2	S30144	osmotin-like prote
448	79.5	5.8	550	2	E85574	probable fumarate	521	74.5	5.4	601	2	G70983	probable glycosyl
449	79	5.7	274	2	T20435	hypothetical prote	522	74.5	5.4	638	1	A31845	nitrous-oxide redu
450	79	5.7	295	2	T19220	hypothetical prote	523	74.5	5.4	791	2	T31885	probable iron-regu
451	79	5.7	333	2	T20436	hypothetical prote	524	74.5	5.4	832	2	A31246	neurogenic protein
452	79	5.7	782	2	A61625	tenascin-like prot	525	74.5	5.4	833	2	S19087	gene Delta protein
453	79	5.7	921	2	S40495	collagen alpha 1(I	526	74.5	5.4	880	2	S00670	neurogenic repetit
454	79	5.7	1758	2	T29350	hypothetical prote	527	74.5	5.4	931	2	S13580	collagen alpha 1(I
455	79	5.7	1759	2	T29351	collagen alpha 2(I	528	74.5	5.4	1496	1	CGH2V	collagen alpha 2(I
456	78.5	5.7	294	2	T22639	hypothetical prote	529	74.5	5.4	1690	1	CGH1B	collagen alpha 4(I
457	78.5	5.7	310	2	T22641	hypothetical prote	530	74.5	5.4	1763	2	S16366	collagen alpha 2(I
458	78.5	5.7	504	2	T34995	probable integral	531	74	5.4	246	2	S29328	complement subcomp
459	78.5	5.7	1315	2	A56101	collagen alpha 1(X	532	74	5.4	248	1	LNRTPS	pulmonary surfacta
460	78.5	5.7	1774	2	B56101	collagen alpha 1(X	533	74	5.4	273	2	AS0682	probable secreted
461	78.5	5.7	2215	2	S38480	nonstructural prot	534	74	5.4	302	2	A31921	collagen dpy-13 pr
462	78.5	5.7	2214	2	T16305	hypothetical prote	535	74	5.4	325	2	T18594	hypothetical prote
463	78.5	5.7	4135	2	A42629	tenascin-X - bovin	536	74	5.4	457	2	T04226	hypothetical prote
464	78.5	5.7	4545	1	S25111	alpha-2-macroglobu	537	74	5.4	470	2	D41977	retinoid receptor
465	78	5.7	300	2	T36768	secreted serine pr	538	74	5.4	513	2	S11439	cellulose 1,4-beta
466	78	5.7	359	2	E83312	hypothetical prote	539	74	5.4	566	2	S69887	hemagglutinin prec
467	78	5.7	394	2	T33641	hypothetical prote	540	74	5.4	614	2	T33149	hypothetical prote

541	74	5.4	886	2	I50694	collagen alpha 1(I	614	71.5	5.2	895	2	T49010	hypothetical prote
542	74	5.4	1124	1	I58388	protein-tyrosine k	615	71.5	5.2	918	2	JC4361	scavenger receptor
543	74	5.4	1413	2	T26467	hypothetical prote	616	71	5.2	181	2	S56532	hypothetical 20K p
544	74	5.4	1670	1	CGH03B	collagen alpha 3(I	617	71	5.2	316	2	S25264	virK protein - Shi
545	74	5.4	1677	2	T14267	Xin protein, stage	618	71	5.2	359	2	E70606	probable regulator
546	73.5	5.3	246	2	T16403	hypothetical prote	619	71	5.2	407	2	AI0595	imidazolonepropion
547	73.5	5.3	294	2	T29838	hypothetical prote	620	71	5.2	458	2	T31631	hypothetical prote
548	73.5	5.3	305	2	B84413	hypothetical prote	621	71	5.2	490	2	T37884	transcription fact
549	73.5	5.3	321	2	T28760	hypothetical prote	622	71	5.2	497	2	B42827	interleukin enhanc
550	73.5	5.3	346	2	JA0159	cysteine proteinas	623	71	5.2	575	2	AY7635	adenine deaminase
551	73.5	5.3	411	2	A65184	arylsulfatase acti	624	71	5.2	575	2	AC2858	adenine deaminase
552	73.5	5.3	482	2	AE0839	succinate-semialde	625	71	5.2	639	2	D70931	hypothetical glyci
553	73.5	5.3	483	2	D83613	succinate-semialde	626	71	5.2	818	2	B75606	hypothetical prote
554	73.5	5.3	525	1	S38794	cellulose 1,4-beta	627	71	5.2	883	2	TS1221	hypothetical prote
555	73.5	5.3	680	1	CGH01D	collagen alpha 1(X	628	71	5.2	1230	2	E64664	outer membrane pro
556	73.5	5.3	724	2	A48569	antigen Emi100 - E1	629	71	5.2	1391	2	T20406	hypothetical prote
557	73.5	5.3	791	2	D64629	iron-regulated out	630	71	5.2	1691	1	S22917	collagen alpha 5(I
558	73.5	5.3	1806	1	CGH01E	collagen alpha 1(X	631	71	5.2	1717	1	A45558	epidermal growth f
559	73	5.3	50	2	S55674	cerastocytin (EC 3	632	71	5.2	2164	1	GNNY89	genome polypeptid
560	73	5.3	295	2	T22833	hypothetical prote	633	71	5.2	2531	2	S18188	notch protein homo
561	73	5.3	360	2	T36763	probable secreted	634	71	5.2	2531	2	T16743	hypothetical prote
562	73	5.3	508	2	B70865	probable transmemb	635	71	5.2	3512	2	T17121	CPY protein - midg
563	73	5.3	597	2	S71352	metalloproteinase	636	70.5	5.1	238	2	S28001	osmotin-like prote
564	73	5.3	662	2	I38400	melanoma-associate	637	70.5	5.1	284	2	T29528	hypothetical prote
565	73	5.3	707	1	TSBYAB	tryptophan synthas	638	70.5	5.1	290	2	AE1176	fructokinases homo
566	73	5.3	728	2	S43768	transcription acti	639	70.5	5.1	325	2	T06784	probable GTP-bind
567	73	5.3	767	2	T05662	hypothetical prote	640	70.5	5.1	325	2	T09613	hypothetical prote
568	73	5.3	881	2	S25445	nitrate reductase	641	70.5	5.1	339	2	T22607	cysteine proteinas
569	73	5.3	997	2	A60776	230k bullous pemph	642	70.5	5.1	356	2	S66348	hypothetical prote
570	73	5.3	1339	2	JC4387	epidermal growth f	643	70.5	5.1	366	2	S11449	collagen short cha
571	73	5.3	1744	2	S40991	collagen alpha 1(I	644	70.5	5.1	396	1	TRYXB4	alpha-lytic protei
572	73	5.3	2207	1	GNNY5P	genome polypeptid	645	70.5	5.1	400	2	T35106	probable secreted
573	73	5.3	2555	2	A40043	notch protein homo	646	70.5	5.1	423	2	A41207	collagen 13, nonfi
574	73	5.3	3061	1	JN0545	genome polypeptid	647	70.5	5.1	585	2	T37526	probable transcrip
575	73	5.3	3623	2	T08618	intrinsic factor-B	648	70.5	5.1	627	2	T35608	polyketide hydroxy
576	72.5	5.3	135	1	TI2M1	trypsin/factor XII	649	70.5	5.1	630	2	T43460	hypothetical prote
577	72.5	5.3	230	2	D85553	probable chaperone	650	70.5	5.1	860	1	EAMS	elastin precursor
578	72.5	5.3	230	2	A90703	probable chaperone	651	70.5	5.1	920	2	A45748	collagen alpha 1(V
579	72.5	5.3	230	2	B64785	molecular chaperon	652	70.5	5.1	1342	2	A36223	kinase-related tra
580	72.5	5.3	286	2	C81681	dihydrodipicolinat	653	70.5	5.1	1414	1	S23809	collagen alpha 2(I
581	72.5	5.3	302	2	T32872	hypothetical prote	654	70.5	5.1	1486	1	B40333	collagen alpha 1(I
582	72.5	5.3	328	2	JC5350	2-nitrotoluene red	655	70.5	5.1	1747	2	A54121	collagen alpha-4 c
583	72.5	5.3	362	2	T35287	probable secreted	656	70.5	5.1	3198	2	A43426	collagen alpha 2 f
584	72.5	5.3	488	2	T47697	Regulator of chrom	657	70	5.1	261	2	S40210	chlorophyll a/b-bi
585	72.5	5.3	606	2	T08180	PF20 protein, micr	658	70	5.1	283	2	JS0170	collagen col-19 -
586	72.5	5.3	1132	2	T03844	telomerase catalyt	659	70	5.1	285	2	S60598	collagen alpha cha
587	72.5	5.3	1497	2	I49607	procollagen type V	660	70	5.1	300	2	T19929	hypothetical prote
588	72.5	5.3	1514	2	T34869	glutamate synthase	661	70	5.1	304	2	T26185	hypothetical prote
589	72	5.2	207	2	T46415	hypothetical prote	662	70	5.1	304	2	T26184	hypothetical prote
590	72	5.2	220	2	T18553	probable O-methylt	663	70	5.1	313	2	T26465	hypothetical prote
591	72	5.2	229	2	D95398	hypothetical prote	664	70	5.1	315	2	C95941	probable transcrip
592	72	5.2	258	2	A29259	Ubx protein - fru1	665	70	5.1	343	2	JQ2370	hemagglutinin - in
593	72	5.2	392	2	A56123	streptogrin D (E	666	70	5.1	389	2	I49263	potential oncogene
594	72	5.2	577	2	B37057	integrin beta-6 ch	667	70	5.1	389	2	AS9392	Wnt10b protein pre
595	72	5.2	673	2	F89101	protein F25E5.7 (i	668	70	5.1	395	1	T45547	arylsulfatase acti
596	72	5.2	691	2	T44543	probable bacteriop	669	70	5.1	402	2	H82228	imidazolonepropion
597	72	5.2	814	2	T49207	receptor kinase-1i	670	70	5.1	485	2	F97228	glu-TRNAGln amidot
598	72	5.2	957	2	T15976	hypothetical prote	671	70	5.1	548	2	H82432	sucrose-6-phosphat
599	72	5.2	1220	2	A56136	jagged protein pre	672	70	5.1	560	2	D84205	hypothetical prote
600	72	5.2	2150	1	GNNYH2	genome polypeptid	673	70	5.1	561	2	C75543	6-aminohexanoate-c
601	72	5.2	2194	1	GNNYE7	genome polypeptid	674	70	5.1	671	1	CGRT1S	collagen alpha 1(I
602	72	5.2	2205	1	GNNY2W	genome polypeptid	675	70	5.1	674	2	S23297	collagen alpha 1(X
603	71.5	5.2	58	2	A45526	collagen homolog A	676	70	5.1	798	2	T28906	hypothetical prote
604	71.5	5.2	236	2	T24799	hypothetical prote	677	70	5.1	863	2	A53034	gag polypeptid -
605	71.5	5.2	283	2	JC5579	chymotrypsin-like	678	70	5.1	877	2	S43197	envelope protein p
606	71.5	5.2	284	2	G70732	probable thiolisufa	679	70	5.1	938	2	C84480	hypothetical prote
607	71.5	5.2	297	2	T18638	hypothetical prote	680	70	5.1	1188	2	D86236	protein F14N23.5 l
608	71.5	5.2	305	2	T20906	hypothetical prote	681	70	5.1	1366	2	T35985	probable large pro
609	71.5	5.2	466	2	T19707	probable indoleace	682	70	5.1	2043	2	T18524	scavenger receptor
610	71.5	5.2	524	2	T04623	cruciferin F2009.2	683	70	5.1	2206	1	GNNY4P	genome polypeptid
611	71.5	5.2	547	2	T29717	hypothetical prote	684	70	5.1	2206	1	GNNY27	genome polypeptid
612	71.5	5.2	665	1	VCMVKA	env polypeptid pr	685	70	5.1	2206	2	S03822	genome polypeptid
613	71.5	5.2	793	2	AH2126	hypothetical prote	686	70	5.1	4391	2	A38096	perlecan precursor

687	69.5	5.1	126	2	S47010	Ig heavy chain V4.	760	68.5	5.0	337	2	H86582	CT 368 hypothetica
688	69.5	5.1	184	2	E82345	probable galactosy	761	68.5	5.0	357	2	H89819	conserved hypothet
689	69.5	5.1	244	1	LNMSMC	mannose-binding le	762	68.5	5.0	372	2	S60207	fomF protein - Str
690	69.5	5.1	248	1	LNDCPS	pulmonary surfacta	763	68.5	5.0	412	2	G86003	probable transport
691	69.5	5.1	250	2	S30157	osmotin precursor	764	68.5	5.0	412	2	A91158	protein transport
692	69.5	5.1	275	2	A84179	endonuclease IV (I	765	68.5	5.0	412	2	B65134	protein transport
693	69.5	5.1	303	2	T19289	hypothetical prote	766	68.5	5.0	427	2	S57776	MFS permease (impo
694	69.5	5.1	337	2	T23794	hypothetical prote	767	68.5	5.0	487	2	AF2692	hypothetical prote
695	69.5	5.1	353	2	S16785	hemagglutinin - in	768	68.5	5.0	528	2	B97474	spore coat protein
696	69.5	5.1	356	2	S18907	collagen alpha 1(I)	769	68.5	5.0	537	2	B33485	conserved hypothet
697	69.5	5.1	382	2	S20375	collagen alpha 3(V	770	68.5	5.0	544	2	G87330	collagen alpha cha
698	69.5	5.1	432	2	F96919	ABC transporter (p	771	68.5	5.0	547	2	A36046	4-alpha-D-((1->4)-
699	69.5	5.1	466	2	T06416	cysteine proteinas	772	68.5	5.0	575	2	JC7727	MPJ-K protein prec
700	69.5	5.1	482	2	S76475	hypothetical prote	773	68.5	5.0	579	2	B45266	nitrous-oxide redu
701	69.5	5.1	545	2	C82617	NH3-dependent NAD	774	68.5	5.0	634	1	S24384	MPJ-P protein prec
702	69.5	5.1	556	2	JC2005	integrin beta-5 ch	775	68.5	5.0	635	2	A45266	collagen alpha 1(I
703	69.5	5.1	739	2	C87559	phosphoribosylform	776	68.5	5.0	673	1	CGBO6C	collagen alpha 1(I
704	69.5	5.1	749	2	I38488	trophinin - huma	777	68.5	5.0	674	2	S13301	collagen alpha 1(I
705	69.5	5.1	1024	2	S18251	collagen alpha 1(I	778	68.5	5.0	677	2	F95910	probable membrane-
706	69.5	5.1	1181	2	C97851	DNA-directed DNA p	779	68.5	5.0	744	1	A34246	collagen alpha 1(V
707	69.5	5.1	1418	2	T45467	collagen alpha 1(I	780	68.5	5.0	744	1	S23298	collagen alpha 1(V
708	69.5	5.1	1464	2	S59856	collagen alpha 1(I	781	68.5	5.0	744	2	S15435	collagen alpha 1(I
709	69.5	5.1	1487	1	CGHU6C	collagen alpha 1(I	782	68.5	5.0	888	2	S28791	collagen alpha 1(I
710	69.5	5.1	1603	2	S23810	collagen alpha 1(I	783	68.5	5.0	915	2	T21772	hypothetical prote
711	69.5	5.1	1986	2	S28353	probable polyketid	784	68.5	5.0	927	2	T21772	hypothetical prote
712	69.5	5.1	2019	1	JQ1322	tenascin precursor	785	68.5	5.0	937	2	I53282	gene PACE4 protein
713	69.5	5.1	2201	1	A32160	tenascin-C - huma	786	68.5	5.0	1049	1	CGBO7S	collagen alpha 1(I
714	69	5.0	38	2	T01677	pseudo-kallikrein	787	68.5	5.0	1419	2	A41182	collagen alpha 1(I
715	69	5.0	224	2	LN6545	finger protein (Cl	788	68.5	5.0	1487	2	B41182	collagen alpha 1(I
716	69	5.0	239	1	S08554	mannose-binding le	789	68.5	5.0	2206	1	GNNY21	genome polyprotein
717	69	5.0	290	2	T24586	hypothetical prote	790	68.5	5.0	2403	2	A59386	sanko - human
718	69	5.0	290	2	T24590	hypothetical prote	791	68.5	5.0	2482	2	I48922	cation-independent
719	69	5.0	294	2	T21668	hypothetical prote	792	68.5	5.0	2483	1	A49617	insulin-like growt
720	69	5.0	297	1	PRSWAG	streptogrisin A (S	793	68.5	5.0	2560	1	I40457	peptide synthetase
721	69	5.0	327	2	S48839	guanine nucleotide	794	68.5	5.0	2715	2	T13049	eyelid - fruit fly
722	69	5.0	329	2	B83162	molybdopterin bios	795	68.5	5.0	3106	1	S53868	laminin alpha-2 ch
723	69	5.0	334	1	S74957	cytochrome c-type	796	68.5	5.0	4544	1	S02392	alpha-2-macroglobu
724	69	5.0	395	2	S41035	hypothetical prote	797	68.5	5.0	4660	2	T42737	gp330 protein prec
725	69	5.0	399	2	H84717	hypothetical prote	798	68	4.9	175	1	A60010	early E1A 20K prot
726	69	5.0	406	2	A47696	acetamidase - Myco	799	68	4.9	177	2	S37749	collagen alpha 2(I
727	69	5.0	435	2	T39719	beta transducin -	800	68	4.9	229	1	S54799	collagen alpha 2(I
728	69	5.0	438	2	T50991	hypothetical prote	801	68	4.9	237	2	A88640	nitrite hydratase
729	69	5.0	441	2	A45565	cysteine proteinas	802	68	4.9	248	1	LNHUMC	protein C34H4.4 (I
730	69	5.0	469	2	A24450	collagen alpha 2(V	803	68	4.9	272	2	H87075	mannose-binding le
731	69	5.0	523	2	B95922	hypothetical nucle	804	68	4.9	289	2	T27708	probable conserved
732	69	5.0	532	2	F70580	hypothetical glyci	805	68	4.9	297	2	T46864	hypothetical prote
733	69	5.0	567	1	C55516	hydrogenase (EC 1.	806	68	4.9	330	2	T26004	nicotinate-nucleot
734	69	5.0	567	2	G85958	probable large sub	807	68	4.9	343	1	HMIVTA	hypothetical prote
735	69	5.0	567	2	G91113	hydrogenase-2 larg	808	68	4.9	349	2	D72175	hemagglutinin HA1
736	69	5.0	613	2	T11464	NADH2 dehydrogenas	809	68	4.9	354	2	A35788	G2R protein - vari
737	69	5.0	635	2	A57131	collagen alpha 2(V	810	68	4.9	358	2	T26281	hemagglutinin - in
738	69	5.0	682	2	D84579	probable Tail-like	811	68	4.9	384	2	S46110	hypothetical prote
739	69	5.0	950	2	S27473	URRS1 protein - sm	812	68	4.9	387	2	B49175	hypothetical prote
740	69	5.0	1366	1	CGHU2S	collagen alpha 2(I	813	68	4.9	404	2	A54871	Notch A protein -
741	69	5.0	1669	1	CGHU4B	collagen alpha 1(I	814	68	4.9	412	2	JC6317	Gal beta-1, 3GalNA
742	69	5.0	1749	2	S75071	hypothetical prote	815	68	4.9	447	2	F82862	glutamate dehydrog
743	69	5.0	1786	1	MMHUB1	laminin beta-1 cha	816	68	4.9	453	2	S49168	conjugal transfer
744	69	5.0	2007	2	S09553	genome polyprotein	817	68	4.9	460	2	A39938	beta tubulin 1 - r
745	69	5.0	2209	1	GNNY2P	genome polyprotein	818	68	4.9	484	2	F98208	phosphotransferase
746	69	5.0	2450	2	T71625	protein-tyrosine-p	819	68	4.9	484	2	AC3078	succinate-semialde
747	69	5.0	4957	2	T03455	ALR protein - huma	820	68	4.9	490	2	B95316	succinate-semialde
748	69	5.0	5262	2	T03454	ALR protein - huma	821	68	4.9	543	2	A41285	interleukin enhanc
749	68.5	5.0	127	2	F82617	ferredoxin XF1964	822	68	4.9	566	1	HMIV	hemagglutinin prec
750	68.5	5.0	155	2	B32669	vasotocin 2 / neur	823	68	4.9	566	1	HMIV17	hemagglutinin prec
751	68.5	5.0	233	2	S31829	pathogenesis-relat	824	68	4.9	605	2	T15291	spingomyelin phos
752	68.5	5.0	250	2	S25114	osmotin-like relat	825	68	4.9	631	2	JC2345	xenin-like protein
753	68.5	5.0	252	2	A55047	collagen alpha 1(V	826	68	4.9	656	2	G85731	Rhs element associ
754	68.5	5.0	285	2	T18814	hypothetical prote	827	68	4.9	680	2	S31216	collagen alpha 1(I
755	68.5	5.0	290	2	A11533	fructokinases homo	828	68	4.9	724	2	T37858	probable peroxidas
756	68.5	5.0	323	2	T19142	hypothetical prote	829	68	4.9	726	2	T35865	probable cyclase -
757	68.5	5.0	329	2	T32783	hypothetical prote	830	68	4.9	743	1	S23779	collagen alpha 1(V
758	68.5	5.0	336	1	S76928	probable aryl alco	831	68	4.9	754	2	A55267	collagen alpha 5(I
759	68.5	5.0	337	2	A72042	conserved hypothet	832	68	4.9	756	2	S67433	hypothetical prote

979	66	4.8	238	1	LNRMTA	mannose-binding le	1052	65.5	4.8	1629	2	C84839	ferredoxin-depende
980	66	4.8	239	2	D82727	6-phosphogluconola	1053	65.5	4.8	2518	2	A12140	polyketide synthas
981	66	4.8	256	2	AE0997	probable biotin bi	1054	65.5	4.8	2823	2	F87908	protein T22A3.8 [i
982	66	4.8	306	2	T21938	hypothetical prote	1055	65.5	4.8	2823	2	T23064	hypothetical prote
983	66	4.8	307	2	T18846	hypothetical prote	1056	65.5	4.8	3102	2	T43291	laminin alpha chai
984	66	4.8	311	2	S48400	carrier protein FL	1057	65.5	4.8	3871	2	T22812	hypothetical prote
985	66	4.8	313	2	A35122	metalloproteinase	1058	65.5	4.8	4848	2	T30289	pristinamycin I sy
986	66	4.8	326	2	JQ1437	hemagglutinin - in	1059	65	4.7	111	2	B82830	hypothetical prote
987	66	4.8	336	2	S41643	syM protein - Rhi	1060	65	4.7	162	2	T49957	ribosomal protein
988	66	4.8	344	2	PQ0319	hemagglutinin - in	1061	65	4.7	181	2	T07661	maturating protein
989	66	4.8	348	2	T23288	hypothetical prote	1062	65	4.7	188	2	A54270	insulin-like growt
990	66	4.8	353	2	D96596	hypothetical prote	1063	65	4.7	229	1	S19713	insulin-like growt
991	66	4.8	355	1	S37460	glutamyl endopepti	1064	65	4.7	229	1	S19713	nitrile hydratase
992	66	4.8	435	2	T51343	hypothetical prote	1065	65	4.7	232	2	F70789	probable protease -
993	66	4.8	553	2	T52362	hypothetical prote	1066	65	4.7	249	2	F70925	hypothetical prote
994	66	4.8	614	2	T05741	hypothetical prote	1067	65	4.7	287	2	D70625	probable transposa
995	66	4.8	687	2	T02459	probable beta-amyl	1068	65	4.7	299	2	T20605	hypothetical prote
996	66	4.8	753	2	S35371	finger protein neu	1069	65	4.7	303	2	S45461	hypothetical prote
997	66	4.8	787	2	T05617	hypothetical prote	1070	65	4.7	311	2	F75366	hypothetical prote
998	66	4.8	854	2	A96574	protein F12M16.30	1071	65	4.7	313	2	H89865	hypothetical prote
999	66	4.8	864	2	T30441	probable capsid-as	1072	65	4.7	313	2	T22828	hypothetical prote
1000	66	4.8	1194	2	C59436	KIAA1391 protein [1073	65	4.7	342	2	A46396	ets-related protei
1001	66	4.8	1364	2	T03059	notch4 - mouse	1074	65	4.7	349	2	T43457	hypothetical prote
1002	66	4.8	2114	2	E96505	hypothetical prote	1075	65	4.7	356	2	T22827	hypothetical prote
1003	66	4.8	2193	2	S52919	polyprotein (IA, 1	1076	65	4.7	358	2	T36415	probable iron-side
1004	66	4.8	3442	2	E82589	hemagglutinin-like	1077	65	4.7	359	1	S28043	cinnamyl-alcohol d
1005	66	4.8	3455	2	B82519	hemagglutinin-like	1078	65	4.7	370	2	T22510	hypothetical prote
1006	66	4.8	3507	2	T34513	hypothetical prote	1079	65	4.7	406	2	S73592	glycine hydroxymet
1007	65.5	4.8	37	2	S03570	trypsin (EC 3.4.21	1080	65	4.7	416	2	H82968	sarcosine oxidase
1008	65.5	4.8	97	2	S26898	Ig heavy chain V r	1081	65	4.7	418	2	T34606	probable fumarylac
1009	65.5	4.8	97	2	JH0428	Ig gamma chain V r	1082	65	4.7	428	2	D83861	hypothetical prote
1010	65.5	4.8	114	2	T72667	cold agglutinin FS	1083	65	4.7	446	2	T10711	anthranilate N-ben
1011	65.5	4.8	117	2	T35913	hypothetical prote	1084	65	4.7	469	2	T36362	probable DNA repai
1012	65.5	4.8	140	2	S78052	Ig heavy chain pre	1085	65	4.7	476	2	T29054	probable transmemb
1013	65.5	4.8	147	2	A84546	50S ribosomal prot	1086	65	4.7	619	2	D86236	hypothetical prote
1014	65.5	4.8	202	2	T35703	hypothetical prote	1087	65	4.7	711	2	S05381	hypothetical prote
1015	65.5	4.8	228	2	T49891	glycine-rich prote	1088	65	4.7	715	2	S52675	probable membrane
1016	65.5	4.8	245	1	C1HU24	complement subcomp	1089	65	4.7	737	2	T02178	hypothetical prote
1017	65.5	4.8	286	2	F71524	dihydrodipicolinat	1090	65	4.7	759	2	T44142	DR1 protein (impor
1018	65.5	4.8	298	2	T27644	hypothetical prote	1091	65	4.7	783	2	T35389	probable serine-th
1019	65.5	4.8	304	2	JC5845	chitinase (EC 3.2.	1092	65	4.7	784	2	JQ0317	hypothetical 82K p
1020	65.5	4.8	311	2	E85867	hypothetical prote	1093	65	4.7	826	2	A60385	monocyte surface a
1021	65.5	4.8	311	2	D91023	hypothetical prote	1094	65	4.7	837	2	E70835	hypothetical glyci
1022	65.5	4.8	327	2	AQ3367	alcohol dehydrogen	1095	65	4.7	866	2	S57936	CotC protein precu
1023	65.5	4.8	350	2	S63248	hypothetical prote	1096	65	4.7	881	2	T49279	hypothetical prote
1024	65.5	4.8	360	2	T37285	collagen dpy-2 - C	1097	65	4.7	984	2	T00326	hypothetical prote
1025	65.5	4.8	363	2	T16831	hypothetical prote	1098	65	4.7	1112	2	S49432	replicase 126K - o
1026	65.5	4.8	371	2	B72461	hypothetical prote	1099	65	4.7	1196	1	DNBEKS	DNA-binding protei
1027	65.5	4.8	396	2	T29773	hypothetical prote	1100	65	4.7	1374	2	T16129	hypothetical prote
1028	65.5	4.8	397	2	S28274	collagen alpha 2(I	1101	65	4.7	1439	2	T02087	gag/pol polyprotei
1029	65.5	4.8	402	1	CG802S	collagen alpha 2(I	1102	65	4.7	1489	2	D70807	hypothetical glyci
1030	65.5	4.8	452	2	T30082	hypothetical prote	1103	65	4.7	1522	2	T00028	brain-specific ang
1031	65.5	4.8	467	1	WZBE61	gene 61 protein -	1104	65	4.7	1603	1	BVASA1	3-dehydroquinatase
1032	65.5	4.8	479	2	C90457	cytochrome b558/56	1105	65	4.7	1707	2	F33526	collagen alpha 2(I
1033	65.5	4.8	486	2	A27353	collagen alpha 1(I	1106	65	4.7	1901	2	F70806	hypothetical glyci
1034	65.5	4.8	576	2	S33327	catalase (EC 1.11.	1107	65	4.7	2083	2	T42721	CRP-ductin-alpha p
1035	65.5	4.8	615	2	A05269	collagen alpha 1(I	1108	65	4.7	2166	2	S11339	calcium channel pr
1036	65.5	4.8	691	2	A54741	erythrocyte membra	1109	65	4.7	2244	2	T08212	calcium channel al
1037	65.5	4.8	730	2	A36226	collagen alpha 1 c	1110	65	4.7	2294	2	T167630	RNA-directed RNA p
1038	65.5	4.8	741	2	G69514	hypothetical prote	1111	65	4.7	2466	2	S05054	protein-tyrosine-p
1039	65.5	4.8	775	2	A61228	collagen alpha 2(I	1112	65	4.7	2490	1	A54971	surface protein ty
1040	65.5	4.8	782	2	B83966	formate dehydrogen	1113	65	4.7	2509	2	G01880	protein-tyrosine-p
1041	65.5	4.8	877	2	T03098	p97 protein - Toxo	1114	65	4.7	2509	2	G01880	protein-tyrosine-p
1042	65.5	4.8	947	2	T23107	hypothetical prote	1115	65	4.7	2509	2	G01880	fatty-acid synthas
1043	65.5	4.8	966	1	P18VBB	RNA 1a protein - b	1116	65	4.7	2509	2	G01880	gamma-r-crystallin
1044	65.5	4.8	969	2	B87083	excinuclease ABC s	1117	64.5	4.7	159	2	I49618	collagen alpha 1(I
1045	65.5	4.8	1137	2	T02097	epidermal synthase	1118	64.5	4.7	171	2	A34493	lipocate biosynthes
1046	65.5	4.8	1210	1	GQHUE	epidermal growth f	1119	64.5	4.7	191	2	D90712	lipocate biosynthes
1047	65.5	4.8	1295	2	A32901	gip1 protein precu	1120	64.5	4.7	191	2	H85562	lipocate-protein li
1048	65.5	4.8	1353	1	JQ2168	E2 glycoprotein pr	1121	64.5	4.7	191	2	D64797	hypothetical prote
1049	65.5	4.8	1360	2	T33922	hypothetical prote	1122	64.5	4.7	210	2	T20973	protein W09G10.1 [
1050	65.5	4.8	1376	1	JQ1534	E2 glycoprotein pr	1123	64.5	4.7	222	2	A88102	minor tail protein
1051	65.5	4.8	1492	2	A40333	collagen alpha 1(I	1124	64.5	4.7	232	2	E90834	

1125	64.5	4.7	242	2	S60143	cellulase (EC 3.2.1)	1198	64	4.7	426	2	D88103	protein W10G11.6 [
1126	64.5	4.7	262	2	A54889	IgE-binding protei	1199	64	4.7	465	1	S47738	cytochrome-c perox
1127	64.5	4.7	266	2	T22706	hypothetical prote	1200	64	4.7	465	2	F91178	cytochrome-c perox
1128	64.5	4.7	277	1	Q0BEC2	HKRFX protein - hu	1201	64	4.7	465	2	G86024	hypothetical prote
1129	64.5	4.7	297	2	T27525	hypothetical prote	1202	64	4.7	487	2	T45923	hypothetical prote
1130	64.5	4.7	301	2	B31219	collagen 2 - Caeno	1203	64	4.7	502	2	S36526	L1 protein - human
1131	64.5	4.7	317	2	T29960	hypothetical prote	1204	64	4.7	504	2	S58745	mucin (clone pGM31
1132	64.5	4.7	318	2	S27977	cuticle collagen d	1205	64	4.7	516	2	S42093	cellulose 1,4-beta
1133	64.5	4.7	328	2	AD1916	hypothetical prote	1206	64	4.7	566	1	HMIVUR	hemagglutinin prec
1134	64.5	4.7	333	2	T15867	alcohol dehydrogen	1207	64	4.7	566	2	S69888	hemagglutinin prec
1135	64.5	4.7	354	2	B75400	phosphoribosylform	1208	64	4.7	595	2	F95379	probable adenine d
1136	64.5	4.7	356	2	T05119	leucoanthocyanidin	1209	64	4.7	563	1	S18572	tetracycline resis
1137	64.5	4.7	387	2	E95933	probable calcium-b	1210	64	4.7	669	2	A35103	cell surface recep
1138	64.5	4.7	398	2	B71284	probable periplasm	1211	64	4.7	697	2	T37946	tryptophan synthas
1139	64.5	4.7	411	2	B91220	probable arylsulfa	1212	64	4.7	717	2	T49238	hypothetical prote
1140	64.5	4.7	411	2	S86066	probable arylsulfa	1213	64	4.7	719	2	A87292	prinosomal protein
1141	64.5	4.7	411	2	S58105	Cu metalloregulato	1214	64	4.7	721	2	F70649	probable Acyl-CoA
1142	64.5	4.7	416	2	T41665	probable dipeptida	1215	64	4.7	728	2	I50719	C-Delta-1 - chicke
1143	64.5	4.7	445	2	D86620	phosphohikimate v	1216	64	4.7	753	2	AH0097	probable biotin su
1144	64.5	4.7	445	2	C72004	phosphohikimate v	1217	64	4.7	823	2	T21104	hypothetical prote
1145	64.5	4.7	460	1	Q0RT	hemopexin precurs	1218	64	4.7	843	2	T13334	probable tail-host
1146	64.5	4.7	529	2	S36578	L1 protein - human	1219	64	4.7	861	2	B49847	nitrate reductase
1147	64.5	4.7	532	2	AE1964	Dnak-type molecula	1220	64	4.7	895	2	AD0541	outer membrane fim
1148	64.5	4.7	547	1	A32244	60K cysteine-rich	1221	64	4.7	963	2	T19140	hypothetical prote
1149	64.5	4.7	553	2	D71515	60K cysteine-rich	1222	64	4.7	998	2	T35745	probable ATP-bindi
1150	64.5	4.7	562	2	A85524	choline dehydrogen	1223	64	4.7	1000	2	A83467	sarcosine oxidase
1151	64.5	4.7	562	2	E90673	choline dehydrogen	1224	64	4.7	1083	2	H86921	probable arabinosy
1152	64.5	4.7	570	2	S42708	proline transport	1225	64	4.7	1955	1	AGCH	agrin precursor -
1153	64.5	4.7	570	2	S04547	proline transport	1226	64	4.7	2042	2	T18399	variant-specific s
1154	64.5	4.7	597	2	JC7615	alpha-glucosidase	1227	64	4.7	2321	2	S78549	notch3 protein - h
1155	64.5	4.7	599	2	T25835	hypothetical prote	1228	64	4.7	3137	2	A37797	reelin precursor -
1156	64.5	4.7	618	2	S32436	collagen alpha 2(I	1229	64	4.7	3461	2	S58870	collagen alpha 3(V
1157	64.5	4.7	626	2	C72033	succinate dehydrog	1230	64	4.7	3635	2	T10053	laminin alpha 5 ch
1158	64.5	4.7	626	2	C86589	succinate dehydrog	1231	64	4.7	7463	2	T36248	CDA peptide synthe
1159	64.5	4.7	644	2	JC2346	kexin-like protein	1232	63.5	4.6	97	2	G34964	ig heavy chain V-I
1160	64.5	4.7	646	2	H95665	protein P2C12.10	1233	63.5	4.6	144	2	S24805	hypothetical prote
1161	64.5	4.7	653	1	S23667	cytochrome c-type	1234	63.5	4.6	152	2	T24064	hypothetical prote
1162	64.5	4.7	653	2	T02080	probable carbonate	1235	63.5	4.6	184	2	D83234	hypothetical prote
1163	64.5	4.7	666	2	F71310	probable periplasm	1236	63.5	4.6	191	2	I46412	keratin KAP5.4 - s
1164	64.5	4.7	678	2	B84856	hypothetical prote	1237	63.5	4.6	191	2	AF0580	lipote-protein li
1165	64.5	4.7	715	2	S70397	zona pellucida gly	1238	63.5	4.6	215	2	AD0455	thiamine-phosphate
1166	64.5	4.7	721	2	C84732	probable homeodoma	1239	63.5	4.6	220	2	S35789	US2 protein - bovi
1167	64.5	4.7	724	2	T71274	hypothetical prote	1240	63.5	4.6	232	1	TL8FLU	minor tail protein
1168	64.5	4.7	730	2	H86295	hypothetical prote	1241	63.5	4.6	234	2	T31753	hypothetical prote
1169	64.5	4.7	884	2	S61569	hypothetical prote	1242	63.5	4.6	253	1	CIHUQB	complement subcomp
1170	64.5	4.7	1374	1	GNVYEC	genome polyprotein	1243	63.5	4.6	256	2	T28853	hypothetical prote
1171	64.5	4.7	1376	1	VG1HJ2	E2 glycoprotein pr	1244	63.5	4.6	269	2	C83516	hypothetical prote
1172	64.5	4.7	1388	2	A53317	collagen alpha 1(X	1245	63.5	4.6	281	2	T32765	hypothetical prote
1173	64.5	4.7	1408	2	S16148	gene serrate prote	1246	63.5	4.6	281	2	C88638	protein F50F6.1 [i
1174	64.5	4.7	1487	2	T02850	hypothetical prote	1247	63.5	4.6	289	2	T34241	hypothetical prote
1175	64.5	4.7	1546	1	CGHU2E	collagen alpha 2(I	1248	63.5	4.6	289	2	T26812	hypothetical prote
1176	64.5	4.7	1712	1	CGHU2B	collagen alpha 2(I	1249	63.5	4.6	290	2	A32249	collagen - sea urc
1177	64.5	4.7	2139	2	A35672	crumbs protein - f	1250	63.5	4.6	291	2	T34494	hypothetical prote
1178	64.5	4.7	3623	2	T09456	intrinsic factor-B	1251	63.5	4.6	294	2	T23916	hypothetical prote
1179	64	4.7	104	2	JH0345	T-cell receptor al	1252	63.5	4.6	308	2	H90452	conserved hypotet
1180	64	4.7	118	1	A31429	hisactophilin [val	1253	63.5	4.6	311	2	B64998	hypothetical prote
1181	64	4.7	128	2	JQ1002	keratin, claw - ch	1254	63.5	4.6	316	2	T20497	hypothetical prote
1182	64	4.7	133	2	B38911	ig heavy chain v r	1255	63.5	4.6	320	2	C81029	3-oxoacyl-(acyl-ca
1183	64	4.7	218	2	T03287	osmotin protein ho	1256	63.5	4.6	320	2	T39110	probable gpase ac
1184	64	4.7	238	2	B75266	phosphoribosylform	1257	63.5	4.6	326	2	T02340	GTP-binding regula
1185	64	4.7	248	1	LNHUP6	pulmonary surfacta	1258	63.5	4.6	328	2	T16970	GTP-binding protei
1186	64	4.7	278	2	A43670	integral membrane	1259	63.5	4.6	335	2	A40038	MHC class I histoc
1187	64	4.7	304	2	T23801	hypothetical prote	1260	63.5	4.6	338	2	T49182	probable chloropla
1188	64	4.7	310	2	T29731	hypothetical prote	1261	63.5	4.6	357	2	H75541	probable oxidoredu
1189	64	4.7	333	2	T50630	hypothetical prote	1262	63.5	4.6	371	2	E88633	protein F56B3.1 [i
1190	64	4.7	346	2	T45069	8-hydroxy-guanine	1263	63.5	4.6	375	2	A95867	probable pyrroloqu
1191	64	4.7	394	1	VGBE17	glycoprotein D pre	1264	63.5	4.6	378	2	AB0894	conserved hypotet
1192	64	4.7	394	1	VGBED1	glycoprotein D - h	1265	63.5	4.6	381	2	T27806	hypothetical prote
1193	64	4.7	401	2	C89102	protein F25E5.10 [1266	63.5	4.6	388	2	T22553	hypothetical prote
1194	64	4.7	411	2	T16982	glutamate dehydrog	1267	63.5	4.6	404	2	T40553	Trp-Asp repeat pro
1195	64	4.7	411	2	T04342	glutamate dehydrog	1268	63.5	4.6	418	2	S31124	hypothetical prote
1196	64	4.7	411	2	T03294	glutamate dehydrog	1269	63.5	4.6	435	2	B87412	conserved hypotet
1197	64	4.7	426	2	AH2144	hypothetical prote	1270	63.5	4.6	445	2	C72695	probable amidase A

1271	63.5	4.6	481	2	A33712	metalloproteinase	1344	63	4.6	437	2	JC7138	alpha-amylase (EC
1272	63.5	4.6	498	2	B84789	probable protein w	1345	63	4.6	437	2	JT0946	alpha-amylase 3E -
1273	63.5	4.6	504	1	P1WL31	l1 protein - human	1346	63	4.6	438	2	D88206	protein nhr-21.a [
1274	63.5	4.6	538	2	S65764	chitinase (EC 3.2.	1347	63	4.6	453	2	A71891	glu-tRNA amidotran
1275	63.5	4.6	556	1	S10901	choline dehydrogen	1348	63	4.6	453	2	AE2955	glutamyl-tRNA amid
1276	63.5	4.6	642	2	A34734	transcription fact	1349	63	4.6	471	2	A39024	collagen alpha 3(I
1277	63.5	4.6	660	2	C90343	conserved hypotet	1350	63	4.6	475	2	AE0855	conserved hypotet
1278	63.5	4.6	680	2	T25832	hypothetical prote	1351	63	4.6	475	2	H91077	probable 4-hydroxy
1279	63.5	4.6	690	2	T08604	hypothetical prote	1352	63	4.6	475	2	T44997	probable 4-hydroxy
1280	63.5	4.6	700	2	T41401	spore outgrowth fa	1353	63	4.6	475	2	AE5923	probable 4-hydroxy
1281	63.5	4.6	724	2	D87530	isoquinoline l-oxi	1354	63	4.6	480	2	F70785	hypothetical prote
1282	63.5	4.6	728	2	S26427	70K structural pro	1355	63	4.6	487	2	T21384	hypothetical prote
1283	63.5	4.6	742	4	C34734	transcription fact	1356	63	4.6	513	1	EUTQ1	cellulose 1,4-beta
1284	63.5	4.6	768	2	A42755	p-selectin precurs	1357	63	4.6	513	2	S45380	cellulose 1,4-beta
1285	63.5	4.6	803	2	C83561	probable type II s	1358	63	4.6	543	2	H82282	viobactin-speci
1286	63.5	4.6	825	4	B34734	transcription fact	1359	63	4.6	545	2	T02079	probable carbonate
1287	63.5	4.6	872	2	A49538	CoC protein precu	1360	63	4.6	582	2	SI0099	transcription fact
1288	63.5	4.6	883	2	T07651	potassium channel	1361	63	4.6	611	2	T27013	hypothetical prote
1289	63.5	4.6	901	2	T04108	receptor kinase ho	1362	63	4.6	622	2	T27155	hypothetical prote
1290	63.5	4.6	907	2	T15792	hypothetical prote	1363	63	4.6	633	2	B40983	collagen alpha 1(X
1291	63.5	4.6	932	2	I52527	PACF4A - mouse (fr	1364	63	4.6	638	2	IS3169	cytokerin 2 - hu
1292	63.5	4.6	1042	2	T26644	hypothetical prote	1365	63	4.6	658	2	AB3253	glucose inhibited
1293	63.5	4.6	1345	2	S46817	hypothetical prote	1366	63	4.6	684	2	F83375	hypothetical prote
1294	63.5	4.6	1381	2	E70806	hypothetical glyci	1367	63	4.6	692	2	B59628	translation elonga
1295	63.5	4.6	1549	2	I49103	type VII collagen	1368	63	4.6	692	2	C83666	translation elonga
1296	63.5	4.6	1573	2	S01845	DNA (cytosine-5-)-	1369	63	4.6	692	2	T44380	translation elonga
1297	63.5	4.6	1649	2	C86822	hypothetical prote	1370	63	4.6	695	2	AB1406	translation elonga
1298	63.5	4.6	1693	2	S76086	beta transducin-li	1371	63	4.6	695	2	AB1782	translation elonga
1299	63.5	4.6	1959	1	AGRT	agrin - rat	1372	63	4.6	695	2	G87316	nuclease, probable
1300	63.5	4.6	2185	1	GNNYBT	genome polyprotein	1373	63	4.6	705	2	C84406	hypothetical prote
1301	63.5	4.6	2185	1	JQ2021	genome polyprotein	1374	63	4.6	760	2	A45174	eye cell developme
1302	63.5	4.6	2195	2	T34264	hypothetical prote	1375	63	4.6	946	2	T16297	hypothetical prote
1303	63.5	4.6	2352	2	T30201	Notch homolog prot	1376	63	4.6	1125	1	S57846	protein-tyrosine k
1304	63.5	4.6	2533	2	T28675	alpha-51D immobili	1377	63	4.6	1170	2	AS3612	launin Blk chain
1305	63.5	4.6	2533	2	T28675	alpha-51D immobili	1378	63	4.6	1203	2	A49175	MoCh B protein -
1306	63.5	4.6	3063	2	S55505	fatty-acid synthas	1379	63	4.6	1331	2	T83310	receptor-adenylate
1307	63.5	4.6	3429	2	T13853	hypothetical prote	1380	63	4.6	1345	2	S55669	tegument protein 7
1308	63	4.6	40	2	A49081	capillary permeabi	1381	63	4.6	1367	2	T33819	hypothetical prote
1309	63	4.6	99	2	S26801	Ig heavy chain v r	1382	63	4.6	1820	2	A55494	latent transformin
1310	63	4.6	119	2	B45937	early chorion prot	1383	63	4.6	2157	1	GNNY1B	genome polyprotein
1311	63	4.6	119	2	S24294	chorion protein -	1384	63	4.6	2437	2	S42612	transmembrane prot
1312	63	4.6	198	2	AB3153	hypothetical prote	1385	63	4.6	2647	2	A37098	gelation factor AB
1313	63	4.6	212	2	E86179	hypothetical prote	1386	63	4.6	3176	2	CGH3A	collagen alpha 3(V
1314	63	4.6	228	2	A44982	collagen UCOLI - p	1387	62.5	4.5	97	2	S14474	Ig heavy chain V r
1315	63	4.6	240	2	F70631	probable sodC prot	1388	62.5	4.5	118	2	S29653	textilotoxin chain
1316	63	4.6	242	1	F75433	probable phosphos	1389	62.5	4.5	144	2	S01391	phospholipase A2 (
1317	63	4.6	245	1	CIHQQC	complement subcomp	1390	62.5	4.5	155	2	C44012	insulin-like growt
1318	63	4.6	248	1	LNHUPS	pulmonary surfacta	1391	62.5	4.5	165	2	S72776	Bi496_F1_41 protei
1319	63	4.6	257	2	T28946	hypothetical prote	1392	62.5	4.5	181	2	A70627	hypothetical prote
1320	63	4.6	265	2	AG0814	cob(I) alamin adeno	1393	62.5	4.5	198	2	I49558	collagen alpha 1(I
1321	63	4.6	269	2	S31666	paired box transcr	1394	62.5	4.5	214	2	T18539	phosphoglycerate m
1322	63	4.6	285	2	T29982	hypothetical prote	1395	62.5	4.5	222	2	S19931	glycine-rich prote
1323	63	4.6	299	2	T24833	hypothetical prote	1396	62.5	4.5	231	2	B3746	Ig Fab region IV-J
1324	63	4.6	302	2	T15936	hypothetical prote	1397	62.5	4.5	247	2	S33197	osmotin-like prote
1325	63	4.6	303	2	E86591	CT580 hypothetical	1398	62.5	4.5	299	2	T29956	hypothetical prote
1326	63	4.6	303	2	D72031	neurosporene hydro	1399	62.5	4.5	306	2	H81036	riboflavin kinase/
1327	63	4.6	308	2	S32172	hypothetical prote	1400	62.5	4.5	313	2	T33010	hypothetical prote
1328	63	4.6	309	2	H69995	probable 3-oxoacyl	1401	62.5	4.5	316	2	T19288	hypothetical prote
1329	63	4.6	320	2	C81972	collagen col-14 -	1402	62.5	4.5	341	2	F70625	hypothetical prote
1330	63	4.6	326	2	JS0169	hypothetical prote	1403	62.5	4.5	352	2	JE0296	thyrotropin releas
1331	63	4.6	331	2	T28623	gene G4R protein -	1404	62.5	4.5	356	2	S61061	hypothetical prote
1332	63	4.6	349	2	C36858	glutamyl endopepti	1405	62.5	4.5	359	2	T22774	hypothetical prote
1333	63	4.6	357	1	S33321	surfactant protein	1406	62.5	4.5	391	2	F87258	acyl-CoA dehydroge
1334	63	4.6	369	2	S33603	hypothetical prote	1407	62.5	4.5	398	2	AG0128	1-deoxy-D-xylulose
1335	63	4.6	383	2	A83518	hypothetical prote	1408	62.5	4.5	398	2	T35255	probable racemase
1336	63	4.6	400	2	C75336	serine proteinase,	1409	62.5	4.5	402	2	S37789	hypothetical prote
1337	63	4.6	403	2	H98327	enantiomer-selecti	1410	62.5	4.5	411	2	S71217	glutamate dehydrog
1338	63	4.6	418	2	T15142	hypothetical prote	1411	62.5	4.5	427	2	S75210	glycine hydroxymet
1339	63	4.6	422	1	A56674	paired box transcr	1412	62.5	4.5	450	2	E70681	probable trpE - My
1340	63	4.6	424	2	C86247	hypothetical prote	1413	62.5	4.5	466	2	A87638	glutamate-1-semial
1341	63	4.6	428	2	T27544	zinc resistance pr	1414	62.5	4.5	473	2	AS6175	adhesive plaque pr
1342	63	4.6	434	2	D96760	hypothetical prote	1415	62.5	4.5	478	2	S31906	beta-1,3-glucanase
1343	63	4.6	436	1	S42234	paired box transcr	1416	62.5	4.5	482	2	S76376	hypothetical prote

1417 62.5 4.5 498 2 A72725 probable beta-lact
1418 62.5 4.5 532 2 T49824 hypothetical prote
1419 62.5 4.5 560 2 T16833 hypothetical prote
1420 62.5 4.5 567 2 A84287 hypothetical prote
1421 62.5 4.5 571 2 A60501 thrombomodulin pre
1422 62.5 4.5 589 2 T23299 hypothetical prote
1423 62.5 4.5 612 2 S53714 probable dinitrifi
1424 62.5 4.5 678 2 B48089 growth arrest-spec
1425 62.5 4.5 684 2 A53019 collagen alpha.1(X
1426 62.5 4.5 695 2 E71463 probable polyribon
1427 62.5 4.5 709 2 S33907 glycerol kinase (E
1428 62.5 4.5 722 2 I48324 DELTA-like 1 - mou
1429 62.5 4.5 731 2 JC7701 ARGA9 protein -
1430 62.5 4.5 784 2 A26601 elastin precursor
1431 62.5 4.5 799 2 A38308 integrin beta-5 ch
1432 62.5 4.5 810 2 C84845 probable salt-indu
1433 62.5 4.5 979 2 D96574 hypothetical prote
1434 62.5 4.5 1030 2 H98568 unknown protein, 2
1435 62.5 4.5 1039 2 A41131 lymphocyte-Peyer's
1436 62.5 4.5 1107 2 T15884 hypothetical prote
1437 62.5 4.5 1160 2 F88369 protein unc-52 (im
1438 62.5 4.5 1257 2 S28764 neurocan precursor
1439 62.5 4.5 1308 2 A47253 epidermal growth f
1440 62.5 4.5 1646 2 A48227 voltage-dependent
1441 62.5 4.5 2203 2 JH0422 voltage-dependent
1442 62.5 4.5 2295 2 C88369 protein unc-52 (im
1443 62.5 4.5 2491 1 A28372 insulin-like growt
1444 62.5 4.5 2591 2 T30288 pristinamycin I sy
1445 62.5 4.5 3375 2 T19821 hypothetical prote
1446 62.5 4.5 43 2 A61168 cocoonase (EC 3.4.
1447 62 4.5 98 2 S39410 nosr protein - Par
1448 62 4.5 99 2 S26807 Ig heavy chain V r
1449 62 4.5 99 2 S26800 Ig heavy chain V r
1450 62 4.5 137 2 B72679 hypothetical prote
1451 62 4.5 161 2 A46189 vasotocin - Pacifi
1452 62 4.5 208 2 E82670 general secretory
1453 62 4.5 215 2 C48150 hibernation-relate
1454 62 4.5 237 2 T16265 hypothetical prote
1455 62 4.5 240 2 S30406 hypothetical prote
1456 62 4.5 247 2 T35602 probable transpasa
1457 62 4.5 283 2 T19731 hypothetical prote
1458 62 4.5 283 2 T29980 hypothetical prote
1459 62 4.5 286 2 C87380 hypothetical prote
1460 62 4.5 298 2 AH0289 conserved hypothet
1461 62 4.5 299 2 A96665 probable aldo/keto
1462 62 4.5 299 2 S68198 protein F2C12.24
1463 62 4.5 302 2 T21257 probable transcrip
1464 62 4.5 308 2 T19846 hypothetical prote
1465 62 4.5 317 2 T19143 hypothetical prote
1466 62 4.5 327 2 T34203 hypothetical prote
1467 62 4.5 328 2 G64901 ABC-type transport
1468 62 4.5 330 2 S08500 QutG protein - Eme
1469 62 4.5 336 2 F81849 probable CDP-6-deo
1470 62 4.5 336 2 A35160 repressor protein
1471 62 4.5 336 2 T20348 hypothetical prote
1472 62 4.5 342 2 A46529 Ig gamma chain (5.
1473 62 4.5 387 2 AC1813 IMP dehydrogenase
1474 62 4.5 393 1 F8BEDZ glycoprotein D pre
1475 62 4.5 399 2 F82657 beta-ketoacyl-[ACP
1476 62 4.5 401 2 B64598 tetrahydroadipicoli
1477 62 4.5 401 2 E82951 probable MFS trans
1478 62 4.5 416 2 S48957 hypothetical prote
1479 62 4.5 426 2 H84349 peroxidase / catal
1480 62 4.5 446 2 D70597 probable signal pe
1481 62 4.5 456 2 C96684 F12P19.15 (impor
1482 62 4.5 462 2 T42565 capsid protein 22
1483 62 4.5 468 2 A69468 ammonium transport
1484 62 4.5 468 2 A12868 phosphomannomutase
1485 62 4.5 502 2 JE0295 Ll protein - human
1486 62 4.5 506 2 C97645 phosphomannomutase
1487 62 4.5 508 2 G84339 phosphoglycerate m

1490 62 4.5 552 2 C86171 hypothetical prote
1491 62 4.5 566 2 S69889 hemagglutinin prec
1492 62 4.5 567 2 AC0885 hydrogenase-2 larg
1493 62 4.5 589 2 B38128 epichelin/granulin
1494 62 4.5 591 2 B70523 hypothetical glyci
1495 62 4.5 592 2 JN0877 protein kinase C (I
1496 62 4.5 606 2 T51880 hypothetical prote
1497 62 4.5 628 2 AB0548 PrP^{Sc} protein (limpo
1498 62 4.5 651 2 JC7705 death receptor-6 -
1499 62 4.5 670 2 S22293 zinc finger protei
1500 62 4.5 693 2 E89822 translational elon

ALIGNMENTS

RESULT 1

I56559

neurospain - mouse

C:Species: Mus musculus (house mouse)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C:Accession: I56559

R:Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nishim

J. Neurosci. 15: 5088-5097, 1995

A:Title: Expression and activity-dependent changes of a novel limbic-serine protease gen

A:Reference number: I56559; MUID:95348817; PMID:7623137

A:Accession: I56559

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-260 <RES>

A:Cross-references: UNIPROT:Q61955; GB:D30785; NID:gl648847; PIDN:BAA06451.1; PID:gl0200;

C:Superfamily: trypsin; trypsin homology

F:33-252/Domain: trypsin homology <TRY>

Query Match 45.3%; Score 622.5; DB 2; Length 260;

Best Local Similarity 49.0%; Pred. No. 3.2e-43;

Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;

QY 5 IFLLLCV---LGLQAATPKIFNGTECGRNSPQWGLFEGTSLRCGGVLIDHRWLTAA 61

Db 13 ILLLLFMGAWAGLTRAQGSKILEGRECIPIHSPQWQAALFQGERLICGGVLVGDWRWLTAA 72

QY 62 HCSGRYWRVLRGEHSLQSLDWTETQIRHGSFVTHPGYLGAS-TSHEHDLRLRLRLPVRV 120

Db 73 HCKKQKYSVRLGDHSLQSRDQPEQIQVAQSIQHPCYNNSPEDSHDMLRLQNSANL 132

QY 121 TSSVQPLPLPNDCATAGTECHVSGNGITNHPNPDPDLLOCLNLSITVSHATGHVYVPEI 180

Db 133 GDKVPVQLANLCPKVGKCIISGWTGVTSPQENFNTLNCAEVKIYSQNKCEAYPGKI 192

QY 181 TSNMYCAGVPQDQACQDSDGSGPLVCGGLVQGLVSGSVGCGQDQIPGVYTYICKYVDW 240

Db 193 TEGMVCASSNGADTCQDSDGSGPLVCDGMLQITSWGSDPCGKPEKPGVYTKICRYTTW 251

QY 241 IRMIMVN 247

Db 252 IKKTMDN 258

RESULT 2

S55066

trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken

N:Alternate names: trypsinogen II

C:Species: Gallus gallus (chicken)

C>Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C:Accession: S55066; S72347

R:Wang, K.; Gan, L.; Lee, I.; Hood, L.

Biochem. J. 307, 471-479, 1995

A:Title: Isolation and characterization of the chicken trypsinogen gene family.

A:Reference number: S55065; MUID:95251611; PMID:7733985

A:Accession: S55066

A:Molecule type: mRNA

A:Residues: 1-248 <WAN1>

A;Cross-references: UNIPROT:Q90629; EMBL:U15157; NID:G603906; PIDN:AAA79914.1; PID:G603904
A;Experimental source: clone 2-P29
A;Accession: S72347
A;Molecule type: DNA
A;Residues: 1-248 <W>N>
A;Cross-references: EMBL:U15157; NID:G603906; PIDN:AAA79914.1; PID:G603907
A;Experimental source: clone 2-P29
A;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
F;17-25/Domain: activation peptide #status predicted <APT>
F;26-248/Product: trypsin II #status predicted <MAT>
F;26-241/Domain: trypsin homology <TRY>
F;65,109,202/Active site: His, Asp, Ser #status predicted

Query Match 41.4%; Score 569.5; DB 2; Length 248;
Best Local Similarity 47.5%; Pred. No. 68-39;
Matches 116; Conservative 39; Mismatches 78; Indels 11; Gaps 6;

QY 5 IFLLLCVLGLS-----QAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLT 59
Db 4 LFLILSLGAAVAFPGGADDDKIVGGYTCEHSVPYQVSLNSGYHF-CGGSLINSQWVL 62
QY 60 AAHCSSGRYWRVGLGHSLSQDWTQIRHSGFSVTHPGVYLGASTSHEHDLRLRLRLPVR 119
Db 63 AAHCYKSRIQVRLGEYNIDVQEDSEVRSSVIRHPKY--SSITLNNDIMLIKASAVE 120
QY 120 VTSSVQPLPNDCATAGTECHVSGWGIHTNPRNFPDILQCLNLSIVSHATCHGVY 179
Db 121 YSADIQPIALPSSCAKAGTECLISGNGTSLNGYNYPELLQCLNAPILSDQCEQAYPGD 180
QY 180 ITSNNMVCAGVP-GQDACQDGGPLVCGVGLQGLVSGWSVGPQGDGIPGVYTVICKV 238
Db 181 ITSNNMVCGLGGKDCQDGGPVCVNGELQGLVSWG-IG-CALKGYGPGVYTVCKNV 238
QY 239 DWIR 242
Db 239 DWIQ 242

RESULT 3
S55067
trypsin (EC 3.4.21.4) I precursor, pancreatic - chicken
N;Alternate names: trypsinogen I
C;Species: Gallus gallus (chicken)
C;Date: 28-Oct-1996 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
A;Accession: S55067; S72345; S55065; S72346; S71155
Biochem. J. 307, 471-479, 1995
R;Wang, K.; Gan, L.; Lee, I.; Hood, L.
A;Title: Isolation and characterization of the chicken trypsinogen gene family.
A;Reference number: S55065; MUID:95251611; PMID:7733885
A;Accession: S55067
A;Molecule type: mRNA
A;Residues: 1-248 <W>N>
A;Cross-references: UNIPROT:Q90627; UNIPROT:Q90628; EMBL:U15156; NID:G603904
A;Experimental source: clone 1-P38
A;Accession: S72345
A;Molecule type: DNA
A;Residues: 1-248 <W>N>
A;Experimental source: clone 1-P38
A;Accession: S55065
A;Molecule type: mRNA
A;Residues: 1-9, 'V', 11-12, 'T', 14-102, 'A', 104-214, 'I', 216-248 <W>N>
A;Cross-references: EMBL:U15155; NID:G603902; PIDN:AAA79912.1; PID:G603903
A;Experimental source: clone P1
A;Accession: S72346
A;Molecule type: DNA
A;Residues: 1-9, 'V', 11-12, 'T', 14-102, 'A', 104-214, 'I', 216-248 <W>N>
A;Cross-references: GB:U15155; NID:G603902; PIDN:AAA79912.1; PID:G603903
A;Experimental source: clone P1
R;Wang, K.
A;Reference number: S71155
submitted to the EMBL Data Library, September 1994

A;Accession: S71155
A;Molecule type: mRNA
A;Residues: 1-102, 'A', 104-248 <W>N>
A;Cross-references: EMBL:U15156; NID:G603904; PIDN:AAA79913.1; PID:G603905
A;Experimental source: clone 1-P38
A;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-25/Domain: activation peptide #status predicted <APT>
F;26-248/Product: trypsin I #status predicted <MAT>
F;26-241/Domain: trypsin homology <TRY>
F;65,109,202/Active site: His, Asp, Ser #status predicted

Query Match 41.3%; Score 567; DB 2; Length 248;
Best Local Similarity 45.5%; Pred. No. 9.6e-39;
Matches 115; Conservative 38; Mismatches 88; Indels 12; Gaps 6;

QY 3 LSIFLLLCVLG-----LSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRW 56
Db 1 MKFLVLVAFLGVAVAFPISEDDDDKIVGGYSCARSAAFPQVSLNSGYHF-CGGSLISSQW 59
QY 57 ULTAHCSSGRYWRVGLGHSLSQDWTQIRHSGFSVTHPGVYLGASTSHEHDLRLRLRL 116
Db 60 VLSSAAHCYKSRIQVRLGEYNLAADQDGEQTSSSKVIRHSGY--NSITLNNDIMLIKUSK 117
QY 117 PVRVTSSVQPLPNDCATAGTECHVSGWGIHTNPRNFPDILQCLNLSIVSHATCHGVY 176
Db 118 AATLSYNTVPLPFTSCVTTAGTCLISGNGTSLSGSLYPPDVLOCLNAPVLSSQCSAY 177
QY 177 PGRITSNMVCAGVP-GQDACQDGGPLVCGVGLQGLVSGWSVGPQGDGIPGVYTVICK 235
Db 178 PGRITSNMICIYGLNGKDCQDGGPVCVNGQLQGFVSWG-IG-CAQKGYGPGVYTVKVC 235
QY 236 KYDWMIRIMRN 248
Db 236 NYVSWIKTTMSN 248

RESULT 4
TRPGTR
trypsin (EC 3.4.21.4) precursor - pig (tentative sequence)
N;Contains: trypsinogen
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text_change 09-Jul-2004
A;Accession: A90641; A90368; A00947
R;Charles, M.; Rovey, M.; Guidoni, A.; Desmuelle, P.
Biochim. Biophys. Acta 69, 115-129, 1963
A;Title: Su le trypsinogene et la trypsine de porc.
A;Reference number: A90641
A;Accession: A90641
A;Molecule type: protein
A;Residues: 1-10 <CHA>
A;Cross-references: UNIPROT:P00761
R;Hermodson, M.A.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.
Biochemistry 12, 3146-3153, 1973
A;Title: Determination of the amino acid sequence of porcine trypsin by sequenator analysis
A;Reference number: A90368; MUID:73258692; PMID:4738933
A;Accession: A90368
A;Molecule type: protein
A;Residues: 9-231 <HER>
A;Note: at position 20, Ile and Val occur alternatively
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; polymorphism; protein digestion; serine proteinase; zymogen
F;1-231/Product: trypsinogen #status experimental <ZYM>
F;1-8/Domain: activation peptide #status experimental <APT>
F;9-231/Product: trypsin #status experimental <MAT>
F;9-224/Domain: trypsin homology <TRY>
F;15-145, 33-49, 117-218, 124-191, 156-170, 181-205/Disulfide bonds: #status predicted
F;48, 92, 185/Active site: His, Asp, Ser #status predicted
F;60, 62, 65, 70/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 40.8%; Score 561; DB 1; Length 231;
Best Local Similarity 46.7%; Pred. No. 2.7e-38;

Matches	107;	Conservative	39;	Mismatches	77;	Indels	6;	Gaps	4;
Qy	21	KIFNGTECGRNSQ	PQWQVGLFEGTSLRCGGVLIDHRWVLTAACHSGSRYYVRLGHSLS	SQL	80				
Db	8	KIVGGYTCAANS	IPQVSLNSGSHF-CGGS	SLNSQWVVAACHKYSRIQVRLGHNIDVL	66				
Qy	81	DWTEQIRHSGFSVTHPGYLGASTSHEHDRLRLRLPVRVTSSVQPLPLPNDCATAGTEC	140						
Db	67	EGNEQFINAAKII	THPNFNG--NTLDNDIMLIKLS	SPATLNSRVATVSLPRSCAAAGTEC	124				
Qy	141	HVSGWGIITHNPRNPFPDLLOCLNLSIVSHAT	CHGVYPGRIITSNMVCAGVB-GODACOGD	199					
Db	125	LISGWGNVTKSGSSYP	SLQCLKAPVLSDSCCKSYPGQITGNM	ICVGFLEGGKDSQCGD	184				
Qy	200	SGGPELVCGGVQLQGLVWSKGSVP	CGQDGIPIGVYTVICKYVDWIRMNRN	248					
Db	185	SGGPVVCNGLOIGTVISG	Y--GCAQKNKPGYTVKVCNVNMI	OOTIAAN	231				

RESULT 5

A35871

trypsin (EC 3.4.21.4) precursor, pancreatic - African clawed frog

C/Species: *Xenopus laevis* (African clawed frog)

C/Date: 09-Nov-1990 #sequence_revision 09-Sep-1990 #text_change 09-Jul-2004

C/Accession: A35871; S12117

R/Shi, Y.B.; Brown, D.D.

Genes Dev. 4, 1107-1113, 1990

A/Title: Developmental and thyroid hormone-dependent regulation of pancreatic genes in *Xenopus laevis*

A/Reference number: A35871; PMID:91007255; PMID:2210372

A/Accession: A35871

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-243 <SHI>

A/Cross-references: UNIPROT:P19799; EMBL:X53458; NID:g65162; PIDN:CAA37538.1; PID:g65163

C/Superfamily: trypsin; trypsin homology

C/Keywords: hydrolase; protein digestion; serine proteinase

F/1-15/Domain: signal sequence #status predicted <SIG>

F/16-20/Domain: activation peptide #status predicted <APT>

F/21-236/Domain: trypsin homology <TRY>

F/28-243/Product: trypsin I #status predicted <MAT>

F/27-157,45-61,129-230,136-203,168-182/Disulfide bonds: #status predicted

F/60,104,197/Active site: His, Asp, Ser #status predicted

[illegible]

RESULT 6
A53968
serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C:Species: Homo sapiens (man)

C; Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
 C; Accession: A53968
 R; Hanson, L.; Stromqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.
 J; Biol. Chem. 269, 19420-19426, 1994
 A; Title: Cloning, expression, and characterization of stratum corneum chymom
 A; Reference number: A53968; PMID:8034709
 A; Accession: A53968
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-253 <HAN>
 A; Cross-references: UNIPROT:P49862; GB:133404; NID:G521214; PIDN:AAC37551.1.1
 C; Genetics:
 A; Gene: GDB:PRSS6; SCCE
 A; Cross-references: GDB:377730
 A; Map position: 7q35-7q35
 C; Superfamily: trypsin; trypsin homology
 F; 30-245/Domain: trypsin homology <TRY>

Query Match	40.4%;	Score	555;	DB	2;	Length	253;
Best Local Similarity	44.6%;	Pred.	No. 9.2e-38;				
Matches	115;	Conservative	37;	Mismatches	90;	Indels	16;
Gaps	6						

Qy	1	MGLSIFLLLCVLGLS-----QAATPKIFNCTECGRNSQPWQVGLFEGTSLRCGGVL	1	52
Db	1	MARSLLLPLQILLSLALETAGHEAOGDKIIDGAPCARGSHPWQVALLSGNQLHCGGVLV	60	
Qy	53	DHRWLVTAAHCSGRYVVRIGHSLSQLDWTQEI RHSGFSVTHPGYLGASTSHSHDLRL	112	
Db	61	NERWLVTAAHCKWNEYVTVHLGSDTLG--DRRAQRIKAKSFRHEGY--STOTHVNDMLV	116	
Qy	113	RLRLPVRTSSVQPLPLPNDCATAGTECHVSGWGITNHRNPPFDLLQLCLNLSIVSHATC	172	
Db	117	KLNSQARLSMVKVRLPSRCEPPGTTCTVSGMGTTTSPDVTFFSDLMCDVDKVLISPDQC	176	
Qy	173	HGVYPRGRTSNMVCAGVPG--QDACGDSGGPLVCGGVTLGLVSWGSVGRCGQDGTPEV	230	
Db	177	TKVYKDLLENSLMCA-GIPDSKKNACNGDSGGPLVCRGTLQGLVSWGTF-PCGQPNPDGV	234	
Qy	231	YTYICKVVDWIRMNRN	248	
Db	235	YTVQCKFTKWINDTMKKH	252	

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RESULT 7
B25528
  trypsin (EC 3.4.21.4) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: B25528
R:Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
  Nucleic Acids Res. 14, 8307-8330, 1986
A:Title: Sequence organisation and transcriptional regulation of the mouse
A:Reference number: A93646; MUID:87066713; PMID:3641189
A:Accession: B25528
A:Molecule type: mRNA
A:Residue: 1-246 <STR>
A:Cross-references: UNIPROT:P07146; GB:X04574; NID:g54918; PIDN:CAR28243.1;
C:Superfamily: trypsin; trypsin homology
C:Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F:/1-23/Domain: signal sequence #status predicted <SIG>
F:/24-246/Product: trypsin #status predicted <MAT>
F:/24-239/Domain: trypsin homology <TRY>
F:/30-160, 48-64, 132-233, 139-206, 171-185/Disulfide bonds: #status predicted
F:/63, 107, 200/Active site: His, Asp, Ser #status predicted
F:/75, 77, 80, 85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
Query Match 40.2%; Score 553; DB 2; Length 246;

```

	Matches	113;	Conservative	45;	Mismatches	81;	Indels	14; Gaps
Qy	3	L S I F L L C V L G S Q A -----A T P K I N G T E C R N S O P W O U G L E F G T S L R C G G V L D H R W L	58					
Dd	1	M S A L I T A L V G A A V P P W D D D D K I V G G Y T C R E S S V P Y O S L N A G Y H F -C G S G L I N D Q W V	59					

	Qy	59	TAAHCGSGSYWYRLGHSLSQLDWTETQHGGFVSTHPGYLGASTSHEHDLLRRLRPV	118
	Dd	60	SAAHCYKRIQVRLGEHNINVLGNVEGFVDSSAKIRHPNY--NSWTILDNDIMIKLASPV	117
	Qy	119	RVTSSVOPLPDPNCATAGTECHUSGWG--ITNHPRNPPDLLLOCLNLISVSHTACHGVY	176
	Dd	118	TLNARVASVPLPSSCAPAGTQTLCISGNGNTLISNGWN--PDLLQCDVPALVLPQADCEASY	175
	Qy	177	PGRITSNNWCAGGP-VGDACOGDSGGGPLVC GGVLQGLVSMGSVPCQGIGIPVTTYIC	235
	Dd	176	PGETDNMIVCVFLGGDKSDCSQDSGGFPVNCBELGIVSWGY--GCAQPDAFGVTKVC	233
	Qy	236	KYYDWIWMIMRN	248
	Dd	234	NYYDWIONTIADN	246

RESULT 8

TRBOTR

trypsin (EC 3.4.21.4) precursor - bovine

N;Contains: trypsinogen

C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Apr-1984 #sequence revision 28-Feb-1986 #text_change 18-Jul-1997

C;Accession: A90164; A00946; S08774

R;Mikes, O.; Holeysovsky, V.; Tomasek, V.; Sorm, F.

Biochem. Biophys. Res. Commun. 24, 346-352, 1966

A;Title: Covalent structure of bovine trypsinogen. The position of the remaining amides.

A;Reference number: A90164; MUID:67168848; PMID:5967094

A;Accession: A90164

A;Molecule type: protein

A;Residues: 1-57, 'Q', 59-67, 'Q', 69-150, 'N', 152-176, 'N', 178-229 <MK>

R;Hartley, B.S.

Philos. Trans. R. Soc. Lond. B257, 77-87, 1970

A;Reference number: A93755

A;Contents: annotation; revisions

R;Titani, K.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.

Biochemistry 14, 1358-1366, 1975

A;Title: Amino acid sequence of dogfish trypsin.

A;Reference number: A00950; MUID:75146445; PMID:1092332

A;Contents: annotation; revisions

A;Note: the sequence agrees with that shown

R;Bode, W.; Schwager, P.

J. Mol. Biol. 98, 693-717, 1975

A;Title: The refined crystal structure of bovine beta-trypsin at 1.8 angstrom resolution

A;Reference number: A92954; MUID:76072097; PMID:512

A;Contents: annotation; X-ray crystallography; binding sites for calcium, substrate, and

C;Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.

C;Comment: Autocatalytic cleavage after Lys-6 leads to beta-trypsin by releasing a terminal

8 pseudotrypsin. A cleavage may also occur after Arg-105.

C;Superfamily: trypsin; trypsin homology

C;Keywords: hydrolyase; pancreas; protein digestion; serine proteinase; zymogen

F;1-229/Product: trypsinogen #status experimental <ZYM>

F;1-6/Domain: activation peptide #status experimental <APT>

F;7-222/Domain: trypsin homology <TRY>

F;7-131,132-229/Product: alpha-trypsin #status experimental <MPT>

F;6-7/Cleavage site: Lys-116 (enteropeptidase) #status experimental

F;13-143,31-47,115-216,122-189,152-168,179-203/Disulfide bonds: #status experimental

F;46,90,183/Active site: His, Asp, Ser #status experimental

F;58,60,63,68/Binding site: calcium (Glu, Asn, Val, Glu) #status experimental

F;131-132/Cleavage site: Lys-Ser (autolytic) #status experimental

[illegible]

Qy	141	HYVSGHGIITNHPNPPDLLQCLNLSIVSHATCHVGRITSNMVCAGGVP--QDACAQGD	199
Db	123	LSLGGNTKSGSTSPVDVLKLPKAPILSDSSKSAYPEQITSNMFCAGYLEGGKDSQGD	182
Qy	200	SGGPIVCGGVLQGLVSWGSGVPGCGDQIGPVYTVICFYDWMIRMRNN	248
Db	183	SGGPVVCCKLQIGIVSWG--GCAQKKNKPGYTVKVCNYSWIKQTASN	229

```

RESULT 9
S13813
trypsin (EC 3.4.21.4) - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C/Accession: S13813
R/ie Huorou, I.; Wicker, C.; Guilloreau, P.; Toullec, R.; Puigserver, A.
Eur. J. Biochem. 193, 767-773, 1990
A/Rittle: Isolation and nucleotide sequence of cDNA clone for bovine pancreatic
A/Reference number: S13813; NUID:91065383; PMID:1701147
A/Accession: S13813
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-247 <HUR>
A/Cross-references: UNIPROT:Q29463; ENBL:X54703; NID:g829; PIDN:CAA38513.1; PI
C/Superfamily: trypsin; trypsin homology
C/Keywords: hydrolase; protein digestion; serine proteinase
F/24-239/Domain: trypsin homology <TRY>
F/63,107,200/Active site: His, Asp, Ser #status predicted

```

Query Match	40.0%;	Score	550;	DB	2;	Length	247;	
Best Local Similarity	45.7%;	Pred. No.	2.3e-34;					
Matches 113;	Conservative	40;	Mismatches	83;	Indels	10;	Gaps	5
QY	7	LLLCVLGLSQA----	ATPKIENGTECGRNSQPWQVGLFECTSLRCGGVLIIDHRWVLTAAH	62				
DB	5	LILA FVGA AVFPSSDDDKI VGGVYTC AENSVPYQVSLNAGYHF--CGGSLINDQMWVYSAAH	63					
QY	63	CSGSRYWVRLGEHSLSQLDWTQI RHSGFSVTHPGYLGASTSHEHDLRLRLRLPVRVTS	122					
DB	64	CYQYHHQVRLGEYINLDVLEGGEQIFDASKIRHPKY--SSWTJDNLDLLIKLSTPAVINA	121					
QY	123	SVQPLFLPNDCATAGTECHVSGWGITNHRNPPFDLLQCLNLISIVSHATCHGVYPGRIITS	182					
DB	122	RVSTLTLLPSACASAGTECLISGWNGLTSSGVNYPDLLQCLVAPLLSHADCEASYPGQITN	181					
QY	183	NNVCAGGVP--GODACQGSGGPLVCGGVLOGLSVWSGVP CGGDGTPGVVYTYICKVVDWI	241					
DB	182	NNICAGFTEGGKDSQCGHSGGFPVACNGLOQLGIWSGY--CCAQKGRFPVYTKVCNVVDWI	239					
QY	242	RMIMRNN	248					
DB	240	OETIAAN	246					

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RESULT 10
TRDG
  trypsin (BC 3.4.21.4) precursor, anionic - dog
N;Alternate names: cationic trypsinogen
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: A26273
R;Pinsky, S.D.; LaForge, K.S.; Scheele, G.
  Mol. Cell. Biol. 5, 2669-2676, 1985
A;Title: Differential regulation of trypsinogen mRNA translation: full-length
A;Reference number: A26273; PMID:86284628; PMID:3841794
A;Accession: A26273
A;Molecule type: mRNA
A;Residues: 1-247 cPIN>
A;Cross-references: UNIPROT:P06872; GB:M11589; NID:g164094; PIDN:AAA30899.1; P
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>

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A>Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of
A:Reference number: A00948; MUID:82265624; PMID:6896710
A:Accession: A00948
A:Molecule type: mRNA
A:Residues: 1-246 <MAC>
A:Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
C:Genetics:
A:Introns: 14/1; 67/2; 152/1; 197/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-23/Domain: activation peptide #status predicted <APT>
F:24-246/Product: trypsin I #status predicted <ENZ>
F:24-239/Domain: trypsin homology <TRY>
F:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F:63,107,200/Active site: His, Asp, Ser #status predicted
F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
Query Match 39.5%; Score 543; DB 1; Length 246;
Best Local Similarity 44.5%; Pred. No. 8.4e-37;
Matches 110; Conservative 47; Mismatches 76; Indels 14; Gaps 7;
QY 3 LSIFILLCVLGSQA---ATPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRWL 58
DB 1 MSALLILALVGAAPFLEDDDDKIVGGYTCPEHSVPYQVSLNSGYHF-CGGLINDQWV 59
QY 59 TAAHCSGRYVRLGHEHLSQLDWTQIRHSGFVTHPGYLGASTSHEHDLRLRLRPV 118
DB 60 SAACHYKSRIOVRLGHEHNLVLEGEQFINAKIKHPNY--SSWTNLDNIMLKSPV 117
QY 119 RVTSSVQPLPNDCATAGTECHVSGWG--ITNHPNPPDLLQCLNLSIVSHATCHGVY 176
DB 118 KLNARVAPVALPSACAPAGTQCLISGWNLTSGVNN--PDLLQCVDPVLSQADCEAAY 175
QY 177 PGRITSNMVACGVP-GQDACGDSGGLVCGVQLGVLGWSGSGPCGQDGIPGVYTYIC 235
DB 176 PGEITSSMICVFLGEGKDCQDGGPVVCGQLGIVSWG--GCALPDNPGVYTKVC 233
QY 236 KYVDWIR 242
DB 234 NFVGHQ 240
RESULT 14
trypsin (EC 3.4.21.4) III precursor - Atlantic salmon (fragment)
C:Species: Salmo salar (Atlantic salmon)
C:Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: S66657; S31779
R:Male, R.; Lorens, J.B.; Smalas, A.O.; Torrisen, K.R.
A>Title: Molecular cloning and characterization of anionic and cationic variants of tryp
A:Reference number: S66657; MUID:96035908; PMID:7556223
A:Accession: S66657
A:Molecule type: mRNA
A:Residues: 1-238 <MAL>
A:Cross-references: UNIPROT:P35033; EMBL:X70074; NID:g64387; PIDN:CAA49679.1; PID:g64388
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:1-7/Domain: signal sequence (fragment) #status predicted <SIG>
F:8-15/Domain: activation peptide #status predicted <APT>
F:16-238/Product: trypsin III #status predicted <MAT>
F:16-231/Domain: trypsin homology <TRY>
F:22-152,40-56,124-225,131-198,163-177,188-212/Disulfide bonds: #status predicted
F:155,99,192/Active site: His, Asp, Ser #status predicted
Query Match 39.3%; Score 540; DB 2; Length 238;
Best Local Similarity 47.2%; Pred. No. 1.4e-36;
Matches 108; Conservative 37; Mismatches 78; Indels 6; Gaps 4;
QY 21 KIFNGTECGRNSQPVQVGLFEGTSLRCGGVLIDHRWLTAHCSGRYVRLGHEHLSQL 80
DB 15 KIVGGECKRNSASYQASLQSGYHF-CGGLISSTWVWSAAHCYKSRIOVRLGHEHNAVN 73

QY 81 DWTEQIRHSGFVTHPGYLGASTSHEHDLRLRLRPVVTSSVQPLPNDCATAGTEC 140
DB 74 EGTEQFIDSVKVIHPSY--NSRNLNDNIMLKSPASLNSVSTVALPSSCASSGTRC 131
QY 141 HVSGHGITHNPNPPDLLQCLNLSIVSHATCHGVYPCGRITSNMVCAGVP-GQDACG 199
DB 132 LVSGWNLSSGSSNYPDTLRLDLPLSSSCNSNAYPGQITSNMFCAGFMGGKDCQD 191
QY 200 SGGPLVCGVQLGVLGWSGSGPCGQDGIPGVYTYICKYVDWIRIMRN 248
DB 192 SGGPVVCGQLGQVSWG--GCAQRNKPVGYYTKVCTRSMISSTMSN 238
RESULT 15
S05494
trypsin (EC 3.4.21.4) IV precursor - rat
N:Alternate names: 23K protein; trypsinogen IV precursor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: S05494
R:Luetteke, H.; Rausch, U.; Vasiloudes, P.; Scheele, G.A.; Kern, H.F.
A>Title: A fourth trypsinogen (P23) in the rat pancreas induced by CCK.
Nucleic Acids Res. 17, 6736, 1989
A:Reference number: S05494; MUID:89386010; PMID:2780302
A:Accession: S05494
A:Molecule type: mRNA
A:Residues: 1-247 <LUB>
A:Cross-references: UNIPROT:P12788; EMBL:X15679; NID:g56813; PIDN:CAA33718.1; PID:g56814
C:Superfamily: trypsin; trypsin homology
C:Keywords: calcium binding; hydrolase; protein digestion; serine proteinase; zymogen
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-23/Domain: activation peptide #status predicted <APT>
F:24-247/Product: trypsin IV #status predicted <MAT>
F:24-240/Domain: trypsin homology <TRY>
F:30-161,49-65,133-233,140-207,172-186/Disulfide bonds: #status predicted
F:64,108,201/Active site: His, Asp, Ser #status predicted
F:76,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
Query Match 38.8%; Score 533.5; DB 2; Length 247;
Best Local Similarity 43.4%; Pred. No. 4.9e-36;
Matches 109; Conservative 41; Mismatches 94; Indels 7; Gaps 4;
QY 1 MGLSIF--LLLCVLGLSQAATPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRWL 58
DB 1 MKISIFFAPLGAVALPVNDDDKIVGGYTCPKHLPYQVSLHDGISHQCGSLISDQWVL 60
QY 59 TAAHCSGRYVRLGHEHLSQLDWTQIRHSGFVTHPGYLGASTSHEHDLRLRLPV 118
DB 61 SAACHYKSRKLOVRLGHEHNLVLEGEQFIDAEKIRHPEY--NKDTLNDNIMLKSP 118
QY 119 RVTSSVQPLPNDCATAGTECHVSGWGITHNHPNPPDLLQCLNLSIVSHATCHGVY 178
DB 119 VNSQVSTVSLPRSCASTDAQCLVSGWNTVSGYKYPALLOCLEAPVLSSCKKSPG 178
QY 179 RITSNMVACGVP-GQDACGDSGGLVCGVQLGVLGWSGSGPCGQDGIPGVYTYICKY 237
DB 179 QITSNMFCGLFLEGKDCQDGGPVVCGNBIQGVSWG--CAMRKPVGYYTKVCNY 236
QY 238 VDWIRIMRN 248
DB 237 LSWIOETMANN 247
Search completed: March 5, 2005, 20:46:44
Job time : 56 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 5, 2005, 20:42:30 ; Search time 174 Seconds
(without alignments)
729.860 Million cell updates/sec

Title: US-10-015-385A-194

Perfect score: 1374

Sequence: 1 MGLSIFLLCVLGLSQAATP.....GVYTYCKVDWIRMNRN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	1374	100.0	248	1	KLKC_HUMAN	Q9ukr0	homo sapien
2	952.5	69.3	234	2	Q9CV76	Q9cv76	mus musculus
3	630.5	45.9	260	1	KLK8_HUMAN	Q60259	homo sapien
4	627.5	45.7	260	2	Q81W69	Q81w69	homo sapien
5	622.5	45.3	260	1	NRPN_MOUSE	Q61955	mus musculus
6	621.5	45.2	260	1	NRPN_RAT	Q88780	rattus norv
7	618.5	45.0	250	1	KLKB_HUMAN	Q9ubx7	homo sapien
8	611	44.5	255	2	Q7JIG6	Q7jig6	saguinus oe
9	610	44.4	250	2	Q63ZF2	Q63zf2	rattus norv
10	608	44.3	254	2	Q8CGR4	Q8cgr4	mus musculus
11	601	43.7	275	2	Q81XD7	Q81xd7	homo sapien
12	599	43.6	255	2	Q6IS10	Q6isi0	homo sapien
13	599	43.6	256	1	KLKP_HUMAN	Q9h2r5	homo sapien
14	597.5	43.5	249	2	Q9QYN4	Q9qyn4	mus musculus
15	597.5	43.5	276	2	Q9QYN3	Q9qyn3	m hippostas
16	595	43.3	255	2	Q96RQ0	Q96rq0	homo sapien
17	588.5	42.8	293	2	Q9D140	Q9di40	mus musculus
18	588	42.8	276	2	Q8CGR6	Q8cgr6	mus musculus
19	586	42.6	250	2	Q8CGR5	Q8cgr5	mus musculus
20	578	42.1	242	2	Q8OV54	Q8ovs4	mus musculus
21	576	41.9	246	2	Q6P3Z0	Q6p3z0	mus musculus
22	569.5	41.4	248	1	TRV3_CHICK	Q90629	gallus gall
23	569.5	41.4	251	1	KLKE_HUMAN	Q9p0g3	homo sapien
24	569.5	41.4	251	2	Q6B089	Q6b089	homo sapien
25	568.5	41.4	250	1	KLK9_HUMAN	Q9ukq9	homo sapien
26	567	41.3	277	1	KLXD_HUMAN	Q9ukr3	homo sapien
27	566	41.2	248	1	TRV2_CHICK	Q90628	gallus gall
28	565	41.1	248	1	TRV1_CHICK	Q90627	gallus gall
29	564.5	41.1	293	1	KLK5_HUMAN	Q9Y337	homo sapien
30	564	41.0	276	1	KLKA_HUMAN	Q43240	homo sapien
31	563	41.0	244	1	TRV2_XENLA	P70059	xenopus lae

32	563	41.0	248	2	Q7SZT1	Q7szt1	xenopus lae
33	562	40.9	255	2	Q6GNU2	Q6gnu2	xenopus lae
34	561	40.8	231	1	TRYP_PIG	P00761	sus scrofa
35	561	40.8	243	1	KLK6_HUMAN	P00760	bos taurus
36	561	40.8	244	1	TRY1_BOVIN	Q92876	homo sapien
37	557	40.5	237	2	Q6GYJ5	Q6gyj5	struthio ca
38	555	40.4	243	1	TRY1_XENLA	P19799	xenopus lae
39	555	40.4	243	2	Q7SZ06	Q7sz06	xenopus lae
40	555	40.4	253	1	KLK7_HUMAN	P49862	homo sapien
41	553.5	40.3	246	2	Q88301	O88301	mus musculus
42	553.5	40.3	253	2	Q91Y82	Q91y82	mus musculus
43	553	40.2	246	1	TRY2_MOUSE	P07146	mus musculus
44	550.5	40.1	247	2	Q9D7V7	Q9d7v7	mus musculus
45	550	40.0	247	1	TRY2_BOVIN	Q29463	bos taurus
46	549.5	40.0	247	2	Q9CPN9	Q9cpn9	m mus muscu
47	548	39.9	246	2	Q6IE66	Q6ie66	rattus norv
48	546.5	39.8	251	2	O54854	O54854	rattus norv
49	546	39.7	247	1	TRY2_CANFA	P06872	canis fami
50	545	39.7	246	1	TRY1_CANFA	P06871	canis fami
51	544.5	39.6	247	1	TRY3_RAT	P08426	rattus norv
52	544	39.6	253	2	Q8N5N9	Q8n5n9	homo sapien
53	543	39.5	246	1	TRY1_RAT	P00762	rattus norv
54	543	39.5	246	2	Q792Z1	Q792z1	mus musculus
55	541.5	39.4	247	2	Q9CPN7	Q9cpn7	mus musculus
56	540	39.3	238	1	TRY3_SALSA	P35033	salmo salar
57	540	39.3	246	2	Q792Y8	Q792y8	mus musculus
58	538.5	39.2	249	2	Q91VE3	Q91ve3	m thymopsin
59	536	39.0	246	2	Q7TT42	Q7tt42	mus musculus
60	536	39.0	246	2	Q9ROT7	Q9rot7	m pancreati
61	535.5	39.0	245	2	Q6R670	Q6r670	oreochromis
62	535.5	39.0	261	2	Q6H320	Q6h320	bos taurus
63	534.5	38.9	245	2	Q6R671	Q6r671	oreochromis
64	533.5	38.8	245	2	Q792Y9	Q792y9	mus musculus
65	533.5	38.8	247	1	TRY4_RAT	P12788	rattus norv
66	533	38.8	246	1	TRY2_RAT	P00763	rattus norv
67	533	38.8	246	2	Q9Z1R9	Q9z1r9	mus musculus
68	532	38.7	246	2	Q9QUR9	Q9qur9	mus musculus
69	528	38.4	246	2	Q792Z0	Q792z0	mus musculus
70	528	38.4	263	2	Q6H319	Q6h319	sus scrofa
71	527.5	38.4	261	1	KLK7_RAT	P36373	rattus norv
72	525	38.2	240	2	Q98TH0	Q98th0	engraulis j
73	523.5	38.1	246	2	Q7M754	Q7m754	mus musculus
74	522	38.0	244	2	Q8QGW3	Q8qgw3	anguilla ja
75	521.5	38.0	246	1	KLK_PIG	P00752	sus scrofa
76	521.5	38.0	261	1	KLK6_MOUSE	P15947	mus musculus
77	520.5	37.9	258	2	Q63ZF4	Q63zf4	rattus norv
78	519	37.8	246	1	TRYA_RAT	P32821	rattus norv
79	518	37.7	246	1	TRYB_RAT	P32822	rattus norv
80	518	37.7	261	1	KLK8_RAT	P36374	rattus norv
81	514.5	37.4	242	2	Q7TIR8	Q7tir8	pangasius h
82	514	37.4	239	2	Q63275	Q63275	rattus norv
83	513.5	37.4	231	1	TRY2_SALSA	P35032	salmo salar
84	513.5	37.4	239	1	KLK2_CAVPO	P12323	cavia porce
85	513.5	37.4	243	2	Q8AV83	Q8av83	brachydanio
86	513.5	37.4	261	2	Q9NIQ1	Q9niq1	saguinus oe
87	513.5	37.4	278	2	Q9NM20	Q9nm20	mus musculus
88	512	37.3	279	2	Q6IE55	Q6ie55	rattus norv
89	511.5	37.2	261	2	Q29474	Q29474	canis fami
90	510.5	37.2	238	2	Q9W7Q6	Q9w7q6	paralichthy
91	510.5	37.2	261	1	KLK3_MOUSE	P00756	mus musculus
92	509.5	37.1	222	2	Q8AV11	Q8av11	oncorhynch
93	509.5	37.1	235	2	Q63274	Q63274	rattus norv
94	508	37.0	242	1	TRY1_SALSA	P35031	salmo salar
95	508	37.0	242	2	Q9W7Q7	Q9w7q7	paralichthy
96	507	36.9	244	2	O42159	Q42159	petromyzon
97	507	36.9	259	2	Q632F5	Q632f5	rattus norv
98	506	36.8	245	2	O42160	Q42160	petromyzon
99	505	36.8	242	2	Q7SX90	Q7sx90	brachydanio
100	505	36.8	249	2	Q92046	Q92046	diesostichu
101	505	36.8	260	1	ESTA_CANFA	P09582	canis fami
102	505	36.8	282	2	Q76B45	Q76b45	blarina bre
103	504.5	36.7	269	2	Q8IU55	Q8iu55	homo sapien
104	503	36.6	241	2	Q98TG9	Q98tg9	engraulis j

105	503	36.6	263	1	KLKR_PRANA	P32824 praomys nat	178	458.5	33.4	261	1	KLK2_HUMAN	P20151 homo sapien
106	502	36.5	249	2	Q9W6K0	Q9W6K0 nototenia	179	452	32.9	260	2	Q71QJ4	Q71QJ4 trimeresuru
107	501	36.5	259	1	KLK2_RAT	P6376 ratiss norv	180	451	32.8	260	2	Q7T229	Q7T229 bothrops ja
108	501.5	36.5	237	2	Q915I5	Q91515 fugu rubrip	181	450	32.8	260	2	Q8UVX1	Q8UVX1 agkistrodon
109	501	36.5	242	2	Q93266	Q93266 pseudopleur	182	449	32.7	258	1	VSP1_TRIST	Q91516 trimeresuru
110	501	36.5	247	1	TR12_HUMAN	P07478 homo sapien	183	448	32.6	258	2	Q8AY78	Q8AY78 trimeresuru
111	501	36.5	247	2	Q9W7Q5	Q9W7Q5 paralichthy	184	446.5	32.5	257	2	Q71QI5	Q71QI5 trimeresuru
112	499.5	36.4	241	1	TRXK_GADMO	Q91041 gadus morhu	185	445.5	32.4	257	1	VSP3_TRIMU	Q91509 trimeresuru
113	499	36.3	239	2	Q8N1C9	Q8N1C9 homo sapien	186	444.5	32.4	249	2	Q8JFQ7	Q8JFQ7 gadus morhu
114	498	36.2	249	2	Q788V0	Q788V0 disostichu	187	443	32.4	258	1	VSP2_AKAC	Q818x1 agkistrodon
115	498	36.2	254	1	KLK4_HUMAN	Q9Y5K2 homo sapien	188	443	32.2	258	1	VSP3_BOTJA	Q9PTU8 bothrops ja
116	497	36.2	257	2	Q61E61	Q61E61 rattus norv	189	439.5	32.0	257	1	VSP7_TRIMU	Q9Q584 trimeresuru
117	497	36.2	258	1	KLK1_PAPHA	Q28773 papio hamad	190	439	32.0	279	2	VSP7_GJ8	Q9Y9J8 agkistrodon
118	497	36.2	261	1	Q725F4	P725F4 homo sapien	191	438	31.9	259	1	VSP1_VIPLE	Q9PT41 vipera lebe
119	496.5	36.1	261	1	KLK5_MOUSE	P15945 mus musculu	192	437.5	31.8	257	1	VSP2_TRIMU	Q91508 trimeresuru
120	496	36.1	242	2	Q92059	Q92059 paranotothe	193	437.5	31.8	257	1	VSP4_TRIMU	Q91510 trimeresuru
121	496	36.1	247	2	Q42158	Q42158 petromyzon	194	436.5	31.8	233	2	Q9PT51	Q9PT51 agkistrodon
122	496	36.1	247	2	Q42608	Q42608 petromyzon	195	436.5	31.8	250	2	Q93955	Q93955 praomys nat
123	496	36.1	262	2	Q86U61	Q86U61 homo sapien	196	436.5	31.8	257	1	VSP1_TRIMU	Q91507 trimeresuru
124	495.5	36.1	257	1	KLK1_MACFA	Q07276 macaca fasc	197	436.5	31.8	257	1	VSP5_TRIMU	Q91511 trimeresuru
125	495.5	36.1	261	1	KLXB_MOUSE	P15946 mus musculu	198	435.5	31.7	257	2	Q71QI7	Q71QI7 trimeresuru
126	495	36.0	261	2	Q725F3	Q725F3 homo sapien	199	435	31.7	258	1	VSP2_TRIBE	Q94F67 trimeresuru
127	495	36.0	261	2	Q6H322	Q6H322 equus cabal	200	434	31.6	258	1	VSP3_TRIBE	Q94F66 trimeresuru
128	494.5	36.0	247	1	TRV1_HUMAN	P07477 homo sapien	201	434	31.6	260	1	VSPB_TRIGA	Q13061 trimeresuru
129	493.5	35.9	248	2	Q66L05	Q66L05 xenopus lae	202	434	31.6	260	2	Q71QI9	Q71QI9 trimeresuru
130	493	35.9	262	1	KLK1_HUMAN	P06870 homo sapien	203	433.5	31.6	257	2	Q71QJ0	Q71QJ0 trimeresuru
131	492	35.8	262	2	Q66U59	Q66U59 homo sapien	204	433	31.5	260	1	VSP1_AKHP	Q9Y9J2 agkistrodon
132	491.5	35.8	241	1	TRV1_GADMO	P16049 gadus morhu	205	432	31.4	236	1	VSPA_DABRU	P18964 daboia russ
133	491	35.7	256	1	KLK4_MOUSE	P00757 mus musculu	206	432	31.4	257	2	Q9PTL3	Q9PTL3 agkistrodon
134	490.5	35.7	229	1	TRYP_SOUAC	P00764 squalus aca	207	432	31.4	260	1	VSP2_AKHP	Q9Y9I6 agkistrodon
135	490.5	35.7	261	1	KLK2_MOUSE	P36368 mus musculu	208	432	31.4	260	2	Q73800	Q73800 agkistrodon
136	489.5	35.6	261	1	KLK1_MOUSE	P61759 mus musculu	209	431.5	31.4	205	2	Q96JEO	Q96JEO homo sapien
137	489	35.6	244	1	KLK1_RAT	P63375 rattus norv	210	431.5	31.4	257	2	Q71QJ1	Q71QJ1 trimeresuru
138	488	35.5	247	2	Q8NHM4	Q8NHM4 homo sapien	211	431.5	31.4	261	1	KLK2_HORSE	Q6H321 equus cabal
139	487.5	35.5	251	2	Q9DBQ8	Q9DBQ8 mus musculu	212	431.5	31.4	261	1	KLK3_MOUSE	P04071 mus musculu
140	486	35.4	242	2	Q6R179	Q6R179 tautogolabr	213	431	31.4	260	1	VSPA_TRIGA	P01060 trimeresuru
141	485.5	35.3	234	2	Q9R048	Q9R048 mus musculu	214	431	31.4	260	2	Q8AY81	Q8AY81 trimeresuru
142	485.5	35.3	261	2	Q88309	Q88309 mus musculu	215	431	31.4	262	1	VSP1_AKCA	Q91053 agkistrodon
143	484.5	35.3	251	2	Q8N2U3	Q8N2U3 homo sapien	216	429.5	31.3	205	2	Q96JE2	Q96JE2 homo sapien
144	484.5	35.3	259	1	KLKX_MOUSE	P15948 mus musculu	217	429	31.2	176	2	Q8K5D7	Q8K5D7 mus musculu
145	484.5	35.3	304	1	TRV3_HUMAN	P35030 homo sapien	218	429	31.2	258	1	VSP3_TRIGA	Q13063 trimeresuru
146	484	35.2	255	2	Q9Z0M1	Q9Z0M1 mus musculu	219	429	31.2	260	2	Q71QI0	Q71QI0 trimeresuru
147	483.5	35.2	261	1	KLK1_RAT	P00758 rattus norv	220	428.5	31.2	262	2	Q9QHK3	Q9QHK3 crotalus at
148	483.5	35.2	265	2	Q68G17	Q68G17 rattus norv	221	427	31.1	260	2	Q93502	Q93502 agkistrodon
149	482	35.1	255	2	Q9JIS2	Q9JIS2 mus musculu	222	426.5	31.0	257	1	VSPC_TRIGA	Q13062 trimeresuru
150	481.5	35.0	261	1	KLX9_MOUSE	P15949 mus musculu	223	425	30.9	260	1	VSP1_AKAC	Q918x2 agkistrodon
151	481	35.0	254	2	Q9XSN6	Q9XSN6 sus scrofa	224	424.5	30.9	257	2	Q71QJ3	Q71QJ3 trimeresuru
152	480.5	35.0	263	1	KLXR_MOUSE	Q9Jm71 mus musculu	225	423	30.8	204	2	Q96JEL	Q96JEL homo sapien
153	479	34.9	261	1	KLK3_MACMU	P33619 macaca mula	226	423	30.8	238	1	VSP1_AKHA	P81176 agkistrodon
154	479	34.9	261	2	Q6DT45	Q6DT45 macaca fasc	227	422.5	30.7	234	2	Q9YGS1	Q9YGS1 agkistrodon
155	478.5	34.8	248	2	Q6GPX7	Q6GPX7 xenopus lae	228	422.5	30.7	259	2	Q8UUK2	Q8UUK2 crotalus ad
156	478.5	34.8	250	2	Q93265	Q93265 pseudopleur	229	422	30.7	256	2	Q7SYF1	Q7SYF1 cerastes ce
157	477.5	34.8	256	2	Q61E12	Q61E12 rattus norv	230	421.5	30.7	163	2	Q66H01	Q66H01 xenopus lae
158	477.5	34.8	261	1	KLK1_MOUSE	P00755 mus musculu	231	420.5	30.6	257	2	Q71QI8	Q71QI8 trimeresuru
159	477.5	34.8	263	1	KLKX_MOUSE	Q61754 mus musculu	232	419.5	30.5	234	2	Q8UUU1	Q8UUU1 agkistrodon
160	477	34.7	247	2	Q66PG9	Q66PG9 fugu rubrip	233	419	30.5	258	2	Q8QHK2	Q8QHK2 crotalus at
161	476.5	34.7	344	2	Q9W6J9	Q9W6J9 disostichu	234	418.5	30.5	257	2	Q71QI6	Q71QI6 trimeresuru
162	476.5	34.7	675	2	Q9W6J8	Q9W6J8 disostichu	235	418	30.4	260	2	Q8AY82	Q8AY82 trimeresuru
163	475.5	34.6	219	2	Q91036	Q91036 gadus morhu	236	417	30.3	236	1	VSPG_DABRU	P18965 daboia russ
164	472.5	34.4	235	2	Q61PG8	Q61PG8 fugu rubrip	237	415.5	30.2	178	2	Q93594	Q93594 dicentrarch
165	471	34.3	249	2	Q6DIW2	Q6DIW2 xenopus tro	238	415.5	30.2	257	2	Q71QH8	Q71QH8 trimeresuru
166	470.5	34.2	257	2	Q6LDS3	Q6LDS3 homo sapien	239	414	30.1	237	2	Q8UUU2	Q8UUU2 agkistrodon
167	470.5	34.2	261	1	KLK3_HUMAN	P07288 homo sapien	240	413	30.1	258	1	VSP1_TRIGA	Q13059 trimeresuru
168	470	34.2	258	2	Q71QI1	Q71QI1 trimeresuru	241	413	30.1	258	2	Q7SZE1	Q7SZE1 glycydus sa
169	469.5	34.2	261	1	KLX8_MOUSE	P07628 mus musculu	242	413	30.1	260	1	VSP1_TRIFL	P05620 glycydus sh
170	469.5	34.2	261	2	Q8C232	Q8C232 mus musculu	243	411.5	29.9	228	1	VSPA_LACMU	P33589 lachesis mu
171	468	34.1	259	1	KLK2_RAT	P00759 rattus norv	244	411	29.9	239	2	Q6T5L0	Q6T5L0 glycydus sh
172	467.5	34.0	261	1	KLKQ_MOUSE	P36369 mus musculu	245	411	29.9	258	2	Q71QH7	Q71QH7 trimeresuru
173	467	34.0	258	2	Q71QH6	Q71QH6 trimeresuru	246	411	29.9	260	2	Q7SZC3	Q7SZC3 gallus gall
174	462.5	33.7	261	2	Q8K0C6	Q8K0C6 mus musculu	247	409	29.8	260	1	VSP2_VIPLE	Q9PT40 vipera lebe
175	461.5	33.6	259	1	KLX9_RAT	P07647 rattus norv	248	408.5	29.7	257	2	Q8JH62	Q8JH62 vipera lebe
176	461	33.6	258	2	Q8AY80	Q8AY80 trimeresuru	249	408	29.7	235	1	VSP2_AKBI	Q9Pn3 agkistrodon
177	458.5	33.4	250	1	TRYP_PLEPL	P35034 pleuronecte	250	407	29.6	237	2	Q93421	Q93421 agkistrodon

251	251	407	29.6	258	1	VSP2_AKCA	042207 agkistrodon	324	361.5	26.3	267	2	Q7SZ51	Q7sz51 brachydanio
252	252	407	29.6	258	2	Q8AY79	Q8ay79 trimeresuru	325	361	26.3	255	2	Q6WGR1	Q6wgr1 ictalurus p
253	253	407	29.6	258	1	VSP2_TRIFL	Q13057 trimeresuru	326	361	26.3	267	2	Q640E1	Q640e1 xenopus lae
254	254	406.5	29.6	231	1	VSP1_AKCA	P09872 agkistrodon	327	359.5	26.2	259	2	Q6AZC2	Q6azc2 brachydanio
255	255	406.5	29.6	257	2	Q71QH5	P09872 trimeresuru	328	359.5	26.2	269	2	Q61SU5	Q61su5 homo sapien
256	256	405.5	29.5	257	2	Q71QI3	Q71q13 trimeresuru	329	359.5	26.2	277	1	TRY2_ANOGA	P35036 anopheles g
257	257	405	29.5	234	2	Q7SZE2	Q7sze2 agkistrodon	330	359.5	26.2	342	1	PS88_MOUSE	Q9sed1 mus musculus
258	258	403.5	29.4	233	2	Q61WFI	Q61wfi bothrops al	331	359	26.1	342	2	Q6P326	Q6p326 xenopus tro
259	259	402.5	29.3	232	1	VSP1_BOTJA	P81824 bothrops ja	332	359	26.1	311	2	Q8OXZ3	Q80x03 rattus norv
260	260	402.5	29.3	257	2	Q9YGVJ9	Q9ygv19 agkistrodon	333	359	26.1	430	2	Q804X0	Q804x0 fagu rubrip
261	261	402	29.3	255	1	VSPA_BOTAT	P04371 bothrops at	334	358.5	26.1	245	1	MCT1_SHEEP	P80931 ovis aries
262	262	402	29.3	260	1	VSP1_TRIJE	Q9df68 trimeresuru	335	358.5	26.1	444	1	FA7_RABIT	P98139 oryctolagus
263	263	402	29.3	260	1	VSP6_TRIMU	Q9df68 trimeresuru	336	358	26.1	812	1	PLMN_BOVIN	P06868 bos taurus
264	264	400	29.1	234	1	VSP2_AKCA	P82981 agkistrodon	337	357.5	26.0	232	2	Q9XY45	Q9xy45 ctenocephal
265	265	400	29.1	258	2	Q802F0	Q802f0 agkistrodon	338	357.5	26.0	371	2	Q8MS52	Q8ms52 drosophila
266	266	399.5	29.1	257	2	Q8QG86	Q8qg86 bothrops in	339	357.5	26.0	643	2	Q97506	Q97506 sus scrofa
267	267	399	29.0	260	2	Q71QJ2	Q71qj2 trimeresuru	340	357	26.0	262	1	GRAA_HUMAN	P12544 homo sapien
268	268	397	28.9	235	2	Q90Z47	Q90z47 agkistrodon	341	357	26.0	263	1	CTRB_HUMAN	P17538 homo sapien
269	269	397	28.9	260	2	Q71QI4	Q71q14 trimeresuru	342	357	26.0	271	1	CTRI_PENVA	Q00871 penaeus van
270	270	395.5	28.8	264	2	Q9ER05	Q9er05 mus musculus	343	357	26.0	806	1	PLMN_MACEU	O18783 macropus eu
271	271	395	28.7	260	2	Q71QH9	Q71qh9 trimeresuru	344	357	26.0	1019	1	LFC_TACTR	P28175 tachyples
272	272	394.5	28.7	257	1	VSP2_BOTJA	O13069 bothrops ja	345	357	26.0	1019	2	Q8T9S1	Q8t9s1 tachyples
273	273	393.5	28.6	264	2	Q9D7F8	Q9d7f8 mus musculus	346	356.5	25.9	261	2	Q9W7Q4	Q9w7q4 paralichthy
274	274	393	28.6	260	1	VSPA_AKCA	Q918w9 agkistrodon	347	356.5	25.9	321	1	TRYG_HUMAN	Q9nr12 homo sapien
275	275	392	28.5	258	2	Q71QI2	Q71q12 trimeresuru	348	356.5	25.9	321	2	Q9GRZ8	Q9grz8 homo sapien
276	276	391.5	28.5	264	2	Q9EQZ8	Q9eqz8 rattus norv	349	355.5	25.9	260	2	Q9V7G4	Q9v7g4 drosophila
277	277	391	28.5	253	2	Q8WZB4	Q8wzb4 homo sapien	350	355.5	25.9	276	1	MCT6_MOUSE	P21845 mus musculus
278	278	389	28.3	258	1	CFAD_HUMAN	P00746 homo sapien	351	355	25.8	342	1	PS88_RAT	Q9es87 rattus norv
279	279	389	28.3	258	2	Q8JH85	Q8jhb85 vipera lebe	352	354.5	25.8	249	2	Q6QX59	Q6qx59 lepeophthei
280	280	388.5	28.3	257	1	VSP3_TRIFL	O13058 trimeresuru	353	354.5	25.8	311	2	Q8WZM5	Q8wzm5 trichoderma
281	281	388	28.2	269	1	EL2_PIG	P08419 sus scrofa	354	354.5	25.8	331	2	Q8RIA6	Q8ria6 mus musculus
282	282	387	28.2	189	1	Q8NFV7	Q8nfv7 homo sapien	355	354.5	25.8	331	2	Q8OX17	Q8ox17 mus musculus
283	283	387	28.2	243	2	Q86VJ5	Q86vj5 homo sapien	356	354	25.8	260	2	Q9W7P9	Q9w7p9 paralichthy
284	284	387	28.2	258	2	Q98TT5	Q98tt5 agkistrodon	357	354	25.8	271	1	EL2_MOUSE	P05208 mus musculus
285	285	386.5	28.1	257	1	VSP3_AKCA	Q918x0 agkistrodon	358	353.5	25.7	263	1	CTFA_GADMO	P47796 gadus norhu
286	286	386	28.1	232	1	VSPA_BOTJA	P81661 bothrops ja	359	353.5	25.7	270	1	TRYT_MERUN	P50342 meriones un
287	287	386	28.1	258	2	Q91961	Q91961 agkistrodon	360	353.5	25.7	333	2	Q7Q5Z6	Q7q5z6 anopheles g
288	288	386	28.1	258	2	Q9W7S1	Q9w7s1 agkistrodon	361	353	25.7	274	1	MCT6_RAT	P50343 rattus norv
289	289	386	28.1	260	2	Q676S7	Q676s7 bitis gabon	362	353	25.7	314	1	TEST_HUMAN	Q9y5m0 homo sapien
290	290	385.5	28.1	188	1	KLK3_RAT	P15950 rattus norv	363	353	25.7	456	1	PRTC_CANFA	Q28278 canis famil
291	291	385.5	28.1	264	1	CTRL_HUMAN	P40313 homo sapien	364	353	25.7	459	1	PRTC_PIG	Q9g1p2 sus scrofa
292	292	385.5	28.1	264	2	Q9D960	Q9d960 mus musculus	365	352.5	25.7	263	2	Q6PGS4	Q6pgs4 xenopus lae
293	293	385.5	28.1	269	2	Q81UW0	Q81uw0 homo sapien	366	352.5	25.7	321	2	Q6GNK3	Q6gnk3 xenopus lae
294	294	384.5	28.0	195	2	Q07277	Q07277 homo sapien	367	352	25.6	111	2	Q6GNK2	Q6gnk2 homo sapien
295	295	382.5	27.8	1524	2	Q91674	Q91674 xenopus lae	368	352	25.6	260	1	GRAA_MOUSE	P11032 mus musculus
296	296	381	27.7	263	1	CFAD_RAT	P32038 rattus norv	369	352	25.6	277	2	Q7T0T6	Q7t0t6 xenopus lae
297	297	380.5	27.7	235	2	Q8NAE0	Q8nae0 homo sapien	370	352	25.6	304	1	DISP_RAT	P83748 rattus norv
298	298	380	27.7	157	2	Q6B338	Q6b338 symphysodon	371	352	25.6	505	2	Q966V4	Q966v4 halocynthia
299	299	380	27.7	455	2	Q7SY86	Q7sy86 xenopus lae	372	351.5	25.6	460	1	PRTC_MOUSE	P33587 mus musculus
300	300	379	27.6	220	2	Q8NCW4	Q8ncw4 homo sapien	373	351	25.5	310	1	DISP_MOUSE	Q9gy29 mus musculus
301	301	378	27.5	261	2	Q6DHD9	Q6dhd9 brachydanio	374	351	25.5	456	1	PRTC_BOVIN	P00745 bos taurus
302	302	374.5	27.3	259	1	CFAD_MOUSE	P03953 mus musculus	375	350.5	25.5	265	2	Q804G1	Q804g1 brachydanio
303	303	372.5	27.1	228	2	Q6FHW3	Q6fhw3 homo sapien	376	350.5	25.5	274	2	O16133	O16133 anopheles s
304	304	372.5	27.1	261	2	Q8CUF4	Q8cuf4 rattus norv	377	350.5	25.5	274	2	Q17086	Q17086 anopheles s
305	305	371	27.0	271	1	EL2_RAT	P00774 rattus norv	378	350.5	25.5	434	2	Q7T3B6	Q7t3b6 brachydanio
306	306	370.5	27.0	204	2	Q86V17	Q86v17 homo sapien	379	350	25.5	263	2	Q6QPI1	Q6qp11 homo sapien
307	307	370.5	27.0	259	1	CFAD_PIG	P51779 sus scrofa	380	350	25.5	268	2	Q6QCS9	Q6qcs9 xenopus lae
308	308	370.5	27.0	263	1	CTR2_CANFA	P04813 canis famil	381	350	25.5	268	2	Q642S8	Q642s8 xenopus tro
309	309	370	26.9	234	1	VSP1_AKGRH	P26324 agkistrodon	382	350	25.5	271	2	O18487	O18487 penaeus van
310	310	370	26.9	270	2	Q819P2	Q819p2 apllysina fi	383	349.5	25.4	261	2	Q66HW9	Q66hw9 brachydanio
311	311	369	26.9	330	2	Q6NVR7	Q6nvr7 xenopus tro	384	349.5	25.4	269	1	EL2A_HUMAN	P08217 homo sapien
312	312	368.5	26.8	343	1	PS88_HUMAN	Q16651 homo sapien	385	349.5	25.4	269	2	Q61CV2	Q61cv2 homo sapien
313	313	368	26.8	256	1	TRP3_PSEAM	Q93267 pseudopleur	386	349.5	25.4	277	2	Q96899	Q96899 scolopendra
314	314	368	26.8	418	1	HATT_HUMAN	P06235 homo sapien	387	349.5	25.4	371	2	Q8CJ16	Q8cj16 rattus norv
315	315	367.5	26.7	638	1	KAL_HUMAN	P03952 homo sapien	388	349.5	25.4	445	2	Q8CJ17	Q8cj17 rattus norv
316	316	366	26.6	258	1	VSP2_AKGRH	P47797 agkistrodon	389	349.5	25.4	558	2	Q6L711	Q6l711 rattus norv
317	317	366	26.6	260	2	Q9W7Q3	Q9w7q3 paralichthy	390	349.5	25.4	1130	2	Q7QIM7	Q7qim7 anopheles g
318	318	365.5	26.6	245	2	Q9XY60	Q9xy60 ctenocephal	391	349	25.4	1019	1	LFC_CARRO	Q26422 carinoscoc
319	319	365	26.6	263	2	Q7SX97	Q7sx97 brachydanio	392	349	25.4	1083	2	Q26423	Q26423 carinoscoc
320	320	363.5	26.5	339	2	Q91A44	Q91a44 mus musculus	393	348.5	25.4	429	2	Q8AVB0	Q8avb0 brachydanio
321	321	363	26.4	340	2	Q8BJV6	Q8bjv6 mus musculus	394	348.5	25.4	503	2	Q8AYE4	Q8aye4 brachydanio
322	322	362.5	26.4	246	1	MCT1_MERUN	P50340 meriones un	395	348.5	25.4	799	2	Q6PF94	Q6pf94 mus musculus
323	323	362.5	26.4	387	2	Q9XY57	Q9xy57 ctenocephal	396	348.5	25.4	811	1	TMS6_MOUSE	Q9dbi0 mus musculus

397	348.5	25.4	818	2	Q6PBA6	Q6pba6 brachydanio	470	339.5	24.7	258	1	GRAM RAT	Q03238 rattus norv
398	348	25.3	267	1	TRY7 ANOGA	P35041 anopheles g	471	339.5	24.7	271	2	Q803Z4	Q80324 brachydanio
399	348	25.3	269	1	Q61SN8	Q61sn8 homo sapien	472	339.5	24.7	333	1	PLMN CANFA	P80009 canis famil
400	348	25.3	278	2	Q7ENF6	Q7pnf6 anopheles g	473	339	24.7	321	2	Q61E60	Q61e60 rattus norv
401	347.5	25.3	344	2	Q6QF08	Q640f8 xenopus lae	474	339	24.7	335	2	Q8VIF2	Q8vif2 mus musculus
402	347	25.3	275	2	Q6FHB8	Q6flb8 homo sapien	475	339	24.7	458	1	PRTC RABIT	Q28661 oryctolagus
403	347	25.3	461	1	PRTC HUMAN	P04070 homo sapien	476	339	24.7	461	1	FA9 HUMAN	P00740 homo sapien
404	346.5	25.2	267	1	Q9BK47	Q9bk47 luidia foli	477	339	24.7	461	1	FA9_PANTR	Q95nd7 pan troglod
405	346.5	25.2	269	1	EL2 BOVIN	Q29461 bos taurus	478	339	24.7	625	1	FALL_HUMAN	P03951 homo sapien
406	346.5	25.2	334	2	Q4E507	Q4e507 papio hamad	479	339	24.7	812	1	PLMN_RAT	Q01177 rattus norv
407	346.5	25.2	351	2	Q816K0	Q816k0 holotrichia	480	338.5	24.6	256	2	Q18599	Q18599 drosophila
408	346.5	25.2	435	1	TMS4 MOUSE	Q8vca5 mus musculus	481	338.5	24.6	258	1	EL1_HUMAN	Q9unil1 homo sapien
409	346.5	25.2	435	1	Q9NPF2	Q9ncv5 anopheles g	482	338.5	24.6	258	2	Q867B0	Q867b0 canis famil
410	346.5	25.2	446	1	PA7 MOUSE	P70375 mus musculus	483	338.5	24.6	307	2	Q02569	Q02569 cullex quinq
411	346.5	25.2	456	1	Q7QC30	Q7qc30 anopheles g	484	338.5	24.6	307	2	Q8ZND6	Q8znd6 homo sapien
412	346.5	25.2	461	1	PRTC RAT	P31394 rattus norv	485	338.5	24.6	455	2	Q8CDR0	Q8cdr0 mus musculus
413	346.5	25.2	612	2	Q68FY8	Q68fy8 rattus norv	486	338.5	24.6	562	2	Q7PN85	Q7pn85 anopheles g
414	346.5	25.2	612	2	Q804W7	Q804w7 fugu rubrip	487	338.5	24.6	704	1	CRAR MOUSE	P98064 mus musculus
415	346	25.2	311	1	TRYG MOUSE	Q9qu17 mus musculus	488	338.5	24.6	802	2	Q6UXD8	Q6uxd8 homo sapien
416	346	25.2	322	2	Q920S2	Q920s2 mus musculus	489	338	24.6	210	2	Q63Z11	Q63z11 xenopus lae
417	345.5	25.1	454	2	Q4E506	Q4e506 papio hamad	490	338	24.6	365	2	Q97366	Q97366 holotrichia
418	345.5	25.1	467	2	Q967X8	Q967x8 panulirus a	491	338	24.6	388	2	Q44330	Q44330 manduca sex
419	345	25.1	253	1	TRXD_DROER	P54626 drosophila	492	338	24.6	418	2	Q7FGU3	Q7fgu3 anopheles g
420	344.5	25.1	117	2	Q9PUF3	Q9puf3 bothrops ja	493	338	24.6	625	1	THRB_BOVIN	P00735 bos taurus
421	344.5	25.1	187	2	Q6PK75	Q6pk75 homo sapien	494	337.5	24.6	238	1	TRY5_AEDAE	P29787 aedes aegyp
422	344.5	25.1	275	2	Q6B051	Q6b051 homo sapien	495	337.5	24.6	261	2	Q6GX60	Q6gx60 lepeophthei
423	344.5	25.1	855	2	Q72410	Q7z410 homo sapien	496	337.5	24.6	264	1	GRAK HUMAN	P49863 homo sapien
424	344.5	25.1	1059	2	Q72411	Q7z411 homo sapien	497	337.5	24.6	282	2	Q9DA13	Q9da13 mus musculus
425	344	25.0	257	2	Q8BZ04	Q8bz04 mus musculus	498	337.5	24.6	317	2	Q9DGR3	Q9dgr3 xenopus lae
426	344	25.0	265	2	Q6QX61	Q6qx61 lepeophthei	499	337.5	24.6	328	2	Q80Z40	Q80z40 rattus norv
427	344	25.0	275	1	TRB2_HUMAN	P02231 homo sapien	500	337.5	24.6	432	2	Q6GNA2	Q6gna2 xenopus lae
428	344	25.0	282	2	Q6NZY1	Q6nzy1 homo sapien	501	337.5	24.6	471	2	Q8CFE0	Q8cfe0 mus musculus
429	344	25.0	417	2	Q8BZ10	Q8bz10 mus musculus	502	337	24.5	247	2	Q17039	Q17039 anopheles g
430	343.5	25.0	266	2	Q4E644	Q4e644 macaca fasc	503	337	24.5	263	2	Q9D8X8	Q9d8x8 mus musculus
431	343.5	25.0	273	1	MCT7_MOUSE	Q02844 mus musculus	504	337	24.5	275	2	Q96RZ6	Q96rz6 homo sapien
432	343.5	25.0	273	2	Q921N4	Q921n4 mus musculus	505	337	24.5	432	2	Q6UX37	Q6ux37 homo sapien
433	343.5	25.0	457	1	TMS5_HUMAN	Q9h3s3 homo sapien	506	337	24.5	434	1	UROK_CHICK	P15120 gallus gall
434	343	25.0	275	1	TRYT CANFA	P15944 canis famil	507	337	24.5	437	1	TMS4_HUMAN	Q9nr54 homo sapien
435	343	25.0	284	2	Q8NF86	Q8nf86 homo sapien	508	336.5	24.5	247	1	MCT1_PAPHA	P52195 papio hamad
436	343	25.0	318	2	Q7RTY9	Q7rty9 homo sapien	509	336.5	24.5	251	1	MCT3_SHEEP	Q46683 ovis aries
437	342.5	24.9	248	2	Q16126	Q16126 boitonia vi	510	336.5	24.5	260	2	Q8F2V9	Q8f2v9 xenopus tro
438	342.5	24.9	248	2	Q9XY52	Q9xy52 ctenocephal	511	336.5	24.5	329	2	Q42272	Q42272 xenopus lae
439	342.5	24.9	271	2	Q8HYJ2	Q8hyj2 bos taurus	512	336.5	24.5	428	2	Q8WPM7	Q8wpm7 oikopleura
440	342.5	24.9	273	1	MCT7 RAT	P27435 rattus norv	513	336.5	24.5	638	1	KAL_MOUSE	P26262 mus musculus
441	342.5	24.9	273	2	Q6P6W8	Q6p6w8 rattus norv	514	336	24.5	227	2	Q81X14	Q81x14 homo sapien
442	342.5	24.9	433	2	Q8JHD0	Q8jhd0 brachydanio	515	336	24.5	263	2	Q9CR35	Q9cr35 m muscu
443	342.5	24.9	433	2	Q90YK1	Q90yk1 brachydanio	516	336	24.5	263	2	Q9DC86	Q9dc86 mus musculus
444	342.5	24.9	517	2	Q8K0D2	Q8kod2 mus musculus	517	336	24.5	273	1	TRYT_SHEEP	Q9xsm2 ovis aries
445	342.5	24.9	624	1	FALL_MOUSE	Q91y47 mus musculus	518	336	24.5	280	2	Q64ID5	Q64id5 anthonomus
446	342.5	24.9	810	1	PLMN_HUMAN	P00747 homo sapien	519	336	24.5	402	2	Q7QB73	Q7qb73 anopheles g
447	342.5	24.9	811	1	TMS6_HUMAN	Q8iu80 homo sapien	520	336	24.5	416	1	FA9_BOVIN	P00741 bos taurus
448	342	24.9	275	1	TRB1_HUMAN	Q15661 homo sapien	521	336	24.5	485	2	Q7PKK0	Q7pkk0 anopheles g
449	342	24.9	355	2	Q7PQR9	Q7pqr9 anopheles g	522	336	24.5	556	2	Q803D5	Q803d5 brachydanio
450	342	24.9	812	1	PLMN_MOUSE	P20918 mus musculus	523	336	24.5	654	2	Q6QNF4	Q6qnf4 canis famil
451	341.5	24.9	258	1	GRAK RAT	P49864 rattus norv	524	336	24.5	790	1	PLMN_PIG	P06867 sus scrofa
452	341.5	24.9	455	1	TMS5_MOUSE	Q9er04 mus musculus	525	335.5	24.4	258	2	Q61SM6	Q61sm6 homo sapien
453	341.5	24.9	573	2	Q9Y516	Q9y516 drosophila	526	335.5	24.4	266	1	EL1_BOVIN	Q28153 bos taurus
454	341.5	24.9	1134	2	Q7RTY7	Q7rty7 homo sapien	527	335.5	24.4	275	1	TRYT_PIG	Q9n2d1 sus scrofa
455	341	24.8	251	2	Q9GLN2	Q9gln2 bos taurus	528	335.5	24.4	389	2	Q9PVX7	Q9pvx7 xenopus lae
456	341	24.8	263	2	Q63ZK0	Q63zk0 xenopus lae	529	335.5	24.4	558	2	Q86YM4	Q86ym4 homo sapien
457	341	24.8	328	2	Q61RA4	Q61ra4 xenopus lae	530	335	24.4	216	2	Q9UD19	Q9ud19 homo sapien
458	341	24.8	719	2	Q67B90	Q67b90 homo sapien	531	335	24.4	318	2	Q8MYN6	Q8my6 nilaparvata
459	341	24.8	572	2	Q8JY98	Q8jy98 homo sapien	532	335	24.4	433	2	Q804X5	Q804x5 gallus gall
460	340.5	24.8	246	1	MCT4_MOUSE	P21812 mus musculus	533	335	24.4	701	2	Q9JJS9	Q9jjs9 rattus norv
461	340.5	24.8	274	1	TRY1_ANOGA	P35035 anopheles g	534	335	24.4	703	2	Q8CHN8	Q8chn8 rattus norv
462	340.5	24.8	446	1	FAV_RAT	Q8ksu6 rattus norv	535	334.5	24.3	247	2	Q70500	Q70500 rattus norv
463	340.5	24.8	624	2	Q9DAT3	Q9dat3 mus musculus	536	334.5	24.3	263	1	GRAK_MOUSE	Q35205 mus musculus
464	340	24.7	273	2	Q9XSM1	Q9xsm1 ovis aries	537	334.5	24.3	275	2	Q7YS62	Q7ys62 equus cabal
465	340	24.7	280	2	Q8N171	Q8n171 homo sapien	538	334.5	24.3	537	2	Q9BYE1	Q9bye1 homo sapien
466	340	24.7	297	2	Q88781	Q88781 rattus ratt	539	334.5	24.3	581	2	Q9BYE2	Q9bye2 homo sapien
467	340	24.7	360	2	Q17489	Q17489 anopheles g	540	334	24.3	234	2	Q15096	Q15096 homo sapien
468	339.5	24.7	247	2	Q08732	Q08732 mesocricetu	541	334	24.3	264	2	Q8QGF6	Q8qgf6 xenopus lae
469	339.5	24.7	253	1	TRYB_DROER	P54625 drosophila	542	333.5	24.3	253	2	Q8MKZ1	Q8mkz1 drosophila

543	333.5	24.3	253	2	Q8SXZ4	Q8sxz4 drosophila	616	328.5	23.9	365	2	Q7Q1D1	Q7q1d1 anopheles g
544	333.5	24.3	275	1	Q7PNF7	Q7pnf7 anopheles g	617	328.5	23.9	524	2	Q7SXH8	Q7sxh8 brachydanio
545	333.5	24.3	290	1	PR27 HUMAN	Q9bqr3 homo sapien	618	328.5	23.9	615	2	Q6GNK4	Q6gnk4 xenopus lae
546	333.5	24.3	824	1	Q6ICC2	Q6icc2 homo sapien	619	328.5	23.9	681	2	Q7ZT70	Q7zt70 lampetra ja
547	333	24.2	245	1	CTRA BOVIN	P00766 bos taurus	620	328.5	23.9	683	2	Q8MRH5	Q8mrh5 drosophila
548	333	24.2	256	2	Q9ROK0	Q9rok0 mus musculus	621	328.5	23.9	786	1	STUB DROME	Q05319 drosophila
549	333	24.2	285	1	FA9_CAYPO	P16295 cavia porce	622	328.5	23.9	787	2	Q9VEY6	Q9vey6 drosophila
550	333	24.2	320	1	Q7TOX2	Q7tox2 xenopus lae	623	328	23.9	226	1	COGS_UCAPU	P00771 uca pugilati
551	333	24.2	355	2	Q7PEW0	Q7pew0 anopheles g	624	328	23.9	328	2	Q6BEA2	Q6bea2 rattus norv
552	333	24.2	360	2	Q7PEV7	Q7pev7 anopheles g	625	328	23.9	452	1	FA9 CANFA	P19540 canis famil
553	332.5	24.2	247	2	Q35342	Q35342 mesocricetu	626	328	23.9	767	2	Q9DGR2	Q9dgr2 xenopus lae
554	332.5	24.2	254	2	Q8TG37	Q8tg37 aedes aegyp	627	327.5	23.8	247	1	MCT1 MACFA	P56335 macaca fasc
555	332.5	24.2	260	2	Q8T4P6	Q8t4p6 lepeophthei	628	327.5	23.8	263	2	Q9TYI6	Q9tyi6 penaeus van
556	332.5	24.2	262	2	Q8T4P7	Q8t4p7 lepeophthei	629	327.5	23.8	266	2	Q27761	Q27761 penaeus van
557	332.5	24.2	263	2	Q7Z1D5	Q7z1d5 lepeophthei	630	327.5	23.8	269	2	Q96QV5	Q96qv5 homo sapien
558	332.5	24.2	264	2	Q7YSS9	Q7yss9 lepeophthei	631	327.5	23.8	269	2	Q6ISM5	Q6ism5 homo sapien
559	332.5	24.2	490	1	TMS2 MOUSE	Q9jiq8 mus musculus	632	327.5	23.8	269	2	Q6GN82	Q6gn82 xenopus lae
560	332.5	24.2	638	1	KAL_RAT	P14272 rattus norv	633	327	23.8	259	1	DERF3 DERFA	P49275 dermatophag
561	332.5	24.2	810	1	PLMN ERIEU	Q29485 erinaceus e	634	327	23.8	263	2	Q7SY84	Q7sy84 xenopus lae
562	332.5	24.2	810	1	PLMN MACMU	P12545 macaca mula	635	327	23.8	270	2	Q27824	Q27824 uca pugilati
563	332	24.2	247	2	Q7OT74	Q7ot74 equus cabal	636	327	23.8	466	2	Q6SA95	Q6sa95 felis silve
564	332	24.2	251	2	Q7Q9W2	Q7q9w2 anopheles g	637	327	23.8	600	2	Q7ZTR2	Q7ztr2 xenopus lae
565	332	24.2	258	2	Q97399	Q97399 phaeton coc	638	326.5	23.8	248	1	GRAC MOUSE	P08882 mus musculu
566	332	24.2	266	2	Q92077	Q92077 gadus morhu	639	326.5	23.8	263	2	Q6GNF7	Q6gnf7 xenopus lae
567	332	24.2	277	2	Q8SQ44	Q8sq44 sus scrofa	640	326.5	23.8	266	1	ELI_PIG	P00772 sus scrofa
568	332	24.2	355	2	Q8NFU1	Q8nfu1 anopheles g	641	326.5	23.8	266	2	Q91X79	Q91x79 mus musculu
569	331.5	24.1	250	2	Q8T4P4	Q8t4p4 lepeophthei	642	326.5	23.8	369	2	Q7QKL1	Q7qkl1 anopheles g
570	331.5	24.1	254	2	Q8MMK9	Q8mmk9 aedes aegyp	643	326.5	23.8	490	2	Q7TN04	Q7tn04 mus musculu
571	331.5	24.1	256	1	TRYA DROME	P04814 drosophila	644	326	23.7	248	1	GRZ1 RAT	Q06505 rattus norv
572	331.5	24.1	260	2	Q8T4P5	Q8t4p5 lepeophthei	645	326	23.7	271	1	CTR2_PENVA	P36178 penaeus van
573	331.5	24.1	263	2	Q9PWQ6	Q9pwq6 gadus morhu	646	326	23.7	329	2	Q7PEV8	Q7pev8 anopheles g
574	331.5	24.1	264	2	Q6PPY5	Q6ppy5 xenopus lae	647	326	23.7	432	2	Q7QKL4	Q7qkl4 anopheles g
575	331.5	24.1	275	1	TRY3 ANOGA	P03037 anopheles g	648	325.5	23.7	259	2	Q8IRE0	Q8ire0 drosophila
576	331	24.1	263	1	CTRB_RAT	P07338 rattus norv	649	325.5	23.7	261	1	DER3 DERPT	P39575 dermatophag
577	331	24.1	622	1	THRB_HUMAN	P00734 homo sapien	650	325.5	23.7	268	2	O46151	O46151 pacifastacu
578	331	24.1	622	2	Q7Z7P3	Q7z7p3 homo sapien	651	325.5	23.7	306	1	BSS4 MOUSE	Q9er10 mus musculu
579	331	24.1	722	2	Q8AW90	Q8aw90 lampetra ja	652	325.5	23.7	891	2	Q9VY38	Q9vv38 drosophila
580	331	24.1	722	1	Q9PSZ5	Q9psz5 lampetra ja	653	324.5	23.6	146	2	Q9DDE1	Q9dde1 brachydanio
581	330.5	24.1	247	1	MCT1 HUMAN	P23946 homo sapien	654	324.5	23.6	228	2	Q7Q153	Q7q153 anopheles g
582	330.5	24.1	256	1	TRYA DROER	P54624 drosophila	655	324.5	23.6	263	2	Q7PUB9	Q7pub9 anopheles g
583	330.5	24.1	269	2	Q61SP9	Q6isp9 homo sapien	656	324.5	23.6	275	1	TRYA HUMAN	P15157 homo sapien
584	330.5	24.1	560	2	Q14520	Q14520 homo sapien	657	324.5	23.6	391	2	Q9V3Z2	Q9v3z2 drosophila
585	330.5	24.1	638	2	Q8R0P5	Q8r0p5 mus musculu	658	324	23.6	253	1	TRYB_HROME	P35004 drosophila
586	330	24.0	236	2	Q7SIG3	Q7sig3 salmo salar	659	324	23.6	257	1	GRAM DROME	P51124 homo sapien
587	330	24.0	253	2	Q9V5Y3	Q9v5y3 drosophila	660	324	23.6	266	2	Q9W7Q0	Q9w7q0 paralichthy
588	330	24.0	266	2	Q81916	Q81916 blomia trop	661	324	23.6	459	1	FA9 MOUSE	P16294 mus musculu
589	330	24.0	282	1	FA9_RAT	P16296 rattus norv	662	324	23.6	1019	1	ENTK_HUMAN	P98073 homo sapien
590	330	24.0	4548	1	APOA HUMAN	P08519 homo sapien	663	323.5	23.5	277	2	Q80WM7	Q80wm7 mus musculu
591	329.5	24.0	237	2	Q29464	Q29464 bos taurus	664	323.5	23.5	299	2	Q9VS87	Q9vsa87 drosophila
592	329.5	24.0	248	2	Q8T4P2	Q8t4p2 lepeophthei	665	323.5	23.5	328	2	Q8BJR6	Q8bjr6 mus musculu
593	329.5	24.0	253	1	TRYD DROME	P42276 drosophila	666	323.5	23.5	466	1	FA7 HUMAN	P08709 homo sapien
594	329.5	24.0	262	2	Q7Z1D6	Q7z1d6 lepeophthei	667	323.5	23.5	490	2	Q6P7D7	Q6p7d7 rattus norv
595	329.5	24.0	266	2	Q8WR10	Q8wr10 paralichthode	668	323.5	23.5	608	2	Q9FTW7	Q9ftw7 struthio ca
596	329.5	24.0	269	1	EL2B_HUMAN	P08218 homo sapien	669	323.5	23.5	875	1	NETR_HUMAN	P56730 homo sapien
597	329.5	24.0	320	2	Q7PEV6	Q7pev6 anopheles g	670	323	23.5	281	2	O46137	O46137 lumbricus r
598	329.5	24.0	578	2	Q6Q017	Q6q017 bos taurus	671	323	23.5	296	2	Q9VDV1	Q9vdv1 drosophila
599	329.5	24.0	1420	1	APOA MACMU	P14417 macaca mula	672	323	23.5	540	2	Q800Y7	Q800y7 meleagris g
600	329	23.9	216	1	VSEP_LACMU	P84036 lachesis mu	673	323	23.5	653	2	Q8VCS4	Q8vcs4 mus musculu
601	329	23.9	264	2	O08643	O08643 mus musculu	674	323	23.5	653	2	Q8VCS4	Q8vcs4 mus musculu
602	329	23.9	279	2	Q9NMS4	Q9nms4 mus musculu	675	322.5	23.5	249	2	Q6QX62	Q6qx62 lepeophthei
603	329	23.9	307	2	Q7TML0	Q7tml0 mus musculu	676	322.5	23.5	258	2	Q9W5U8	Q9w5u8 drosophila
604	329	23.9	572	2	Q8BIK6	Q8bik6 mus musculu	677	322.5	23.5	324	1	TEST MOUSE	Q9jhj7 mus musculu
605	329	23.9	575	2	Q7Q9W3	Q7q9w3 anopheles g	678	322.5	23.5	336	2	Q80YD8	Q80yd8 mus musculu
606	329	23.9	722	2	Q6NUP5	Q6nuf5 xenopus lae	679	322.5	23.5	372	2	Q9Y1K6	Q9y1k6 anopheles g
607	328.5	23.9	239	2	Q8T4P3	Q8t4p3 lepeophthei	680	322.5	23.5	581	2	Q9XZM7	Q9xzm7 strongyloce
608	328.5	23.9	245	1	CTRB GADMO	P80646 gadus morhu	681	322	23.4	210	2	Q68DS2	Q68ds2 homo sapien
609	328.5	23.9	253	1	TRYG DROME	P42277 drosophila	682	322	23.4	699	1	CRAR_HUMAN	P48740 h complemen
610	328.5	23.9	260	1	MCT1 RAT	P09650 rattus norv	683	322	23.4	1303	2	Q6GS84	Q6gs84 oikopleura
611	328.5	23.9	261	2	Q8T4P1	Q8t4p1 lepeophthei	684	321.5	23.4	263	2	O62562	O62562 penaeus van
612	328.5	23.9	275	2	Q86TM8	Q86tm8 homo sapien	685	321.5	23.4	265	2	Q7SYI8	Q7syi8 xenopus lae
613	328.5	23.9	276	2	Q86UAS	Q86uas homo sapien	686	321.5	23.4	266	2	Q9D936	Q9d936 mus musculu
614	328.5	23.9	338	1	PLMN HORSE	P80010 equus cabal	687	321.5	23.4	679	2	Q96PQ8	Q96pq8 homo sapien
615	328.5	23.9	364	2	Q9NA59	Q9nas9 anopheles g	688	321	23.4	226	1	DDN1_BOVIN	P80219 bos taurus

689	321	23.4	230	2	Q61E13	Q61E13 rattus norv	762	314	22.9	629	2	Q6AZS7	Q6AZS7 xenopus lae
690	321	23.4	247	1	MCT2 MERUN	P50341 meriones un	763	314	22.9	855	1	STM4 HUMAN	Q9Y5Y6 homo sapien
691	321	23.4	248	1	NKPI_RAT	P18291 rattus norv	764	313.5	22.8	261	1	EU13_SURMA	Q9Y370 euroglyphus
692	321	23.4	269	1	TRYM_CANFA	P19236 canis famil	765	313.5	22.8	321	2	Q80Y38	Q80Y38 mus musculus
693	321	23.4	411	2	QVUF0	P19236 drosophila	766	313.5	22.8	326	2	Q9D9M0	Q9D9M0 mus musculus
694	321	23.4	655	1	HGFA_HUMAN	Q04756 homo sapien	767	313.5	22.8	364	2	Q9I7V4	Q9I7V4 drosophila
695	320.5	23.3	247	1	GRAB_MOUSE	P04187 mus musculus	768	313.5	22.8	425	2	Q804X7	Q804X7 gallus gall
696	320.5	23.3	312	2	Q7M755	P07M755 mus musculus	769	313	22.8	241	2	Q9I7L2	Q9I7L2 drosophila
697	320	23.3	249	2	Q9W7Q1	Q9W7Q1 paralichthy	770	313	22.8	336	2	Q8CIR9	Q8CIR9 mus musculus
698	320	23.3	489	2	Q7Q432	Q7Q432 anopheles g	771	313	22.8	420	2	Q90504	Q90504 eptatretus
699	320	23.3	536	2	Q7PX72	Q7PX72 anopheles g	772	313	22.8	613	2	Q03711	Q03711 xenopus lae
700	319.5	23.3	265	2	Q6NGN0	Q6NGN0 xenopus lae	773	313	22.8	697	2	Q8CG43	Q8CG43 rattus norv
701	319.5	23.3	559	2	Q6P7U0	Q6P7U0 mus musculus	774	313	22.8	733	2	Q920S0	Q920S0 mus musculus
702	319.5	23.3	607	2	Q6DPJ5	Q6DPJ5 xenopus lae	775	313	22.8	733	2	Q8CD27	Q8CD27 mus musculus
703	319	23.2	241	2	Q7PPF7	Q7PPF7 anopheles g	776	313	22.8	855	2	Q9JJI7	Q9JJI7 rattus norv
704	319	23.2	264	2	Q81PY7	Q81PY7 drosophila	777	312.5	22.7	241	2	Q81VP2	Q81VP2 homo sapien
705	319	23.2	270	2	Q641D1	Q641D1 anthonomus	778	312.5	22.7	271	2	Q819R6	Q819R6 culex pipie
706	319	23.2	320	2	Q8CIR7	Q8CIR7 rattus norv	779	312.5	22.7	274	1	TRY5_ANOGA	P35039 anopheles g
707	319	23.2	461	2	Q95ND6	Q95ND6 pan troglod	780	312.5	22.7	300	2	Q96EF3	Q96EF3 homo sapien
708	319	23.2	1034	1	ENTK_PIG	P98074 sus scrofa	781	312.5	22.7	390	2	Q9Y157	Q9Y157 drosophila
709	318.5	23.2	343	1	PLMN_SHEEP	P81286 ovis aries	782	312.5	22.7	615	1	FA12_HUMAN	P00748 homo sapien
710	318.5	23.2	418	2	Q61E15	Q61E15 rattus norv	783	312.5	22.7	680	2	Q868H5	Q868H5 branchiosto
711	318.5	23.2	490	2	Q920K3	Q920K3 rattus norv	784	312.5	22.7	1234	2	Q7PIQ7	Q7PIQ7 anopheles g
712	318	23.1	232	2	Q94508	Q94508 dermatophag	785	312.5	22.7	1322	2	Q9PNR7	Q9PNR7 anopheles g
713	318	23.1	258	2	Q7YRZ7	Q7YRZ7 bos taurus	786	312.5	22.7	1322	2	Q9NJ55	Q9NJ55 anopheles g
714	318	23.1	261	2	Q962G7	Q962G7 culex pipie	787	312	22.7	295	2	Q8CIP7	Q8CIP7 rattus norv
715	318	23.1	265	2	Q18488	Q18488 penaeus van	788	312	22.7	374	2	Q8I862	Q8I862 dermaceator
716	318	23.1	271	1	FA9_PIG	P16293 sus scrofa	789	312	22.7	597	2	Q35727	Q35727 mus musculus
717	318	23.1	274	1	FA9_SHEEP	P16291 ovis aries	790	312	22.7	597	2	Q6PER0	Q6PER0 mus musculus
718	318	23.1	295	1	Q69E28	Q69E28 homo sapien	791	312	22.7	609	2	Q80YC5	Q80YC5 mus musculus
719	318	23.1	618	1	THRB_MOUSE	P19221 mus musculus	792	311.5	22.7	255	2	Q25227	Q25227 lucilia cup
720	317.5	23.1	245	1	CTRB_BOVIN	P00767 bos taurus	793	311.5	22.7	255	2	Q7TN10	Q7TN10 mus musculus
721	317.5	23.1	246	1	GRAH_HUMAN	P20718 homo sapien	794	311.5	22.7	293	2	Q23528	Q23528 caenorhabdi
722	317.5	23.1	248	2	Q9XYX9	Q9XYX9 rhyzopertha	795	311.5	22.7	566	1	TPA_BOVIN	Q28198 bos taurus
723	317.5	23.1	256	1	TRTE_DROER	P54627 drosophila	796	311.5	22.7	645	2	Q7PWE4	Q7PWE4 anopheles g
724	317.5	23.1	374	2	Q9VUG2	Q9VUG2 drosophila	797	311.5	22.7	761	1	NETR_MOUSE	Q08762 mus musculus
725	317.5	23.1	559	1	TPA_MOUSE	P11214 mus musculus	798	311.5	22.7	1322	2	Q9NAT0	Q9NAT0 anopheles g
726	317.5	23.1	604	1	CFAT_RAT	Q9WUW3 rattus norv	799	311	22.6	249	2	Q6IE11	Q6IE11 rattus norv
727	317.5	23.1	617	2	Q8JIS1	Q8JIS1 triakis scy	800	311	22.6	250	2	Q9V514	Q9V514 drosophila
728	317	23.1	248	2	Q63636	Q63636 rattus norv	801	311	22.6	261	1	CATG_MOUSE	P28293 mus musculus
729	317	23.1	624	2	Q9SME7	Q9SME7 oryctolagus	802	311	22.6	431	1	ACRO_RABIT	P48038 oryctolagus
730	316.5	23.0	246	1	MCT1_MOUSE	P11034 mus musculus	803	311	22.6	433	1	UROK_BOVIN	Q05589 bos taurus
731	316.5	23.0	441	2	Q81917	Q81917 manduca sex	804	311	22.6	1035	1	ENTK_BOVIN	P98072 bos taurus
732	316.5	23.0	607	2	Q91001	Q91001 gallus gall	805	311	22.6	1042	1	CORI_HUMAN	Q9Y5Q5 homo sapien
733	316	23.0	246	2	Q9XY46	Q9XY46 ctenocephal	806	310.5	22.6	247	1	MCT2_RAT	P00770 rattus norv
734	316	23.0	259	2	Q69E27	Q69E27 homo sapien	807	310.5	22.6	259	2	Q7PFI7	Q7PFI7 anopheles g
735	316	23.0	263	2	Q02570	Q02570 culex quinq	808	310.5	22.6	371	2	Q8MRV3	Q8MRV3 drosophila
736	316	23.0	269	2	Q9CQ52	Q9CQ52 m mus muscu	809	310.5	22.6	473	2	Q7PV63	Q7PV63 anopheles g
737	316	23.0	269	2	Q9D7T9	Q9D7T9 mus musculus	810	310.5	22.6	559	1	TPA_RAT	P19637 rattus norv
738	315.5	23.0	264	1	TRY3_ABDAAE	P29786 aedes aegypt	811	310.5	22.6	1374	2	Q9VSU0	Q9VSU0 drosophila
739	315.5	23.0	264	2	Q62561	Q62561 penaeus van	812	310.5	22.6	1449	2	Q9UI12	Q9UI12 drosophila
740	315.5	23.0	265	1	Q66KR6	Q66KR6 xenopus lae	813	310.5	22.6	1450	2	Q8IQB8	Q8IQB8 drosophila
741	315.5	23.0	266	1	ELJ_RAT	P00773 rattus norv	814	310.5	22.6	1462	2	Q9UI13	Q9UI13 drosophila
742	315.5	23.0	314	2	Q9VR15	Q9VR15 drosophila	815	310.5	22.6	2382	2	Q9BI19	Q9BI19 drosophila
743	315.5	23.0	374	2	Q7QCS5	Q7QCS5 anopheles g	816	310.5	22.6	2409	2	Q960G6	Q960G6 drosophila
744	315.5	23.0	392	1	EAST_DROME	P13582 drosophila	817	310.5	22.6	2786	2	Q9VSU2	Q9VSU2 drosophila
745	315.5	23.0	453	2	Q812A6	Q812A6 mus musculus	818	310	22.6	275	1	FA9_RABIT	P16292 oryctolagus
746	315.5	23.0	492	1	FA10_BOVIN	P00743 bos taurus	819	310	22.6	327	2	Q7O530	Q7O530 anopheles g
747	315	22.9	248	2	Q63224	Q63224 rattus norv	820	310	22.6	483	2	Q8T8X4	Q8T8X4 drosophila
748	315	22.9	280	2	Q66NX6	Q66NX6 canis famil	821	310	22.6	483	2	Q9VK10	Q9VK10 rattus norv
749	315	22.9	323	2	Q960Q4	Q960Q4 homo sapien	822	310	22.6	1111	2	Q80YN4	Q80YN4 rattus norv
750	315	22.9	617	1	THRB_RAT	P18292 rattus norv	823	309.5	22.5	246	2	Q9EPR0	Q9EPR0 mus musculus
751	315	22.9	686	1	MAS2_HUMAN	Q00187 homo sapien	824	309.5	22.5	255	2	Q9Y7A9	Q9Y7A9 metarhizium
752	314.5	22.9	256	1	TRVE_DROME	P35005 drosophila	825	309.5	22.5	265	2	Q9VVT3	Q9VVT3 drosophila
753	314.5	22.9	261	2	Q61DF4	Q61DF4 drosophila	826	309.5	22.5	284	2	Q7Q493	Q7Q493 anopheles g
754	314.5	22.9	283	2	Q6UWY2	Q6UWY2 homo sapien	827	309.5	22.5	482	1	FA10_RAT	Q63207 rattus norv
755	314.5	22.9	453	1	TMS3_MOUSE	Q8KIT0 mus musculus	828	309.5	22.5	868	2	Q9Y1V3	Q9Y1V3 polyandroca
756	314.5	22.9	609	2	Q7M761	Q7M761 mus musculus	829	309	22.5	285	2	Q8CG42	Q8CG42 rattus norv
757	314.5	22.9	680	2	Q868H7	Q868H7 branchiosto	830	309	22.5	404	2	Q7QKL2	Q7QKL2 anopheles g
758	314	22.9	275	1	TRY4_ANOGA	P35038 anopheles g	831	308.5	22.5	240	2	Q6IE06	Q6IE06 rattus norv
759	314	22.9	280	2	Q7Q494	Q7Q494 anopheles g	832	308.5	22.5	246	1	MCT9_MOUSE	Q35164 mus musculus
760	314	22.9	280	2	Q66NX5	Q66NX5 canis famil	833	308.5	22.5	260	2	Q6VP06	Q6VP06 sarcopes s
761	314	22.9	422	2	Q8WVC1	Q8WVC1 homo sapien	834	308	22.4	125	2	Q804G0	Q804G0 sphoeroides

835	308	22.4	300	2	Q819P4	Q819P4 aurelia aur	908	302	22.0	269	2	Q7PW17	Q7PW17 anopheles g
836	308	22.4	317	1	BSS4_HUMAN	Q9GN4 homo sapien	909	302	22.0	321	2	Q6MZL2	Q6MZL2 homo sapien
837	308	22.4	334	2	Q6UXE0	Q6UXE0 homo sapien	910	302	22.0	394	1	URTG_DESRO	P49150 desmodus ro
838	308	22.4	335	2	Q86PB3	Q86PB3 drosophila	911	302	22.0	477	1	URTB_DESRO	P15638 desmodus ro
839	308	22.4	377	2	Q9VB68	Q9VB68 drosophila	912	301.5	21.9	241	2	Q8BW11	Q8BW11 m mus muscu
840	308	22.4	408	2	Q8MR95	Q8MR95 drosophila	913	301.5	21.9	394	2	P91817	P91817 tachypleus
841	308	22.4	498	2	Q6GPF9	Q6GPF9 xenopus lae	914	301.5	21.9	505	2	Q7QCV2	Q7QCV2 anopheles g
842	307.5	22.4	255	2	Q7BPF16	Q7BPF16 anopheles g	915	301	21.9	255	1	CATG_HUMAN	P08311 homo sapien
843	307.5	22.4	471	2	Q804X6	Q804X6 gallus gall	916	301	21.9	255	2	Q34289	Q34289 salvelinus
844	307.5	22.4	676	2	Q6UDJ6	Q6UDJ6 cyprinus ca	917	301	21.9	268	2	Q17030	Q17030 anopheles g
845	307	22.3	135	2	Q62284	Q62284 mus muscu	918	301	21.9	279	2	Q7PX39	Q7PX39 anopheles g
846	307	22.3	250	2	Q17036	Q17036 anopheles g	919	301	21.9	279	2	Q7TNX3	Q7TNX3 mus muscu
847	307	22.3	259	1	CTR1_ANOGA	Q27289 anopheles g	920	301	21.9	283	2	Q95V22	Q95V22 lumbricus b
848	307	22.3	318	2	Q7Q9W4	Q7Q9W4 anopheles g	921	301	21.9	417	2	Q8VHK8	Q8VHK8 mus muscu
849	307	22.3	417	1	HEPS_HUMAN	P05981 homo sapien	922	301	21.9	417	2	Q8VDV1	Q8VDV1 mus muscu
850	307	22.3	726	2	Q7QBP4	Q7QBP4 anopheles g	923	301	21.9	431	1	URTB_DESRO	P98121 desmodus ro
851	306.5	22.3	308	2	Q9W454	Q9W454 drosophila	924	301	21.9	728	2	Q9GRS4	Q9GRS4 homo sapien
852	306.5	22.3	365	1	Q7OGL1	Q7OGL1 anopheles g	925	300.5	21.9	239	2	Q7T2H1	Q7T2H1 xenopus lae
853	306.5	22.3	375	1	PCB_TACTR	P21902 tachypleus	926	300.5	21.9	276	2	P91894	P91894 arenicola m
854	306.5	22.3	418	2	Q8SZK2	Q8SZK2 drosophila	927	300.5	21.9	278	2	Q68FN6	Q68FN6 brachydanio
855	306.5	22.3	468	2	Q9U0G3	Q9U0G3 pacifastacu	928	300.5	21.9	386	2	Q8I924	Q8I924 bombyx mori
856	306	22.3	162	2	Q6UBM2	Q6UBM2 homo sapien	929	300.5	21.9	424	2	Q9VA88	Q9VA88 drosophila
857	306	22.3	247	2	Q8N1D2	Q8N1D2 homo sapien	930	300.5	21.9	433	2	Q8MHY7	Q8MHY7 oryctolagus
858	306	22.3	266	2	Q6AZC0	Q6AZC0 brachydanio	931	300.5	21.9	433	2	Q8MIL0	Q8MIL0 oryctolagus
859	306	22.3	362	2	Q9W453	Q9W453 drosophila	932	300.5	21.9	442	1	UROK_PIG	P04185 sus scrofa
860	306	22.3	685	2	Q91WP0	Q91WP0 mus muscu	933	300.5	21.9	562	2	Q8SQ23	Q8SQ23 sus scrofa
861	305.5	22.2	228	2	Q9XY49	Q9XY49 ctenocephal	934	300	21.8	245	1	GILX_HELHO	P43685 heloderma h
862	305.5	22.2	246	2	Q91VB1	Q91VB1 mus muscu	935	300	21.8	270	2	Q8WR11	Q8WR11 paralithode
863	305.5	22.2	256	1	HYPA_HYPLI	P35587 hypoderma l	936	300	21.8	291	2	Q8IQ89	Q8IQ89 drosophila
864	305.5	22.2	274	2	Q6GNF0	Q6GNF0 xenopus lae	937	300	21.8	417	2	Q8VHJ4	Q8VHJ4 rattus norv
865	305.5	22.2	383	2	Q77102	Q77102 manduca sex	938	300	21.8	698	2	Q9PU71	Q9PU71 xenopus lae
866	305.5	22.2	418	2	Q9VA87	Q9VA87 drosophila	939	299.5	21.8	241	2	Q63637	Q63637 rattus norv
867	305.5	22.2	441	2	Q804X2	Q804X2 fugu rubrip	940	299.5	21.8	246	1	MCTX_MOUSE	Q00356 mus muscu
868	305	22.2	247	1	GRAB_HUMAN	P10144 h granzyme	941	299.5	21.8	254	2	Q6DBS8	Q6DBS8 brachydanio
869	305	22.2	281	2	Q67BC3	Q67BC3 homo sapien	942	299.5	21.8	257	2	Q19023	Q19023 macaca mula
870	305	22.2	307	2	Q641D2	Q641D2 anthonomus	943	299.5	21.8	258	1	CTR2_ANOGA	Q17025 anopheles g
871	305	22.2	391	2	Q7PFX3	Q7PFX3 anopheles g	944	299.5	21.8	272	2	Q7Q9W5	Q7Q9W5 anopheles g
872	305	22.2	395	2	Q9BZM1	Q9BZM1 homo sapien	945	299.5	21.8	282	2	Q7PT16	Q7PT16 anopheles g
873	305	22.2	532	2	Q7PX73	Q7PX73 anopheles g	946	299.5	21.8	325	2	Q15944	Q15944 sarcophaga
874	304.5	22.2	258	2	Q9XY53	Q9XY53 ctenocephal	947	299.5	21.8	372	2	Q9W2C8	Q9W2C8 drosophila
875	304.5	22.2	271	2	Q7Q820	Q7Q820 anopheles g	948	299.5	21.8	430	2	Q6RUJ3	Q6RUJ3 trichinella
876	304.5	22.2	384	2	Q9XY63	Q9XY63 ctenocephal	949	299.5	21.8	436	1	ACRO_MOUSE	P23378 mus muscu
877	304.5	22.2	492	1	TMS2_HUMAN	Q15393 homo sapien	950	299.5	21.8	465	2	Q9BJL7	Q9BJL7 trichinella
878	304.5	22.2	492	2	Q6ET73	Q6ET73 homo sapien	951	299.5	21.8	615	2	Q8I2Z5	Q8I2Z5 homo sapien
879	304	22.1	268	1	CLCR_HUMAN	Q99895 homo sapien	952	299.5	21.8	974	2	Q9WMD8	Q9WMD8 bufo japoni
880	304	22.1	272	2	Q9XYV6	Q9XYV6 rhizopertha	953	299.5	21.8	1069	1	ENTK_MOUSE	P97435 mus muscu
881	304	22.1	375	2	Q817W8	Q817W8 dermaceron	954	299	21.8	256	2	Q6VLQ1	Q6VLQ1 verticilliu
882	304	22.1	393	2	Q6RX66	Q6RX66 armigeres s	955	299	21.8	437	1	ACRO_RAT	P29293 rattus norv
883	304	22.1	400	2	Q9VCJ8	Q9VCJ8 drosophila	956	298.5	21.7	235	2	Q91004	Q91004 gecko gecko
884	304	22.1	423	2	Q8BM10	Q8BM10 mus muscu	957	298.5	21.7	248	2	Q9VQ98	Q9VQ98 drosophila
885	304	22.1	543	2	Q9BU99	Q9BU99 homo sapien	958	298.5	21.7	249	1	MCT1_CANFA	P21842 canis fami
886	304	22.1	562	1	TPA_HUMAN	P00750 homo sapien	959	298.5	21.7	350	2	Q7QKX0	Q7QKX0 anopheles g
887	304	22.1	589	2	Q6FUA5	Q6FUA5 homo sapien	960	298.5	21.7	407	1	FAT_BOVIN	P22457 bos taurus
888	304	22.1	685	2	Q9Z338	Q9Z338 mus muscu	961	298.5	21.7	433	2	Q8T3A2	Q8T3A2 ciona intes
889	304	22.1	1379	2	Q9V4N6	Q9V4N6 drosophila	962	298.5	21.7	733	2	Q9VTX9	Q9VTX9 drosophila
890	304	22.1	1397	2	Q7KQO9	Q7KQO9 drosophila	963	298	21.7	235	2	Q28731	Q28731 oryctolagus
891	303.5	22.1	240	2	Q7SVQ8	Q7SVQ8 xenopus lae	964	298	21.7	255	2	Q18435	Q18435 helicoverpa
892	303.5	22.1	244	1	MCT2_MOUSE	P15119 mus muscu	965	298	21.7	268	2	Q8T4T4	Q8T4T4 aedes aegypt
893	303.5	22.1	246	1	MCT4_RAT	P97592 rattus norv	966	298	21.7	348	2	Q86WS5	Q86WS5 homo sapien
894	303.5	22.1	278	2	Q7Q492	Q7Q492 anopheles g	967	297.5	21.7	254	2	Q76520	Q76520 stomoxys ca
895	303.5	22.1	309	2	Q27083	Q27083 tachypleus	968	297.5	21.7	256	2	Q6MJY6	Q6MJY6 bdellovibri
896	303.5	22.1	603	1	CFAI_MOUSE	Q61129 mus muscu	969	297.5	21.7	269	2	Q6AZF9	Q6AZF9 xenopus lae
897	303.5	22.1	761	2	Q99J78	Q99J78 rattus norv	970	297.5	21.7	277	2	Q8IQ10	Q8IQ10 drosophila
898	303	22.1	246	1	MCT2_SHEEP	P79204 ovis aries	971	297.5	21.7	293	2	Q7Q8F9	Q7Q8F9 anopheles g
899	303	22.1	259	2	Q6JPG5	Q6JPG5 neodiprion	972	297.5	21.7	408	2	Q9VM19	Q9VM19 drosophila
900	302.5	22.0	119	2	Q9NR68	Q9NR68 homo sapien	973	297.5	21.7	435	1	SNAX_DROME	P05049 drosophila
901	302.5	22.0	223	2	Q9VB44	Q9VB44 drosophila	974	297.5	21.7	472	2	Q7QI82	Q7QI82 anopheles g
902	302.5	22.0	273	1	TRY6_ANOGA	P35040 anopheles g	975	297.5	21.7	486	2	Q7PX74	Q7PX74 anopheles g
903	302.5	22.0	1004	2	P79953	P79953 xenopus lae	976	297.5	21.7	519	2	Q8T3A3	Q8T3A3 ciona intes
904	302.5	22.0	1113	1	COR1_MOUSE	Q92319 mus muscu	977	297.5	21.7	616	2	Q97507	Q97507 sus scrofa
905	302	22.0	247	2	Q8T376	Q8T376 eisenia foe	978	297	21.6	237	1	TRYP_ASTFL	P00765 astacus flu
906	302	22.0	255	1	TRV4_LUCCU	P35044 lucilia cup	979	297	21.6	247	1	MCT5_MOUSE	P21844 mus muscu
907	302	22.0	268	2	Q9W7Q2	Q9W7Q2 paralichthy	980	297	21.6	256	2	Q9XY51	Q9XY51 ctenocephal

981	297	21.6	268	2	Q9BIG0	Q9bi90 aedes aegyp	1054	291.5	21.2	270	2	Q7Q5A6	Q7q5a6 anopheles g
982	297	21.6	284	2	Q8IRX5	Q8irx5 drosophila	1055	291	21.2	239	2	Q6LCU4	Q6lcu4 lumbricus r
983	297	21.6	352	2	Q6UWB4	Q6uwb4 homo sapien	1056	291	21.2	271	2	Q54213	Q54213 streptomyce
984	297	21.6	369	2	Q6AXZ6	Q6axz6 rattus norv	1057	291	21.2	436	1	HEPS MOUSE	O35453 mus musculu
985	297	21.6	454	1	TMS3 HUMAN	P57727 homo sapien	1058	291	21.2	678	2	Q9JJS8	Q9jjs8 rattus norv
986	297	21.6	477	1	UR11_DESRO	P98119 desmodus ro	1059	290.5	21.1	483	2	Q7PKJ7	Q7pkj7 anopheles g
987	296.5	21.6	248	1	EL3B_MOUSE	P08883 mus musculu	1060	290.5	21.1	681	2	Q7Q554	Q7q554 anopheles g
988	296.5	21.6	270	1	EL3B_HUMAN	P08861 homo sapien	1061	290	21.1	149	2	Q6DTY8	Q6dty8 hypophthalm
989	296.5	21.6	272	2	Q7VYX6	Q7v5x6 drosophila	1062	290	21.1	256	1	HYPB_HYPLI	P35588 hypoderma l
990	296.5	21.6	273	2	Q7JYN3	Q7jyn3 drosophila	1063	290	21.1	257	2	Q27440	Q27440 aedes aegyp
991	296.5	21.6	581	2	Q960I5	Q960i5 drosophila	1064	290	21.1	390	2	Q8I927	Q8i927 hyphantria
992	296.5	21.6	1047	2	Q9VZH2	Q9vzh2 drosophila	1065	289.5	21.1	246	2	Q9BLI7	Q9bli7 lumbricus r
993	296	21.5	265	2	Q74696	Q74696 phaesphaer	1066	289.5	21.1	248	1	GRAG_MOUSE	P13366 mus musculu
994	296	21.5	279	2	Q9QZ74	Q9qz74 rattus norv	1067	289.5	21.1	257	2	Q6R560	Q6r560 ostrinia nu
995	296	21.5	281	2	Q76898	Q76898 drosophila	1068	289.5	21.1	317	2	Q8K4I7	Q8k4i7 mus musculu
996	296	21.5	314	2	Q6RUT2	Q6rut2 mus musculu	1069	289	21.0	260	2	Q7RTY3	Q7rty3 homo sapien
997	296	21.5	318	2	Q8OUR4	Q8our4 mus musculu	1070	289	21.0	278	2	Q7QHS0	Q7qhs0 anopheles g
998	295.5	21.5	339	2	Q9GME0	Q9gme0 ornithorhyn	1071	289	21.0	339	2	Q9QX91	Q9qx91 rattus norv
999	295.5	21.5	239	2	Q9I218	Q9i218 oncorhynch	1072	289	21.0	366	2	Q9QX85	Q9qx85 rattus norv
1000	295.5	21.5	270	2	Q9VRS4	Q9vrs4 drosophila	1073	289	21.0	376	1	FA10_TROCA	P81428 tropidechis
1001	295.5	21.5	433	1	UROK_MOUSE	P06869 mus musculu	1074	289	21.0	441	2	Q9XXV0	Q9xxv0 bombyx mori
1002	295.5	21.5	449	2	Q9VDU8	Q9vdu8 drosophila	1075	289	21.0	541	2	Q9QX90	Q9qx90 rattus norv
1003	295.5	21.5	453	2	Q6ZMC3	Q6zmc3 homo sapien	1076	289	21.0	583	1	CFAL_HUMAN	P05156 homo sapien
1004	295	21.5	260	2	Q9V6P6	Q9v6p6 drosophila	1077	289	21.0	623	2	Q9JJP3	Q9jjp3 rattus norv
1005	295	21.5	267	2	Q6DGM4	Q6dgm4 brachydanio	1078	289	21.0	643	2	Q9QX84	Q9qx84 rattus norv
1006	295	21.5	268	2	Q84T45	Q84t45 aedes aegyp	1079	288.5	21.0	255	2	Q9XY62	Q9xy62 ctenocephal
1007	295	21.5	269	2	Q95KW7	Q95kw7 bos taurus	1080	288.5	21.0	264	2	Q7Q290	Q7q290 anopheles g
1008	295	21.5	358	2	Q45029	Q45029 drosophila	1081	288.5	21.0	315	2	Q8IRR3	Q8irr3 drosophila
1009	295	21.5	553	2	Q6P7I9	Q6p7i9 xenopus lae	1082	288.5	21.0	317	2	Q8K4D1	Q8k4d1 mus musculu
1010	294.5	21.4	244	2	Q8I6N3	Q8i6n3 eisenia foe	1083	288.5	21.0	438	2	Q6ZWK6	Q6zwk6 homo sapien
1011	294.5	21.4	575	2	Q6IE57	Q6ie57 rattus norv	1084	288.5	21.0	442	2	Q804X1	Q804x1 fugu rubrip
1012	294	21.4	247	2	Q9VHF8	Q9vfh8 drosophila	1085	288.5	21.0	1047	2	Q24019	Q24019 drosophila
1013	294	21.4	259	2	Q9XY61	Q9xy61 ctenocephal	1086	288	21.0	257	2	Q9NB49	Q9nb49 aedes aegyp
1014	294	21.4	265	2	Q9VHF8	Q9vfh8 drosophila	1087	288	21.0	261	2	Q8IRE1	Q8ire1 drosophila
1015	294	21.4	271	2	Q9CTK2	Q9ctk2 culex quinq	1088	288	21.0	405	2	Q8XZW7	Q8xzm7 anopheles g
1016	294	21.4	283	2	Q25394	Q25394 lumbricus r	1089	288	21.0	405	2	Q7PGY0	Q7pgy0 anopheles g
1017	294	21.4	283	2	Q8ITU7	Q8itu7 lumbricus r	1090	288	21.0	421	2	Q60491	Q60491 cavia porce
1018	294	21.4	293	2	Q725A4	Q725a4 homo sapien	1091	288	21.0	730	2	Q6Q1Q8	Q6qlq8 gallus gall
1019	294	21.4	303	2	Q76900	Q76900 drosophila	1092	287.5	20.9	234	2	Q90244	Q90244 acipenser t
1020	293.5	21.4	246	2	Q6IE10	Q6ie10 rattus norv	1093	287.5	20.9	244	2	Q6T375	Q6t375 eisenia foe
1021	293.5	21.4	256	2	Q9XY11	Q9xy11 rhyzopertha	1094	287.5	20.9	249	2	Q7KR00	Q7krd0 drosophila
1022	293.5	21.4	257	2	Q7X0G1	Q7x0g1 phlebotomus	1095	287.5	20.9	472	2	Q6IGB2	Q6igb2 drosophila
1023	293.5	21.4	302	2	Q8SYZ7	Q8syz7 drosophila	1096	287.5	20.9	603	1	FA12_CAVPO	Q94962 cavia porce
1024	293.5	21.4	302	2	Q8SYZ6	Q8syz6 drosophila	1097	287.5	20.9	845	2	Q63ZQ6	Q63zq6 xenopus lae
1025	293.5	21.4	431	1	UROK_HUMAN	P00749 homo sapien	1098	287	20.9	204	2	Q6S9W8	Q6s9w8 homo sapien
1026	293.5	21.4	845	2	Q6GR54	Q6gr54 xenopus lae	1099	287	20.9	244	2	Q6LAW0	Q6lam0 homo sapien
1027	293	21.3	246	2	Q9R2C8	Q9r2c8 rattus norv	1100	287	20.9	256	2	Q25081	Q25081 hypoderma l
1028	293	21.3	247	1	MCT3_RAT	P50339 rattus norv	1101	287	20.9	268	2	Q7RT43	Q7rt43 aedes aegyp
1029	293	21.3	265	1	SER1_DROME	P17205 drosophila	1102	287	20.9	273	2	Q9VEM5	Q9vem5 drosophila
1030	293	21.3	268	2	Q16900	Q16900 aedes aegyp	1103	287	20.9	416	2	Q86T26	Q86t26 homo sapien
1031	293	21.3	268	2	Q8N0R8	Q8n0r8 aedes aegyp	1104	287	20.9	422	1	DES1_HUMAN	Q9ul52 homo sapien
1032	293	21.3	277	2	Q9VPN8	Q9vpn8 drosophila	1105	287	20.9	423	2	Q6UW31	Q6uw31 homo sapien
1033	293	21.3	278	2	Q8WQQ2	Q8wqq2 drosophila	1106	287	20.9	481	1	FA10_MOUSE	Q88947 mus musculu
1034	293	21.3	301	2	Q7Q6U2	Q7q6u2 anopheles g	1107	287	20.9	581	2	Q8I925	Q8i925 hyphantria
1035	293	21.3	427	2	Q6Y2X4	Q6y2x4 manduca sex	1108	286.5	20.9	220	1	CTR2_VESCR	P00769 vespa crabr
1036	293	21.3	433	1	UROK_PAPCY	P16227 papio cynoc	1109	286.5	20.9	220	2	Q7QM61	Q7qm61 anopheles g
1037	293	21.3	777	2	Q8CAN9	Q8can9 mus musculu	1110	286.5	20.9	376	2	Q7PTP7	Q7ptp7 anopheles g
1038	293	21.3	855	1	ST14_MOUSE	P56677 mus musculu	1111	286.5	20.9	425	2	Q7P285	Q7p285 anopheles g
1039	292.5	21.3	235	2	Q90387	Q90387 cynops pyrr	1112	286	20.8	235	2	Q6XGZ4	Q6xgz4 homo sapien
1040	292.5	21.3	336	2	Q9Z1H1	Q9z1h1 mus musculu	1113	286	20.8	254	1	CTRL_HALRU	P35003 halioeius ru
1041	292.5	21.3	390	2	Q8MP08	Q8mp08 bombyx mori	1114	286	20.8	272	2	Q7Q483	Q7q483 anopheles g
1042	292.5	21.3	459	2	Q9GMD9	Q9gmd9 ornithorhyn	1115	286	20.8	416	2	Q8BZ13	Q8bz13 mus musculu
1043	292	21.3	267	2	Q8T639	Q8t639 aedes aegyp	1116	286	20.8	416	2	Q8BZ30	Q8bz30 mus musculu
1044	292	21.3	268	1	CLCR_RAT	P55091 rattus norv	1117	286	20.8	443	2	Q8JHC9	Q8jhc9 brachydanio
1045	292	21.3	270	2	Q8T4A8	Q8t4a8 drosophila	1118	286	20.8	667	2	Q9BJM1	Q9bjm1 trichinella
1046	292	21.3	276	2	Q97398	Q97398 phaeden coc	1119	285.5	20.8	175	2	Q8PLJ9	Q8plj9 squilla ora
1047	292	21.3	332	2	Q8SYS8	Q8sys8 drosophila	1120	285.5	20.8	248	1	MCT8_RAT	P97594 rattus norv
1048	292	21.3	413	2	Q8T9T2	Q8t9t2 aedes aegyp	1121	285.5	20.8	270	1	EL3A_HUMAN	P95093 homo sapien
1049	292	21.3	475	2	Q804W9	Q804w9 fugu rubrip	1122	285.5	20.8	270	2	Q96QL8	Q96ql8 homo sapien
1050	292	21.3	688	2	Q868H6	Q868h6 branchiosco	1123	285.5	20.8	270	2	Q91039	Q91039 gadus morhu
1051	291.5	21.2	216	1	CTR2_VESOR	P00768 vespa orien	1124	285.5	20.8	289	2	Q8MR67	Q8mr67 drosophila
1052	291.5	21.2	235	2	Q9Z1D3	Q9z1d3 rattus norv	1125	285.5	20.8	290	2	Q9VRT2	Q9vrt2 drosophila
1053	291.5	21.2	258	2	Q9NBC9	Q9nbc9 glossina mo	1126	285	20.7	470	2	Q8T3A1	Q8t3a1 ciona intes

1127	284.5	20.7	172	2	Q6T776	Q6t776 homo sapien	1200	277	20.2	273	2	Q9VKA8	Q9vka8 drosophila
1128	284.5	20.7	245	2	Q6DKQ3	P6dkq3 eisenia foe	1201	277	20.2	398	2	Q8Mkp4	Q8mkp4 drosophila
1129	284.5	20.7	253	1	CAC3_BOVIN	P05805 bos taurus	1202	277	20.2	1629	2	Q9V513	Q9v513 drosophila
1130	284.5	20.7	564	2	Q7RTZ1	Q7rtz1 homo sapien	1203	277	20.2	1674	2	Q8SY35	Q8sy35 drosophila
1131	284	20.7	235	2	Q6BAR4	Q6bar4 bos taurus	1204	276.5	20.1	257	2	Q97099	Q97099 anopheles d
1132	284	20.7	243	2	Q01309	Q01309 botryllus s	1205	276.5	20.1	262	2	Q9V5J2	Q9vaj2 drosophila
1133	284	20.7	257	2	Q8EPL8	Q8epl8 aedes aegypt	1206	276	20.1	254	1	PRN3_MOUSE	Q61096 mus musculu
1134	283.5	20.6	268	2	Q9XY56	Q9xy56 ctenocephal	1207	276	20.1	257	2	Q818E4	Q818e4 ochlerotatu
1135	283.5	20.6	707	2	Q8QGV0	Q8qgv0 cyprinus ca	1208	276	20.1	271	1	S24D_ANOGA	Q17004 anopheles g
1136	283	20.6	247	1	TRYP_STMVI	P35048 simulum vi	1209	276	20.1	300	2	Q7Q6U1	Q7q6u1 anopheles g
1137	283	20.6	320	2	Q7GKL3	Q7gkl3 anopheles g	1210	276	20.1	302	2	Q9VCJ0	Q9vcj0 drosophila
1138	283	20.6	382	2	Q7GHL1	Q7ghl1 mus musculu	1211	276	20.1	376	1	FA10_HOPST	P83370 holocephal
1139	282.5	20.6	245	2	Q7FJQ0	Q7fjq0 anopheles g	1212	276	20.1	488	1	FA10_HUMAN	P00742 homo sapien
1140	282.5	20.6	267	2	Q817P0	Q817p0 lumbricus b	1213	276	20.1	717	2	Q8AXR1	Q8axr1 xenopus lae
1141	282.5	20.6	246	2	Q9VLF5	Q9vlf5 drosophila	1214	275.5	20.1	246	2	Q6DKQ2	Q6dkq2 eisenia foe
1142	282.5	20.6	269	2	Q9V929	Q9v929 drosophila	1215	275.5	20.1	249	2	Q8CIQ8	Q8ciq8 mus musculu
1143	282.5	20.6	424	2	Q6R558	Q6r558 ostrinia nu	1216	275.5	20.1	256	2	Q818E5	Q818e5 ochlerotatu
1144	282.5	20.6	687	2	Q69DK8	Q69dk8 sus scrofa	1217	275.5	20.1	258	2	Q6NLM5	Q6nlm5 drosophila
1145	282	20.5	258	2	Q6JKF3	Q6jkf3 neodiprion	1218	275.5	20.1	262	2	Q9V5X9	Q9v5x9 drosophila
1146	282	20.5	259	2	Q18600	Q18600 drosophila	1219	275.5	20.1	296	2	Q8TR906	Q8tr9u6 aedes aegypt
1147	282	20.5	263	2	Q9NB92	Q9nb92 agrotis ips	1220	275	20.0	237	2	Q17035	Q17035 anopheles g
1148	282	20.5	416	1	HEPS_RAT	Q05511 rattus norv	1221	275	20.0	256	2	Q25082	Q25082 hypodema l
1149	282	20.5	686	2	Q6O1Q9	Q6qlq9 gallus gall	1222	275	20.0	260	2	Q9VSJ1	Q9vsj1 drosophila
1150	282	20.5	688	2	Q858H4	Q858h4 branchiosteo	1223	275	20.0	262	2	Q7ZOG3	Q7z0g3 phlebotomus
1151	281.5	20.5	258	2	Q9NGY6	Q9ngy6 aedes aegypt	1224	275	20.0	284	2	Q8AXQ8	Q8axq8 xenopus lae
1152	281.5	20.5	291	2	Q8MLC5	Q8mlc5 drosophila	1225	275	20.0	317	2	Q7Q619	Q7q619 anopheles g
1153	281.5	20.5	388	2	Q7Z1F0	Q7z1f0 cotesia rub	1226	275	20.0	496	2	Q8CHP7	Q8chp7 cavia porce
1154	281.5	20.5	430	2	Q7PNQ4	Q7pnq4 anopheles g	1227	275	20.0	717	2	Q8AXR0	Q8axr0 xenopus lae
1155	281	20.5	262	2	Q7ZOG5	Q7z0g5 phlebotomus	1228	274.5	20.0	695	1	CASP_MESAU	P15156 mesocricetu
1156	281	20.5	267	2	Q9VA66	Q9va66 drosophila	1229	274	19.9	87	2	Q9CQ78	Q9cq78 m mus muscu
1157	281	20.5	329	2	Q7QB72	Q7qb72 anopheles g	1230	274	19.9	265	2	Q9VHF7	Q9vhf7 drosophila
1158	281	20.5	564	2	Q8MKB1	Q8mbk1 oryctolagus	1231	273	19.9	125	2	Q86VI8	Q86vi8 homo sapien
1159	280.5	20.4	227	2	Q7PHB4	Q7phb4 anopheles g	1232	273	19.9	247	1	MCT8_MOUSE	P43430 mus musculu
1160	280.5	20.4	255	2	Q97100	Q97100 anopheles d	1233	273	19.9	254	2	Q8K597	Q8k597 rattus norv
1161	280.5	20.4	270	2	Q7Q0N6	Q7q0n6 anopheles g	1234	273	19.9	257	2	Q818E3	Q818e3 aedes polyn
1162	280.5	20.4	365	2	Q9Y1K7	Q9y1k7 anopheles g	1235	273	19.9	258	1	TRYU_DROER	P54629 drosophila
1163	280.5	20.4	410	2	Q7QJ44	Q7qj44 anopheles g	1236	273	19.9	265	2	Q17800	Q17800 caenorhabdi
1164	280.5	20.4	424	2	Q6R559	Q6r559 ostrinia nu	1237	273	19.9	377	2	Q9VEM8	Q9vem8 drosophila
1165	280.5	20.4	439	2	Q8BHM9	Q8bhm9 m mus muscu	1238	273	19.9	388	2	P79343	P79343 bos taurus
1166	280	20.4	241	1	TRYP_PQB3	P7pqb3 anopheles g	1239	272.5	19.8	258	2	Q9GME1	Q9gme1 ornithorhyn
1167	280	20.4	254	1	TRYP_SARBU	P51588 sarcophaga	1240	272.5	19.8	262	1	TRYU_DROME	P42279 drosophila
1168	280	20.4	267	2	Q8SYK8	Q8syk8 drosophila	1241	272.5	19.8	282	2	Q7PX30	Q7px30 anopheles g
1169	280	20.4	271	2	Q9V4W5	Q9v4w5 drosophila	1242	272.5	19.8	287	2	Q9VTV2	Q9vtv2 drosophila
1170	280	20.4	282	2	Q25395	Q25395 lumbricus r	1243	272.5	19.8	432	1	UROK_RAT	P29598 rattus norv
1171	280	20.4	336	2	Q7RTY5	Q7rtys homo sapien	1244	272.5	19.8	537	2	Q804W8	Q804w8 fugu rubrip
1172	280	20.4	420	2	Q61E14	Q6ie14 rattus norv	1245	272.5	19.8	978	2	P91777	P91777 pacifastacu
1173	280	20.4	494	2	Q9VJD7	Q9vjd7 drosophila	1246	272	19.8	243	2	O01310	O01310 botryllus s
1174	279.5	20.3	745	2	Q9PVI3	Q9pyv3 cyprinus ca	1247	272	19.8	262	1	TRYT_DROME	P42278 drosophila
1175	279	20.3	242	2	Q6T374	Q6t374 eisenia foe	1248	272	19.8	262	2	Q9V5Y0	Q9v5y0 drosophila
1176	279	20.3	248	2	Q920S1	Q920s1 mus musculu	1249	272	19.8	288	2	Q8SX49	Q8sx49 drosophila
1177	279	20.3	267	2	Q9VA67	Q9va67 drosophila	1250	272	19.8	475	1	FA10_CHICK	P25155 gallus gall
1178	279	20.3	280	1	TRYZ_DROME	P42280 drosophila	1251	272	19.8	492	2	Q7Z155	Q7z155 chiromantes
1179	279	20.3	280	2	Q9V5X8	Q9v5x8 drosophila	1252	272	19.8	688	1	C1S_HUMAN	P09871 homo sapien
1180	279	20.3	319	2	Q9VRS5	Q9vrs5 drosophila	1253	272	19.8	688	2	Q8CFG8	Q8cfg8 mus musculu
1181	279	20.3	329	2	Q9GL10	Q9gl10 ovis aries	1254	271.5	19.8	250	2	Q7PWE3	Q7pwe3 anopheles g
1182	279	20.3	385	2	Q25101	Q25101 herdmania m	1255	271.5	19.8	257	2	Q81S83	Q81s83 aedes albop
1183	279	20.3	694	2	Q8R099	Q8r099 mus musculu	1256	271.5	19.8	262	2	Q9NB91	Q9nb91 agrotis ips
1184	279	20.3	694	2	Q6P6T1	Q6p6t1 rattus norv	1257	271.5	19.8	267	2	Q9V942	Q9v942 drosophila
1185	279	20.3	721	2	Q7ZT69	Q7zt69 lampetra ja	1258	271.5	19.8	272	2	Q9VRS3	Q9vrs3 drosophila
1186	278.5	20.3	269	2	Q7PWT2	Q7pwt2 anopheles g	1259	271.5	19.8	833	2	Q96442	Q96442 strongyloce
1187	278.5	20.3	326	2	Q7ZZ80	Q7zz80 brachydanio	1260	271	19.7	247	2	O70164	O70164 mesocricetu
1188	278.5	20.3	330	2	Q61E62	Q6ie62 rattus norv	1261	271	19.7	253	2	Q9XY50	Q9xy50 stenoccephal
1189	278.5	20.3	593	1	FA12_BOVIN	P98140 bos taurus	1262	271	19.7	275	2	Q7Z0B4	Q7z0b4 stomoxys ca
1190	278	20.2	239	2	Q9NKC5	Q9nkc5 drosophila	1263	271	19.7	1801	2	Q8WSJ2	Q8wsj2 bombyx mori
1191	278	20.2	474	2	Q7FZH7	Q7fzh7 anopheles g	1264	270.5	19.7	219	2	Q7PJ75	Q7pj75 anopheles g
1192	278	20.2	490	1	FA10_RABIT	O19045 oryctolagus	1265	270.5	19.7	245	2	Q81E56	Q81e56 rattus norv
1193	278	20.2	501	2	Q7QCVO	Q7qcv0 anopheles g	1266	270.5	19.7	248	1	GRAD_MOUSE	P11033 mus musculu
1194	277.5	20.2	245	2	Q9BLI8	Q9bli8 lumbricus r	1267	270.5	19.7	256	1	TRYV_MANSE	P35046 manduca sex
1195	277.5	20.2	266	2	Q24091	Q24091 drosophila	1268	270.5	19.7	420	2	Q7Q235	Q7q235 anopheles g
1196	277.5	20.2	271	2	Q76519	Q76519 stomoxys ca	1269	270	19.7	253	2	O18440	O18440 helicoverpa
1197	277.5	20.2	845	2	Q9DGR1	Q9dgr1 xenopus lae	1270	270	19.7	297	2	Q7Q6U4	Q7q6u4 anopheles g
1198	277	20.2	252	2	Q76498	O76498 diaprepes a	1271	270	19.7	694	2	Q70542	Q70542 rattus norv
1199	277	20.2	272	2	Q82KG0	Q82kg0 streptomyce	1272	269.5	19.6	248	1	GR22_RAT	Q06606 rattus norv

1419	256	18.6	421	2	Q6ZMR5	06zmr5	homo sapien
1420	256	18.6	463	2	Q6IT10	06it10	pseudonaja
1421	255.5	18.6	260	2	Q6X143	06x143	drosohila
1422	255.5	18.6	254	2	Q6I436	06i436	helicoverpa
1423	255.5	18.6	273	2	Q7Z163	07z163	dermatophag
1424	255.5	18.6	431	2	Q7PV05	07pv05	anopheles g
1425	255	18.6	292	2	Q7PVQ5	07pvq5	anopheles g
1426	255	18.6	405	2	Q7PQK3	07pqk3	anopheles g
1427	254.5	18.5	254	2	Q6I434	06i434	helicoverpa
1428	254.5	18.5	278	2	P91893	p91893	arenicola m
1429	254.5	18.5	357	2	Q7Q092	07q092	anopheles g
1430	254.5	18.5	357	2	Q7Q0X6	07qx6	anopheles g
1431	254.5	18.5	493	2	Q7PV62	07pv62	anopheles g
1432	254.5	18.5	523	2	Q9V819	09v819	drosohila
1433	254.5	18.5	524	2	Q8MR00	08mr00	drosohila
1434	254.5	18.5	827	2	Q7P288	07p288	anopheles g
1435	254	18.5	324	2	Q6BD11	06bd11	drosohila
1436	254	18.5	334	2	Q9VEA0	09vea0	anthosoma
1437	253.5	18.4	282	2	Q641D4	0641d4	antonomus
1438	253	18.4	242	2	Q9XY59	09xy59	ctenoccephal
1439	253	18.4	251	2	Q9VXC9	09vxc9	drosohila
1440	253	18.4	253	2	Q6W741	06w741	pediculus h
1441	253	18.4	272	1	SER3 DROME	p17207	drosohila
1442	253	18.4	287	2	Q675S0	0675s0	oikopleura
1443	252.5	18.4	245	2	Q7Q2Q8	07q2q8	anopheles g
1444	252.5	18.4	254	2	Q7Q6T0	07q6t0	anopheles g
1445	252.5	18.4	282	2	Q8WJD1	08wjd1	canis famli
1446	252.5	18.4	324	2	Q6BD09	06bd09	drosohila
1447	252	18.3	235	2	Q7PRK6	07prk6	anopheles g
1448	252	18.3	295	2	Q18450	018450	helicoverpa
1449	252	18.3	301	2	Q7Q6T0	07q6t0	anopheles g
1450	252	18.3	400	2	Q72081	072081	tachypeus
1451	251.5	18.3	186	2	Q6X655	06x655	marmota mon
1452	251.5	18.3	266	2	Q8MLC2	08mlc2	drosohila
1453	251.5	18.3	267	2	Q9VGB8	09vgb8	drosohila
1454	251.5	18.3	276	2	Q18443	018443	helicoverpa
1455	251.5	18.3	318	2	Q7QC37	07qc37	anopheles g
1456	251.5	18.3	418	2	Q7Q529	07q529	anopheles g
1457	251.5	18.3	520	2	Q8ING0	08ing0	drosohila
1458	251	18.3	285	2	Q7Q5K4	07q5k4	anopheles g
1459	251	18.3	405	2	Q8WQS8	08wqs8	apis mellif
1460	250.5	18.2	226	2	Q6XHU4	06xhu4	drosohila
1461	250.5	18.2	240	2	Q7PYJ1	07pyj1	anopheles g
1462	250.5	18.2	268	2	Q9VT24	09vt24	drosohila
1463	250.5	18.2	305	2	Q8WRL2	08wrl2	drosohila
1464	250.5	18.2	323	2	Q76920	076920	drosohila
1465	250	18.2	124	2	Q8C6G5	08c6g5	mus musculu
1466	250	18.2	203	2	Q9NB77	09nb77	heliothis z
1467	250	18.2	258	2	Q9VS86	09vs86	drosohila
1468	250	18.2	274	2	Q8WUG0	08wug0	glossina fu
1469	249.5	18.2	253	2	Q18442	018442	helicoverpa
1470	249.5	18.2	254	2	Q18447	018447	helicoverpa
1471	249.5	18.2	258	2	Q7Q2P0	07q2p0	anopheles g
1472	249.5	18.2	269	2	Q7PWI5	07pwi5	anopheles g
1473	249.5	18.2	274	2	Q9VRS7	09vrs7	drosohila
1474	249.5	18.2	282	2	Q18655	018655	plodia inte
1475	249.5	18.2	327	2	Q8MS77	08ms77	drosohila
1476	249.5	18.2	362	2	Q6LUJ1	06luj1	photobacter
1477	249.5	18.2	520	2	Q8SY93	08sy93	drosohila
1478	249	18.1	253	2	Q9NGY5	09ngy5	heliothis v
1479	249	18.1	305	2	Q7Q6S4	07q6s4	anopheles g
1480	249	18.1	388	2	Q966V2	0966v2	halocynthia
1481	249	18.1	714	2	Q7PWE5	07pwe5	anopheles g
1482	248.5	18.1	296	2	Q917I1	0917i1	drosohila
1483	248.5	18.1	381	2	Q8WQY4	08wqy4	drosohila
1484	248.5	18.1	746	2	Q01654	001654	halocynthia
1485	248	18.0	141	2	Q6GKZ6	06gkz6	drosohila
1486	248	18.0	257	2	Q8IT49	08it49	pyrocoelia
1487	248	18.0	257	2	Q945U0	0945u0	phytothor
1488	248	18.0	258	2	Q9VZS9	09vzs9	drosohila
1489	248	18.0	277	2	Q7QI41	07qi41	anopheles g
1490	248	18.0	277	2	Q7QNM2	07qnm2	anopheles g
1491	248	18.0	367	2	Q7O169	07o169	mus musculu
1492	248	18.0	374	2	Q80YD5	080yd5	mus musculu
1493	248	18.0	392	2	Q9VMZ3	09vmz3	drosohila
1494	248	18.0	401	2	Q6LH17	06lhi17	photobacter
1495	247.5	18.0	260	2	Q9U414	09u414	plodia inte
1496	247.5	18.0	291	2	Q6V1Y9	06v1y9	lygus lineo
1497	247	18.0	243	2	Q7M4I3	07m4i3	megabombus
1498	247	18.0	278	2	Q7Q8Q5	07q8q5	anopheles g
1499	247	18.0	350	2	Q9VCJ9	09vcj9	drosohila
1500	247	18.0	360	2	Q9W1X6	09w1x6	drosohila

ALIGNMENTS

RESULT 1

KLKC_HUMAN STANDARD; PRT; 248 AA.

AC Q9UKR0; Q9UKR1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein 5)
DE (KLK-L5) (UNQ669/PRO1303).
GN Name-KLK12; Synonyms-KLK15;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20118156; PubMed=10652563;
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
RT "Identification of novel human kallikrein-like genes on chromosome 19q13.3-q13.4";
RL Anticancer Res. 19:2843-2852(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX Yousef G.M., Magklara A., Scorilas A., Diamandis E.P.;
RT "Cloning of new alternatively spliced forms of the kallikrein-like gene 5 (KLK-L5)";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paepser B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaudo C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wicand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [5]
RP SEQUENCE FROM N.A.
RX PubMed=15057824; DOI=10.1038/nature02399;
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J., Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M., Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E., Caenepeel S., Carrano A.V., Caciile C., Chan Y.M., Christensen M., Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Dettler J.C.,

RA Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,
RA Glavina T., Gomez M., Gonzales E., Groza M., Hamon N., Hawkins T.,
RA Layton L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
RA Kobayashi A., Lartionov V., Leem S.-H., Lopez P., Lou Y., Lowry S.,
RA Malfatti S., Martinez D., McCreedy P.M., Medina C., Morgan J.,
RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
RA Furey T.S., DeLong P., Dickson M., Gordon D., Eichler E.B.,
RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
RA Rubin E.M., Lucas S.M.;
RT "The DNA sequence and biology of human chromosome 19.";
RL Nature 428:529-535(2004).
CC -|- SUBCELLULAR LOCATION: Secreted (Probable).
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9UKR0-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9UKR0-2; Sequence=VSP_005403;
CC -|- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC
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CC
CC EMBL; AF135025; AAD26426.2; -;
CC EMBL; AF135025; AAF06065.1; -;
CC EMBL; AF243527; AAG33365.1; -;
CC EMBL; AY358524; AAQ88888.1; -;
CC EMBL; AC011473; AAG23258.1; -;
CC HSSP; P00760; 1EZX.
CC MEROPS; S01.020; -;
CC Genew; HGNC:6360; KLIK12.
CC MIM; 605539; -;
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:004252; F:serine-type endopeptidase activity; NAS.
CC GO; GO:006508; P:proteolysis and peptidolysis; NAS.
CC InterPro; IPR009003; Pept_Ser_Cys.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00089; Trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00020; TRYPSIN_DOM; 1.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
KW Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
KW Signal.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 248 Kallikrein 12.
FT ACT_SITE 62 62 Charge relay system (By similarity).
FT ACT_SITE 108 108 Charge relay system (By similarity).
FT ACT_SITE 200 200 Charge relay system (By similarity).
FT DISULFID 28 161 By similarity.
FT DISULFID 47 63 By similarity.
FT DISULFID 133 235 By similarity.
FT DISULFID 140 206 By similarity.
FT DISULFID 172 186 By similarity.
FT DISULFID 196 222 By similarity.
FT CARBOHYD 24 24 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 163 163 N-linked (GlcNAc...) (Potential).
FT VARSP_LIC 236 248 KYVDWRIMRN -> NSTLVGLGTSWNFNSQPP (in
FT isoform 2).
FT FTIDG_VSP 005403.
SQ SEQUENCE 248 AA; 26733 MW; BB473E98F8BAF703 CRC64;

Query Match 100.0%; Score 1374; DB 1; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.5e-102;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSIFLLCVLGUSQAATPKIFNGTEGRNSQPMQVGLFECTSLRCGVLIDHRWLTA 60
DB 1 MGLSIFLLCVLGUSQAATPKIFNGTEGRNSQPMQVGLFECTSLRCGVLIDHRWLTA 60
QY 61 AHCSGRVWVRLGHSLSQLDWTEQIRHSGFSVTHPGVLGASTSHEDHLRLRLPVRV 120
DB 61 AHCSGRVWVRLGHSLSQLDWTEQIRHSGFSVTHPGVLGASTSHEDHLRLRLPVRV 120
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGIITHNPRNPFLLQCLNLSIVSHATCHGVYPGRI 180
DB 121 TSSVQPLPLPNDCATAGTECHVSGWGIITHNPRNPFLLQCLNLSIVSHATCHGVYPGRI 180
QY 181 TSNMYCAGVPGQDACCQDSGGPLVCGGVLOGLVSWGSGVPGCGQIGIPGVYTYICKYVDW 240
DB 181 TSNMYCAGVPGQDACCQDSGGPLVCGGVLOGLVSWGSGVPGCGQIGIPGVYTYICKYVDW 240
QY 241 TRMIMRNN 248
DB 241 TRMIMRNN 248
RESULT 2
Q9CV76 PRELIMINARY; PRT; 234 AA.
ID Q9CV76
AC Q9CV76; 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Mus musculus adult male tongue cDNA, RIKEN full-length enriched
DE library, clone:231008B01 product:similar to KALLIKREIN 12 (EC
DE 3.4.21.-) (KALLIKREIN-LIKE PROTEIN 5) (KLU-L5) (Fragment).
GN Name=Klik12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]

RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Andreise T., Frankheim M., Attix C., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.,
RT "Sequence analysis of chromosome 19q13.4";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
CC hippocampal plasticity.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O60259-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O60259-2; Sequence=VSP_005401;
CC -!- TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in the
CC pancreas while isoform 2 is expressed in adult brain and
CC hippocampus. Both forms are also found in fetal brain and
CC placenta. Not detected in kidney, spleen, liver and lung.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC
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CC -----
CC EMBL; AB029849; BAA28673.1; -;
CC EMBL; AB012761; BAA28676.1; -;
CC EMBL; AB010780; BAA88684.1; -;
CC EMBL; AB008390; BAA82665.1; -;
CC EMBL; AB008927; BAA82666.1; -;
CC EMBL; AF055982; AAD56050.1; -;
CC EMBL; AF095742; AAD25979.1; -;
CC EMBL; AF095743; AAD29574.1; -;
CC EMBL; AF243527; AAG33361.1; -;
CC EMBL; AY359036; AAG89395.1; -;
CC EMBL; AC011473; AAG23254.1; -;
CC HSSP; P00760; 1EZX.
CC MEROPS; S01.244; -;
CC Genew; HGNC:6369; KLK8.
CC MIM; 605644;
CC GO; GO:0008236; F:serine-type peptidase activity; TAS.
CC GO; GO:0007399; P:neurogenesis; TAS.
CC InterPro; IPR009003; Pept_Ser_Cys.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00089; Trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SRR; 1.
KW Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
KW Signal; Zymogen.
FT SIGNAL 1 28 Potential.
FT PROPEP 29 32 By similarity.
FT CHAIN 33 260 Neuropsin.
FT ACT_SITE 73 73 Charge relay system (By similarity).
FT ACT_SITE 120 120 Charge relay system (By similarity).
FT ACT_SITE 212 212 Charge relay system (By similarity).
FT DISULFID 39 173 By similarity.
FT DISULFID 58 74 By similarity.
FT DISULFID 145 246 By similarity.
FT DISULFID 152 218 By similarity.
FT DISULFID 184 198 By similarity.
FT DISULFID 208 233 By similarity.
FT CARBOHYD 110 210 N-linked (GlcNAc...) (Potential).
FT VARSPLOC 23 A -> AACGSLDLTLKLYAENLPCVHLNQPWPSQPSHCPRG

FT WRSNPLPPAA (in isoform 2).
FT /FTID=VSP_005401.
SQ SEQUENCE 260 AA; 28048 MW; EF439E5B8C83B660 CRC64;
Query Match 45.9%; Score 630.5; DB 1; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.3e-42;
Matches 123; Conservative 24; Mismatches 93; Indels 5; Gaps 3;
QY 5 IFLLL---CVLGLSQATPKIFNGTCGRNSOPWQGLFEGTSLRCGGVLIDHRWVLTAA 61
DB 13 WFLLLGGAWAGHSRAQEDKVLGHECQPHSQPWAALFQGQLLCGGVLVGNWVLTAA 72
QY 62 HCGSRYWVRLGEHSLSDMTWEQIRHSGFSVTHPGYLGAST-SHEHDLRLRLRLPVRV 120
DB 73 HCKPKYTVRLGDHSLQNKDGEQIIPVQSIHPHCYNSDDVEDHNDMLLIQLRDQASL 132
QY 121 TSSVOPLELPNDCATAGTECHVSGWGIITNHPNPPDILLOCLNLISVSHATCGVYPGR 180
DB 133 GSKVKPISLADHCTQPGQKCTVSGMGTVTSRENFPDTLNCAEVKIFPKKCEDAYPGQ 192
QY 181 TSNMVACAGVPGQDACQDSGGPLVCGGVLOGLVSWGSGVPCGQDGIQGVYTYICKYVDW 240
DB 193 TGMVACAGSSKGADTCQDSGGPLVCDALQIGTSWGS-DPCGRSDKFGVYTNICRYLDW 251
QY 241 IRMIM 245
DB 252 IKKII 256
PRELIMINARY; PRT; 260 AA.
RESULT 4
Q81W69
ID Q81W69 PRELIMINARY; PRT; 260 AA.
AC Q81W69;
DC 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Kallikrein 8, isoform 1 preproprotein.
GN Name=KLK8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DB EMBL; BC040887; AAH40887.1; -;

HSSP; P00760; 1EXX.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004298; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase S1a.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYPSIN_DOM; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 260 AA; 28090 MW; EF5934EB96295660 CRC64;

Query Match 45.7%; Score 627.5; DB 2; Length 260;
 Best Local Similarity 50.2%; Pred. No. 2.2e-42;
 Matches 123; Conservative 24; Mismatches 93; Indels 5; Gaps 3;

OY 5 IFLL---CVLGLSQAATPKFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDRWLTA 61
 DB 13 MFLLLGGAWAGHSAQEDKVLGHECPHSPWQAALFQGGQLCGVLGCVNWLTA 72
 OY 62 HCGSGRYVRLGEHLSQLDWTIEQIRHSGFVTHPGYLGAFT-SHEHDLRLRLPLVRV 120
 DB 73 HCKPKYTVRLGDHSLQNKDGEQEPVQSPHPCVNSDVEDHNDLMLQLRDQASL 132
 OY 121 TTSVQPLPLPNDATAGTECHVSGWGTNHPNPPDQLQCLNLSIVSHATGVPGRH 180
 DB 133 GSKVAPISLADHCTQFGQKCTVSGMGTVPSPNFPDNLNCAEVKIFPKKCEDAYPGQ 192
 OY 181 TSNMVCAGVPQDCAQCGSGPLVCGVGLQVLSVSGVPGQDGPVGVYVICKYVDW 240
 DB 193 TDVMCAGSKGADTCQDGGPLVCDGALQGITSGS-DPCGRSDKPGVYVNICRYLW 251
 OY 241 IRMIM 245
 DB 252 IKKII 256

RESULT 5
 NRPN MOUSE
 ID NRPN MOUSE STANDARD; PRT; 260 AA.
 AC Q61955;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Neuropeptide precursor [EC 3.4.21.-] (NP) (Kallikrein 8).
 GN Name=Klk8; Synonyms=Nrpn, Prss19;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Hippocampus;
 RX MEDLINE=95348817; PubMed=7623137;
 RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
 RA Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.;
 RT "Expression and activity-dependent changes of a novel limbic-serine
 RT protease gene in the hippocampus."
 RL J. Neurosci. 15:5088-5097(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yoshida S., Hirata A., Inoue N., Shiosaka S.;
 RT "Cloning and assignment of mouse neuropeptide gene, Prss19 to chromosome
 RT 7B4.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Czech II; TISSUE=Mammary gland;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF N-TERMINUS, CHARACTERIZATION, AND MASS SPECTROMETRY.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=98225202; PubMed=9556608; DOI=10.1074/jbc.273.18.11189;
 RA Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,
 RA Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;
 RT "Characterization of recombinant and brain neuropeptide, a plasticity-
 RT related serine protease.";
 RL J. Biol. Chem. 273:11189-11196(1998).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
 RC TISSUE=Hippocampus;
 RX MEDLINE=99134351; PubMed=9933620; DOI=10.1074/jbc.274.7.4220;
 RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
 RA Shiosaka S., Hakoshima T.;
 RT "Crystal structure of neuropeptide, a hippocampal protease involved in
 RT kindling epileptogenesis.";
 RL J. Biol. Chem. 274:4220-4224(1999).
 CC -!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
 CC hippocampal plasticity. Has a strong proteolytic activity against
 CC fibronectin.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
 CC -!- ENZYME REGULATION: Strongly inhibited by diisopropyl
 CC fluorophosphate, leupeptin and (4-amidinophenyl)methanesulfonyl 1-
 CC fluoride.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed specifically in the limbic system of
 CC mouse brain and is localized at highest concentration in pyramidal
 CC neurons of the hippocampal CA1-3 subfields.
 CC -!- MASS SPECTROMETRY: MW=26613; METHOD=MALDI; RANGE=29-260;
 CC NOTE=Ref.4.
 CC -!- MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260;
 CC NOTE=Ref.4.
 CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 CC subfamily.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; D30785; BAA06451.1; -.
 CC EMBL; AB032202; BAA92435.1; -.
 CC EMBL; BC055895; AAH55895.1; -.
 CC PIR; I56559; I56559.
 CC PDB; 1NPM; X-ray; A/B=33-256.
 CC MEROPS; S01.244; -.
 CC MGD; MGI:892018; Klk8.
 CC InterPro; IPR009003; Pept_Ser_Cys.

DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PS00722; CHYMOTRYPSIN.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW 3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;
Serine protease; Signal; Zymogen.
FT SIGNAL 1 28 Potential.
FT PROPEP 29 32
FT CHAIN 33 260
FT ACT_SITE 73 73
FT ACT_SITE 120 120 Charge relay system (By similarity).
FT ACT_SITE 212 212 Charge relay system (By similarity).
FT DISULFID 39 173
FT DISULFID 58 74
FT DISULFID 145 246
FT DISULFID 152 218
FT DISULFID 184 198
FT DISULFID 208 233
FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
FT STRAND 34 34
FT STRAND 37 38
FT TURN 41 42
FT TURN 45 46
FT TURN 47 52
FT STRAND 53 54
FT TURN 55 64
FT TURN 65 66
FT STRAND 67 70
FT HELIX 72 74
FT STRAND 80 83
FT STRAND 87 87
FT STRAND 88 89
FT TURN 96 98
FT STRAND 100 105
FT TURN 107 108
FT TURN 114 115
FT TURN 118 119
FT STRAND 122 126
FT STRAND 140 141
FT TURN 148 149
FT STRAND 151 156
FT STRAND 170 170
FT STRAND 172 178
FT HELIX 181 187
FT TURN 189 191
FT TURN 194 195
FT STRAND 196 200
FT TURN 202 203
FT STRAND 206 206
FT TURN 209 210
FT TURN 212 213
FT STRAND 215 218
FT TURN 219 220
FT STRAND 221 228
FT STRAND 235 235
FT TURN 236 237
FT STRAND 238 238
FT STRAND 240 244
FT HELIX 245 256
SQ SEQUENCE 260 AA; 28523 MW; BE5F6F6BE37CD60E CRC64;

Query Match 45.3%; Score 622.5; DB 1; Length 260;
Best Local Similarity 49.0%; Pred. No. 5.6e-42;
Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;
5 IFLLLCV---LGLSQAATPKIFNGTEGCRNSQPWQGLFEGTSLRCGGVLIDHRWVLTAA 61
13 ILLLLFMGAWAGLTRAQGSKILLEGECIPHSQPWQAALFQGERLICGGVLVNGDRWVLTAA 72
62 HCSGRYVRLGEHLSQLDWTETQIRHSGFVTHPGYLGA--TSHEHDLRLRLRLPVRV 120

Db 73 HCKKQKYSVRLGDHSLQSRDQPEQBIQVAQSIQHFPYNNSPEDSHDMLRLQNSANL 132
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGIITHNPNPPDLLQCLNLSIVSHATGHVYVPGRI 180
Db 133 GDKVRPVLANLCPKVGQKCIISGWTGTSPOENFNTLNCVAKVIYQNKKERAYPGKI 192
QY 181 TSNMVCAAGVPGQDACQGDSDSGPLVCGGVLOGLVSGVSGPCGQDGIIPGVYTIICKYVDW 240
Db 193 TEGMVCAAGSSNGADTCQGDSSGGLVCDGMLQGITSWGSS-DPCGKPEKPGVYTKICRYTWW 251
QY 241 IRMINRN 247
Db 252 IKKTMDN 258
RESULT 6
NRPN RAT
ID NRPN RAT STANDARD; PRT; 260 AA.
AC O88780;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine protease 1).
GN Name=Klk8; Synonyms=Bspl, Nrpn, Prss19;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer; TISSUE=Brain;
RX MEDLINE=98389725; PubMed=9722524; DOI=10.1074/jbc.273.36.23004;
RA Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Iathe R.;
RT "Serine proteases in rodent hippocampus."
RL J. Biol. Chem. 273:23004-23011(1998).
CC -!- FUNCTION: Suggested to be involved in kindling epileptogenesis and hippocampal plasticity. Has a strong proteolytic activity against fibronectin (By similarity).
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- TISSUE SPECIFICITY: Restricted to hippocampus.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein subfamily.
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DR EMBL; AJ005641; CAA06643.1; -.
DR HSSP; Q61955; INPM.
DR MEROPS; S01.244; -.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PS00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Serine protease; Signal; Zymogen.
FT SIGNAL 1 28 Potential.
FT PROPEP 29 32 By similarity.
FT CHAIN 33 260 Neuropsin.
FT ACT_SITE 73 73 Charge relay system (By similarity).
FT ACT_SITE 120 120 Charge relay system (By similarity).
FT ACT_SITE 212 212 Charge relay system (By similarity).


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CC CC -!- ALTERNATIVE PRODUCTS:
CC CC Event=Alternative splicing; Named isoforms=2;
CC CC Name=1;
CC CC Name=2; Sequence=Displayed;
CC CC IsoId=Q9UBX7-1; Sequences=VSP_005402;
CC CC -!- TISSUE SPECIFICITY: Expressed in brain, skin and prostate. Isoform
CC CC 1 is expressed preferentially in brain; isoform 2 in prostate.
CC CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC CC subfamily.
CC CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC CC modified and this statement is not removed. Usage by and for commercial
CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; AB012917; BAA33404.1; ALT_INIT.
CC CC EMBL; AB013730; BAA88713.1; -.
CC CC EMBL; AB041036; BAA96797.1; -.
CC CC EMBL; AF164623; RAD47815.1; -.
CC CC EMBL; AF243527; AAG33364.1; -.
CC CC EMBL; AY359014; AAG89373.1; -.
CC CC EMBL; AC011473; AAG23257.1; -.
CC CC EMBL; BC022068; AAH22068.1; -.
CC CC HSSP; P00760; 1EZX.
CC CC MEROPS; S01.257; -.
CC CC Genew; HGNC:6359; KLK11.
CC CC H-InvDB; HIX0015375; -.
CC CC MIM; 604434; -.
CC CC GO; GO:0008236; F:serine-type peptidase activity; TAS.
CC CC InterPro; IPR009003; Pept_Ser_Cys.
CC CC InterPro; IPR001254; Peptidase_S1.
CC CC InterPro; IPR001314; Peptidase_S1A.
CC CC Pfam; PF00089; Trypsin; 1.
CC CC PRINTS; PR00722; CHYMOTRYPSIN.
CC CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC CC Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
CC CC Signal; Zymogen.
CC CC SIGNAL 1 18 Potential.
CC CC ACTPROPEP 19 21 Activation peptide (Potential).
CC CC CHAIN 22 250 Kallikrein 11.
CC CC ACT_SITE 62 62 Charge relay system (By similarity).
CC CC ACT_SITE 110 110 Charge relay system (By similarity).
CC CC ACT_SITE 203 203 Charge relay system (By similarity).
CC CC DISULFID 28 163 By similarity.
CC CC DISULFID 47 63 By similarity.
CC CC DISULFID 135 237 By similarity.
CC CC DISULFID 142 209 By similarity.
CC CC DISULFID 174 188 By similarity.
CC CC DISULFID 199 224 By similarity.
CC CC CARBOHYD 99 99 N-linked (GlcNAc...) (Potential).
CC CC CARBOHYD 165 165 N-linked (GlcNAc...) (Potential).
CC CC CARBOHYD 181 181 N-linked (GlcNAc...) (Potential).
CC CC CARBOHYD 210 210 N-linked (GlcNAc...) (Potential).
CC CC VARSPPLIC 1 1 M -> MQRLRWRDKSSGRGLTAKEPKARSSPLQAM
CC CC (in isoform 2).
CC CC /FTID=VSP_005402.
CC CC SEQUENCE 250 AA; 27466 MW; 192D910BBDC7A56 CRC64;
CC CC Query Match 45.0%; Score 618.5; DB 1; Length 250;
CC CC Best Local Similarity 48.2%; Pred. No. 1.1e-41;
CC CC Matches 120; Conservative 35; Mismatches 89; Indels 5; Gaps 4;
CC CC 3 LSIFLLCVLGSQAATPKIFNGTECGRNSQPQWGLFEGTSLRCGGVLIDHRWVLTAAH 62
CC CC 4 LQILLLATGLVGGET-RIIKFCKPQSPQWQAALFEKTELLCGATLIAPRWLTAAH 62
CC CC Db
CC CC 63 CSGSRVWRLGHSLSQLDWTETQIRHSGFVTHPGYLGCA--STSHEHDLRLRLPVRV 120
CC CC -----
CC CC 63 CLKPRYIVHLGQHNLQKEGCEQRTATSPHPGCFNNNSLPNKHNRNDIMLVKMAASPVSI 122
CC CC 121 TSSVQPLPLPNDCATAGTECHVSGWGIITHRNPPDILLOCLNLISIVSHATCHGVYPGRI 180
CC CC 123 TWAVRPLTLSSRCVTAGTSSCLISGWSSTSPQLRPLHTLRCAITITIEHQKCNAYPGNI 182
CC CC 181 TSNMWVACG-GYPGQDACQGDGGLVCGQVLQGLVSWGSGVPCGQDGIPIGVVYTI CKYVD 239
CC CC 183 TDTMWVCASVQEGGKDCQDGGPLVCNQSLQGIISWGQ-DPCAIRTRKGVVTKCKYVD 241
CC CC 240 WIRMTMRNN 248
CC CC 242 MIQETMKNN 250
CC CC -----
CC CC RESULT 8
CC CC Q7JIG6 PRELIMINARY; PRT; 255 AA.
CC CC ID Q7JIG6;
CC CC AC Q7JIG6;
CC CC DT 05-JUL-2004 (TREMELrel. 27, Created)
CC CC DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
CC CC DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
CC CC DE KIKI5.
CC CC OS Saguinus oedipus (Cotton-top tamarin).
CC CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC CC OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
CC CC OX NCBI_TaxID=9490;
CC CC RN [1]
CC CC RP SEQUENCE FROM N.A.
CC CC RX MEDLINE=21094033; PubMed=11177570; DOI=10.1089/104454900750058080;
CC CC RA Olsson A.Y., Persson M., Valtonen-Andre C., Lundwall A.;
CC CC RT "Glandular kallikreins of the cotton-top tamarin: molecular cloning of
CC CC RL the gene encoding the tissue kallikrein.";
CC CC RN [2]
CC CC RP SEQUENCE FROM N.A.
CC CC RA Olsson Y., Persson M., Lundwall A.;
CC CC RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC CC CC -!- SIMILARITY: Belongs to peptidase family S1.
CC CC DR EMBL; AF173845; AAS45302.1; -.
CC CC DR HSSP; P00761; 1AKS.
CC CC DR GO; GO:0004263; F:chymotrypsin activity; IEA.
CC CC DR GO; GO:0008233; F:peptidase activity; IEA.
CC CC DR GO; GO:0004295; F:trypsin activity; IEA.
CC CC DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
CC CC DR InterPro; IPR001254; Peptidase_S1.
CC CC DR InterPro; IPR001314; Peptidase_S1A.
CC CC DR InterPro; IPR009003; Pept_Ser_Cys.
CC CC DR Pfam; PF00089; Trypsin; 1.
CC CC DR PRINTS; PR00722; CHYMOTRYPSIN.
CC CC DR SMART; SM00020; Tryp_Spc; 1.
CC CC DR PROSITE; PS00240; TRYPSIN_DOM; 1.
CC CC DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
CC CC DR Hydrolase; Protease; Serine protease.
CC CC SK SEQUENCE 255 AA; 28078 MW; A040914ABC8FEC8D CRC64;
CC CC Query Match 44.5%; Score 611; DB 2; Length 255;
CC CC Best Local Similarity 49.4%; Pred. No. 4.6e-41;
CC CC Matches 118; Conservative 31; Mismatches 76; Indels 14; Gaps 5;
CC CC 21 KIFNGTECGRNSQPQWGLFEGTSLRCGGVLIDHRWVLTAAHCGSRVWRLGHSLSQL 80
CC CC 20 KLEEGEACAPHSQPWQVALYERGRFNCASLISPHWVLSAAHCQSRFMRVRLGEHLNRKR 79
CC CC 81 DWTQIRHSGFVTHPGYLGASTSHEHDLRLRLPVRVTSVSSVQPLPLPNDCATAGTEC 140
CC CC 80 DGPEQLRTASRVIPHPRY--EARSRHHDIMLRVQPARLTPQVRVPLTRCPHPGEAC 137
CC CC 141 HVSGWGINTH-----PRN--PFPPDLLOCLNLISIVSHATCHGVYPGRITSNMWVACGV 190
CC CC 138 VVSGWGLVSHNPEGTGRQSQVSLPDLTHCANISIIISDASCDKNYPGLRINTWVCAAE 197
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QY 191 -PGDACCQDSCGGLVCGVLSWGSVGGCGQDGPVGVYICKYVDWIRMNRN 248
DB 198 GRGAESCEGSGPLVCGGILGIVSWGVDV-PCDNTTKFGVYTKCRYKWIETMKRN 255

RESULT 9
Q632F2 PRELIMINARY; PRT; 250 AA.
AC Q632F2
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Glandular kallikrein 11 precursor.
GN Name=KLK11;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RX PubMed=15203212; DOI=10.1016/j.ygeno.2004.01.009;
RA Olsson A.Y., Lilja H., Lundwall A.;
RT "Taxon-specific evolution of glandular kallikrein genes and
RL identification of a progenitor of prostate-specific antigen.";
CC Genomics 84:147-156(2004).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
EMBL/GenBank/DDBJ third party annotation (TPA) entry.
KW EMBL; BK001364; DAA05600.1; -.
KW Signal.
FT SIGNAL. 1 18 Potential.
FT CHAIN 22 250 Glandular kallikrein 11.
SQ SEQUENCE 250 AA; 27630 MW; 247B29D3F0DEF8F1 CRC64;

Query Match 44.4%; Score 610; DB 2; Length 250;
Best Local Similarity 46.7%; Pred. No. 5.4e-41;
Matches 115; Conservative 37; Mismatches 90; Indels 4; Gaps 3;

QY 6 FULLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGVLIHHRWVLTAAHCSG 65
DB 6 FTALAVTVGHVGGETRIKGYECRPHSPQWQVALFQKTRLLCGATLIAPKMLLTAAHCKK 65

QY 66 SHYWRVLRGHSLSQLDWTEQIRHSGFVTHPGYVGLA--STSEHDLRLRLRLPVRVTS 123
DB 66 PHYVILLGHELNLEKTDGCSQRRMATESFFPHGFNLSNPKNDRNDIMLVKMSAPFITRA 125

QY 124 VQPLPLNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVGHATGCHVYPCRTSN 183
DB 126 VRPLTSLLCVTVAGTSCLSISGWTGSSPOLRPLHSLRCANVSLIGHKECERAYPGNITDT 185

QY 184 MYCAG-GVPGDACCQDSCGGLVCGVLSWGSVGGCGQDGPVGVYICKYVDWIR 242
DB 186 MLCASVRKEGKDCQDSCGGLVCGVLSWGSVGGCGQDGPVGVYICKYVDWIR 244

QY 243 MTMRNN 248
DB 245 EVMRNN 250

RESULT 10
Q8CGR4 PRELIMINARY; PRT; 254 AA.
AC Q8CGR4
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Proctin.
GN Name=KLK15; Synonyms=KLK15;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
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RX MEDLINE=22325484; PubMed=12437987; DOI=10.1016/S0006-291X(02)02629-3;
RA Olsson A.Y., Lundwall A.;
RT "Organization and evolution of the glandular kallikrein locus in Mus
RL musculus.";
RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M., Mural R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AV152434; AAN78422.1; -.
DR HSSP; P00760; 1EZX.
DR MEROPS; S01.237; -.
DR MGD; MGI:2447533; K1k15.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 254 AA; 28042 MW; AA9E38BEDD01861 CRC64;

Query Match 44.3%; Score 608; DB 2; Length 254;
Best Local Similarity 49.0%; Pred. No. 7.9e-41;
Matches 124; Conservative 30; Mismatches 77; Indels 22; Gaps 7;

QY 5 IFLLLCVLGLSQAAT--PKIFNGTECGRNSQPWQVGLFEGTSLRCGVLIHHRWVLTAAH 62
DB 1 MMLLAFLVLLVSAADGKVLGESECVPHSQWQVALFERGFNCAGFLISPRWVLTAAH 60

QY 63 CSGSRVYWRVLRGHSLSQLDWTEQIRHSGFVTHPGYVGLASTSHEDHLRLRLPVRVTS 122
DB 61 CQTRFMRVLRGHEHLNLRKFDGPEQLASVSRIIPHPGY--EARTHHDIMLRLFKPARLTA 118

QY 123 SVQPLPLNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHAT 171
DB 119 YVRPVALPRRCPLIGEDCVVSGWGLLS--DNNPFGATGSKSHVRLPDTLRCANISISEAS 177

QY 172 CHGVYPGRTSNMCA---GGVPGDACCQDSCGGLVCGVLSWGSVGGCGQDGP 228
DB 178 CNKDYPGRVLPFWCVGVEGG--GTDSCGDSGGPLVCGGALQGVISWGDV-PCDTTTPK 234

QY 229 GVYTYICKYVDWI 241
DB 235 GVYTKVCSYLEWI 247

RESULT 11
Q8IXD7 PRELIMINARY; PRT; 275 AA.
AC Q8IXD7
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Variant form hippostasin/KLK11.
GN Name=KLK11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Nakamura T., Mitsui S., Miki T., Yamaguchi N.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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-!- SIMILARITY: Belongs to peptidase family S1.
CC EMBL; AB078780; BAC54105.1; -.
DR HSSP; P00760; 1EZX.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 275 AA; 30165 MW; 257A42B28F40E2C4 CRC64;

Query Match 43.7%; Score 601; DB 2; Length 275;
Best Local Similarity 44.2%; Pred. No. 31e-40;
Matches 121; Conservative 35; Mismatches 88; Indels 30; Gaps 5;

QY 3 LSIFLLCVLGSQAATPKFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH 62
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
4 LQILILALATGLVGGET-RIIKGFECKPSQPWQAALFEKRLLCGATLIAPRWLLTAAH 62
QY 63 CSG-----SRVVRVLRGEHSLDQWTEQIRHGSFVTHPG 97
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
63 CLKPWVSLTSPHVSPLDSSNYCLSHLSRYIVHLGQHNLOKEEGCEQRTTATESFPHPG 122

QY 98 YLGA--STGHEHDLRLRLRPVTVTSVQPLPLPNDCATAGTECHVSGWGIINPRNPF 155
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
123 FNNSLPNKDRNDIMLVKASPSVITWAVRPLTSLRCVTAAGTSLISGWGSTSPQLRL 182

QY 156 PDLQCLNLSIVSHATGCHGYPERITSNVVACG-GVPGDQACGDSGGPLVCGVQLQGV 214
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
183 PHTLRCAITIIHOKCENAYPGNITDTWVCASVQEGKDSQCGDSGGPLVCGVQLQGV 242

QY 215 SNGSVGPGCGDGIPIGVYVICKYVDWMIRMNN 248
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
243 SNGQ-DPCAITRKPGVYVICKYVDWMIRMNN 275

RESULT 12
Q6IS10 PRELIMINARY; PRT; 255 AA.
AC Q6IS10; Q6IS10 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Kallikrein 15, isoform 4 preproprotein.
GN Name=KLK15;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Feilings F.S., Toshiyuki S., Carninci P., Prange C.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
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"Molecular cloning of the human kallikrein 15 gene (KLK15). Up-regulation in prostate cancer.";
J. Biol. Chem. 276:53-61(2001).
[2]
SEQUENCE FROM N.A.
RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
RA Can L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Paepir B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
[3]
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94289486; PubMed=8018728; DOI=10.1016/0167-4781(94)90018-3;
RA Dhanich M.E., Spiess M.;
RL "A novel serine proteinase-like sequence from human brain.";
RN Biochim. Biophys. Acta 1218:225-228(1994).
[4]
RP SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Brenner S.E.;
RL "An unappreciated role for RNA surveillance.";
RN Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
CC -!- FUNCTION: Protease whose physiological substrate is not yet known.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=Q9H2R5-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9H2R5-2; Sequence=VSP_005405;
CC Note=May be produced at very low levels due to a premature stop
CC codon in the mRNA, leading to nonsense-mediated mRNA decay;
CC Name=3;
CC IsoId=Q9H2R5-3; Sequence=VSP_005406, VSP_005407;
CC Name=4;
CC IsoId=Q9H2R5-4; Sequence=VSP_005404;
CC -!- TISSUE SPECIFICITY: Highest expression in the thyroid gland. Also
CC expressed in the prostate, salivary, and adrenal glands and in the
CC colon testis and kidney.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).

DR EMBL; AF242195; AAC09469.1; --
DR EMBL; AF242195; AAC09470.1; --
DR EMBL; AF242195; AAC09471.1; --
DR EMBL; AF242195; AAC09472.1; --
DR EMBL; AF243527; AAC33354.1; --
DR EMBL; X75363; CA53145.1; ALT_SEQ.
DR HSSP; P00760; 1EZX.
DR MEROPS; S01.081; --
DR Genew; HGNC:20453; KLK15.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.

KW Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
FT SIGNAL; Zymogen. 1 16 Potential.
FT PROPEP 17 21 Activation peptide (Potential).
FT CHAIN 22 256 Kallikrein 15.
FT ACT_SITE 62 62 Charge relay system (By similarity).
FT ACT_SITE 106 106 Charge relay system (By similarity).
FT ACT_SITE 209 209 Charge relay system (By similarity).
FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 232 232 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 122 206 Missing (in isoform 4).
FT VARSPLIC 122 256 Missing (in isoform 2).
FT VARSPLIC 161 161 Missing (in isoform 3).
FT VARSPLIC 162 256 Missing (in isoform 3).
FT CONFLICT 147 160 SHNEPFGTSGPSRQ -> PLSSP (in Ref. 2).
SQ SEQUENCE 256 AA; 28087 MW; B5EBF8D6022786B5 CRC64;

Query Match 43.6%; Score 599; DB 1; Length 256;
Best Local Similarity 47.1%; Pred. No. 4.2e-40;
Matches 121; Conservative 32; Mismatches 88; Indels 16; Gaps 6;

QY 5 IFLLLCVLGLSOAAT--PKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH 62
DB 3 LLLTLTSLFLASTAAQDGDKLLGDECAPHSQPWQVGLYERGRFNCGLSLSPHWVLSAAH 62

QY 63 CSGSRVWRLGHSLSQLDWTEQIRHSQSVTHPGYLGASTSHEHDLRLRLPLRVVTS 122
DB 63 COSRFMRVRLGHNLRKXDGPEQLRTTSRVIPHPRY--EARSHRNDIMLLRLVQPARLNP 120

QY 123 SVQPLPLPNDCATAGTECHVSGWGITNH-----PRN--PPDLOCLNLSIVSHATC 172
DB 121 QVRPAVLPTCPHPGEACVVGSLVSHNEPCTAGSPRSQVSLPDTLHKANISIIDTSC 180

QY 173 HGVPYGRITSNMVCAGGV-PGQACQSGSGGGLVCGVLPQGLVSGVSGPCGQDGPVGY 231
DB 181 DKSYPGLRTNTWVCAGAEGRGAESCEGDSGLVCGGILQGIIVSGWGV-PCDNTTKPGVY 239

QY 232 TVICKYVDWIRMN 248
DB 240 TKVCHYLEWIRETKRN 256

RESULT 14
Q9QYN4 PRELIMINARY; PRT; 249 AA.
AC Q9QYN4; DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hippocastin.
GN Name=2310015108Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
RA Mitui S., Okui A., Kominami K., Uemura H., Yamaguchi N.;
RT "cDNA cloning and tissue-specific splicing variants of mouse
RL Biophys. Acta 1494:206-210(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Yamaguchi N., Mitui S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.

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DR EMBL; AB016226; BRA88825.1; -.
DR HSSP; P00760; 1EZX.
DR MEROPS; S01.257; -.
DR MGD; MGI:1929977; 2310015I08Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS02440; TRYPSIN_DOM; 1.
DR PROSITE; PS01334; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 249 AA; 27604 MW; F9F9CB45D727D5 CRC64;

Query Match 43.5%; Score 597.5; DB 2; Length 249;
Best Local Similarity 47.0%; Pred. No. 5.4e-40;
Matches 118; Conservative 33; Mismatches 95; Indels 5; Gaps 4;

QY 1 MGLSIFLLCVLGLSQAATPKLFGNTECGRNSQPWQVGLFEGTSLRCGGVLIIDHRVLTAA 60
Db 1 MLRLTALALVTGHVGGET-RIIKGYECRPHSPQWQVALLFQKTRLLCGATLAPKWLTA 59

QY 61 AHCGSGRYVVRIGEHSLSQDWTQIRHSGFSVTHPGYLCA--STSHEHDLRLRLRLP 118
Db 60 AHCRKPHYVILLGEHNLEKTDCEQRMRATESFPFHPDFNNSLPNKHNDIMLVKMSSPV 119

QY 119 RVTSSVQPIPLPNDCAATAGTECHVSQWGTINHPNRPFDLLQCLNLSIVSHATCGHYVP 178
Db 120 FETRAVQPIPLSPHCAAGTSCLLISGWGTTSSPQLRLPHSLRCANVSIIEHKECEKAYPG 179

QY 179 RITSNMVACAG-GVPGDAGCGSGPLVCGGVLCGLVSGVCGPCQDGIPIGVYTVICKY 237
Db 180 NITDTMLCASVKEGKDCQSGSGLVLCVNGSLQGIISWGQ-DPCAVTRKPGVYTVICKY 238

QY 238 VDWIRMERN 248
Db 239 FNNWHEVMERN 249

RESULT 15
Q9QYN3 PRELIMINARY; PRT; 276 AA.
ID Q9QYN3
AC Q9QYN3;
DT 01-WAY-2000 (TrEMBLrel. 13, Created)
DT 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hippostasin prostate type (Mus musculus adult male tongue cDNA, RIKEN
DE full-length enriched library, clone:2310015I08 product:protease,
DE serine, 20, full insert sequence) (Mus musculus adult male tongue
DE cDNA, RIKEN full-length enriched library, clone:2310040F07
DE product:protease, serine, 20, full insert sequence).
GN Name:2310015I08Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
TISSE=Prostate;
MEDLINE=20525450; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
Mitsu S., Okui A., Kominami K., Uemura H., Yamaguchi N.;
"cDNA cloning and tissue-specific splicing variants of mouse
hippostasin/TLSP (PRSS20)".;
Biochim. Biophys. Acta 1494:206-210 (2000).
[2]
SEQUENCE FROM N.A.
TISSE=Prostate;
Yamaguchi N., Mitsu S.;
Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
[3]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
[7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
[8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
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CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AB016227; BAA36955.1; -.
DR EMBL; AK009360; BAB26241.2; -.
DR EMBL; AK009720; BAB26461.2; -.
DR HSSP; P00760; 1EZX.
DR MEROPS; S01.257; -.
DR MGD; MGI:1929977; 2310015I08Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
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